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ICE is Nice

Version 1: 9/1/00

Created, Written, Narrated, and Prepared by:

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U.S. Environmental Protection Agency

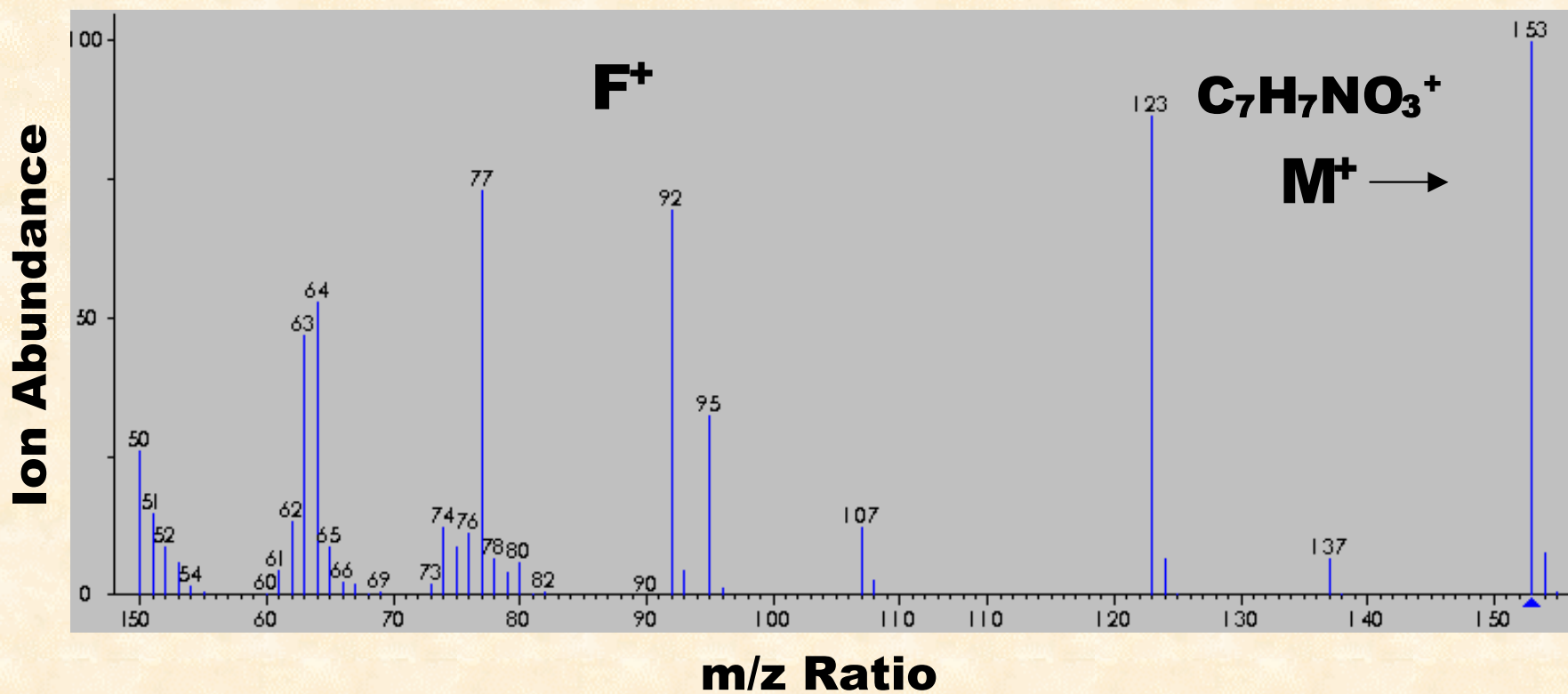
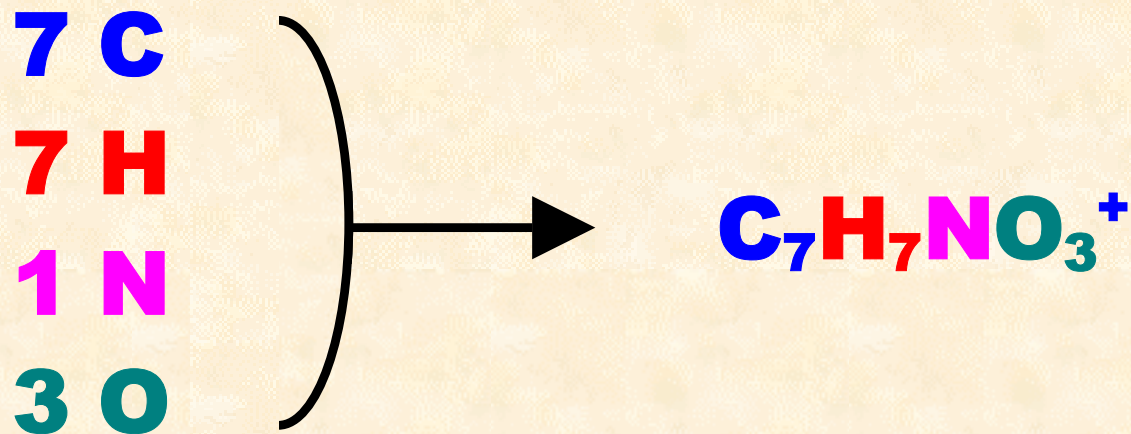
P.O. Box 93478, Las Vegas, NV 89193

William C. Brumley, Ph. D. & G. Wayne Sovocool, Ph. D.

*** Ion Composition Elucidation**

Mt. Hood, Oregon

Click



ICE Instructional Video

Problem Solved by ICE

Scientific Basis, Advantages, Limitations of ICE

Data Acquisition:

***Mass Peak Profiling from Selected Ion
Recording Data (MPPSIRD)***

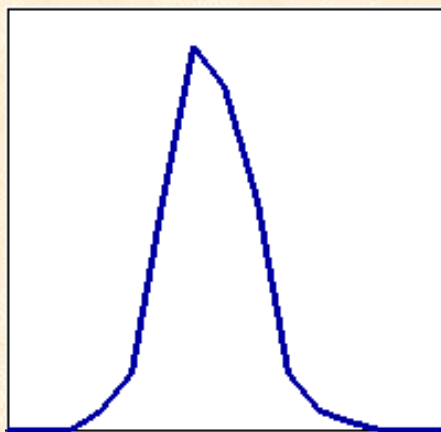
Automated Data Interpretation:

Profile Generation Model (PGM)

3 Example Applications of ICE

Jargon Review

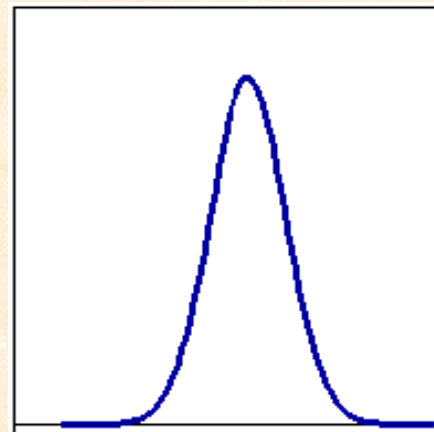
Ion Abundance



Time

Total Ion
or
Single Ion
Chromatogram

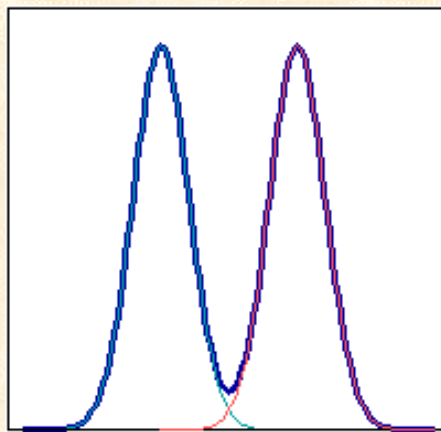
Ion Abundance



m/z

10% valley

Ion Abundance



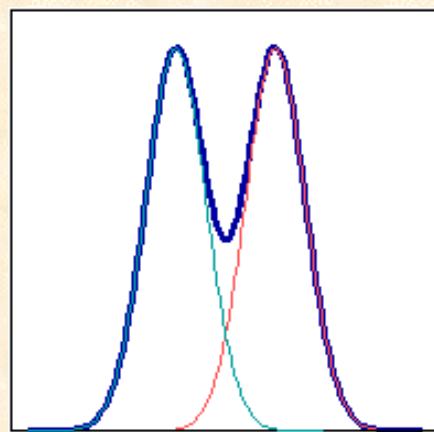
m/z



10,000 (10%)

14,700 (50%)

Ion Abundance

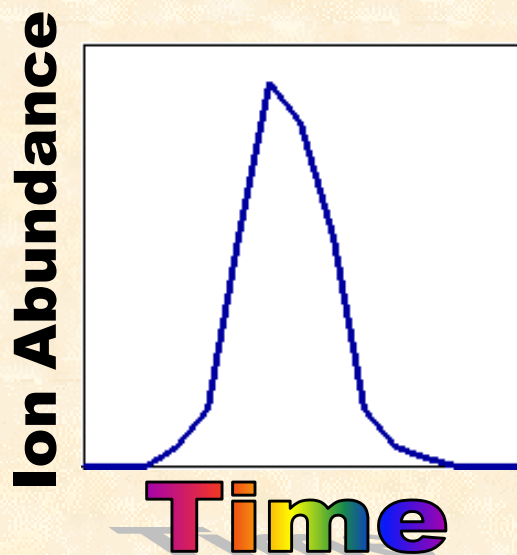


m/z

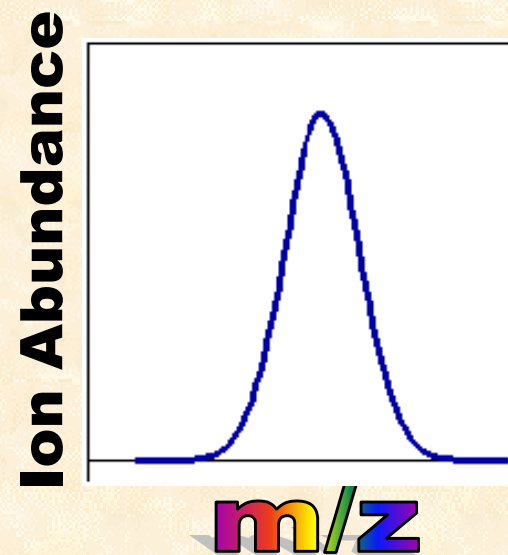
Click

Jargon Review

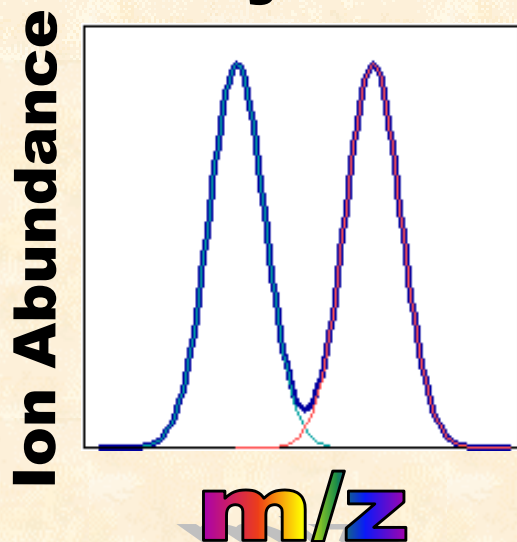
Chromatographic Peak



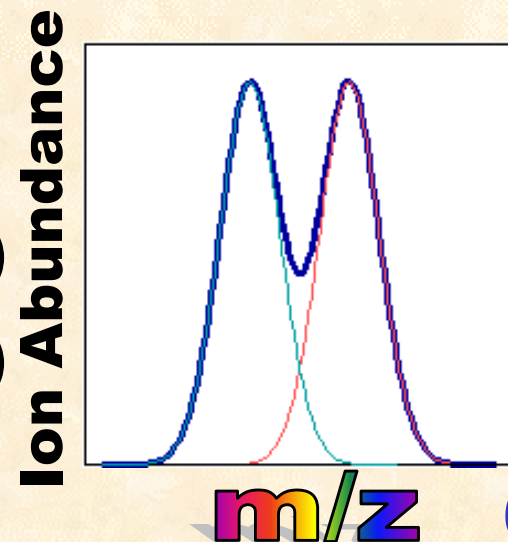
Total Ion
or
Single Ion
Chromatogram



10% valley



10,000 (10%)
14,700 (50%)

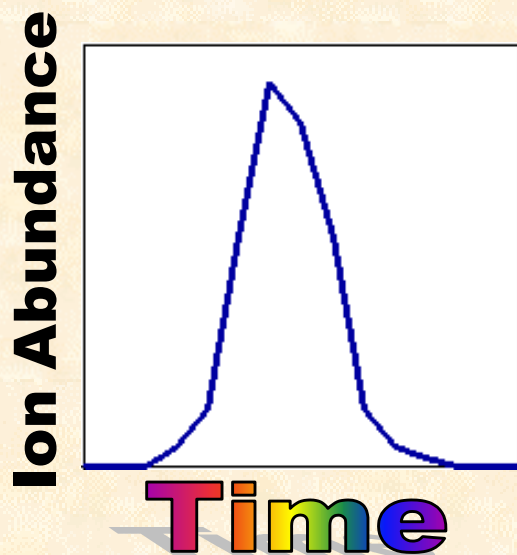


Click

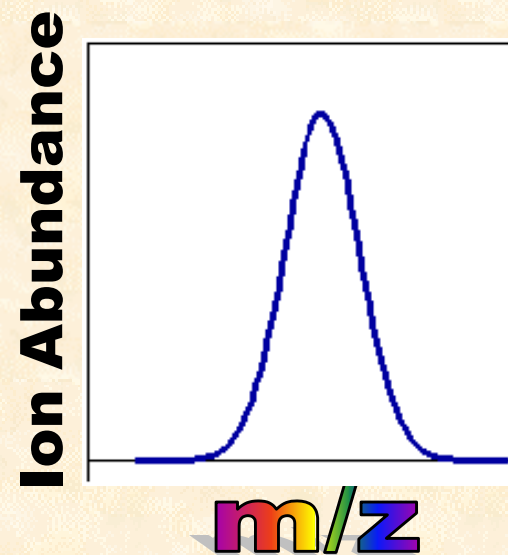
Jargon Review

Chromatographic Peak

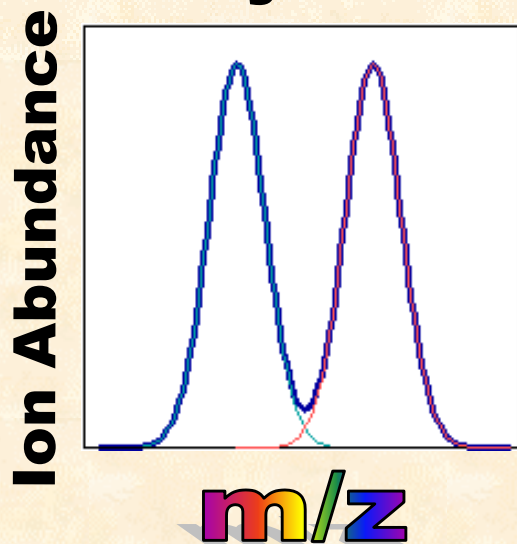
Mass Peak Profile



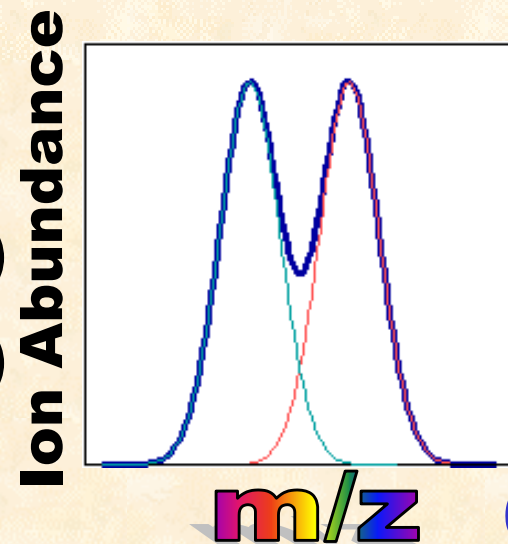
Total Ion
or
Single Ion
Chromatogram



10% valley



— △
10,000 (10%)
14,700 (50%)

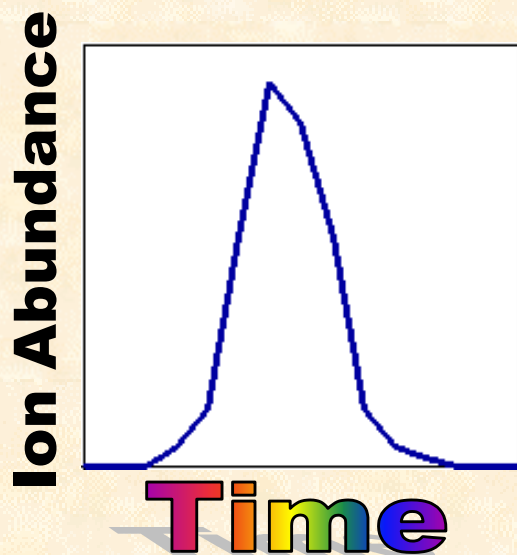


Click

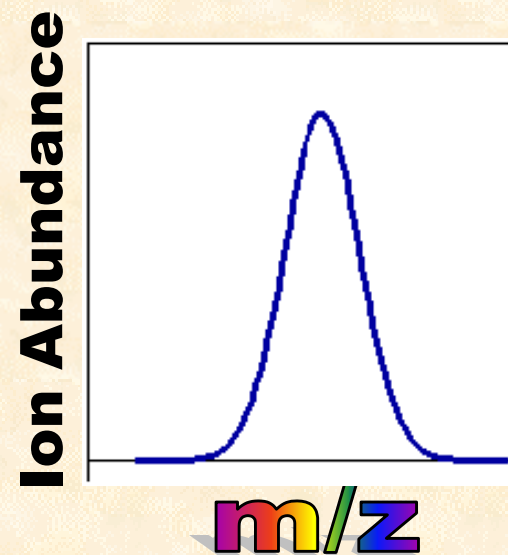
Jargon Review

Chromatographic Peak

Mass Peak Profile

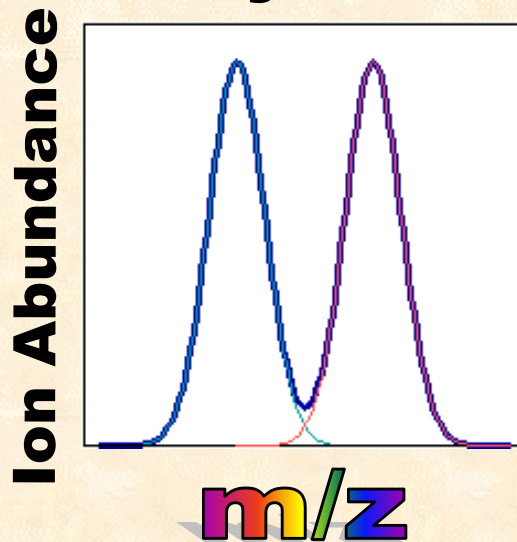


Total Ion
or
Single Ion
Chromatogram



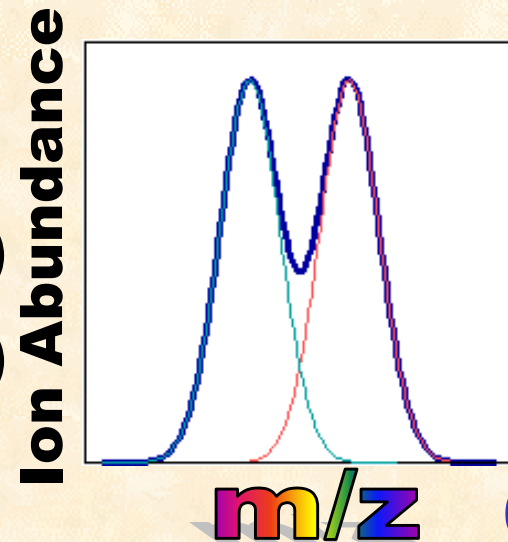
10% valley

Mass Resolution



— Δ

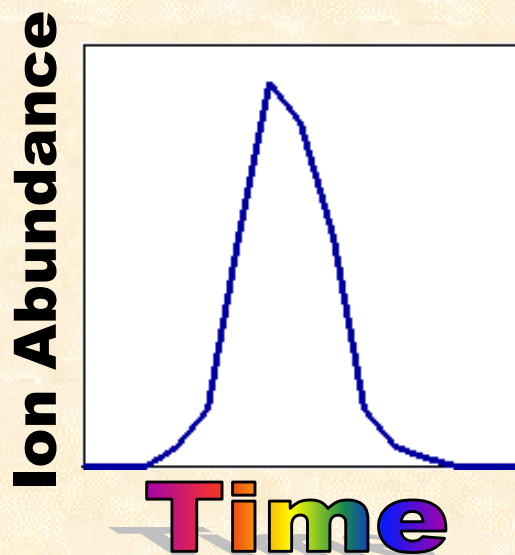
10,000 (10%)
14,700 (50%)



Click

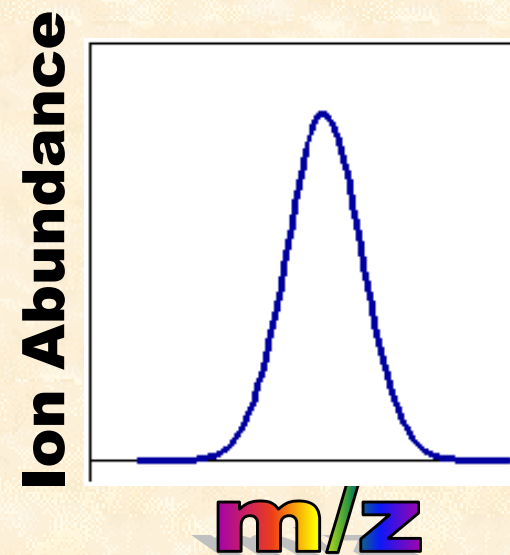
Jargon Review

Chromatographic Peak

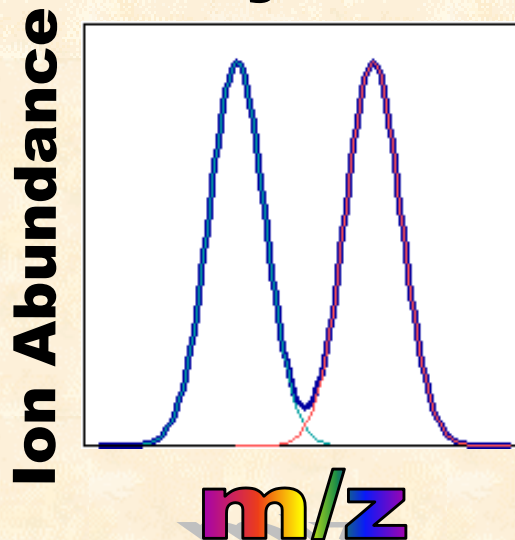


Total Ion
or
Single Ion
Chromatogram

Mass Peak Profile



10% valley

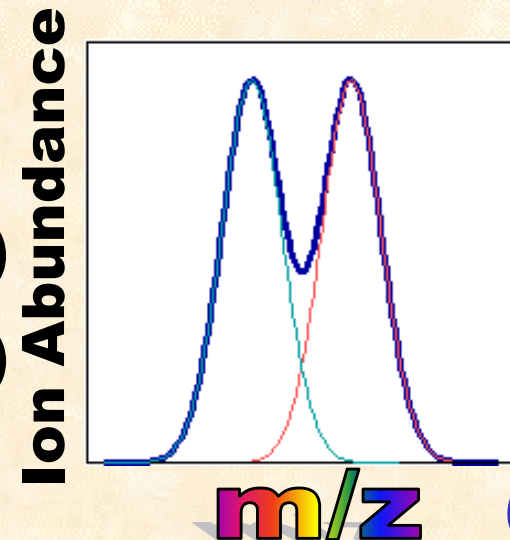


Mass Resolution

$$\bar{M}/\Delta M$$

10,000 (10%)

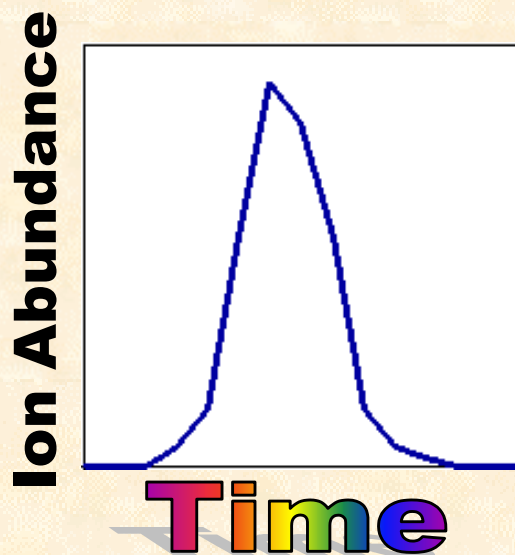
14,700 (50%)



Click

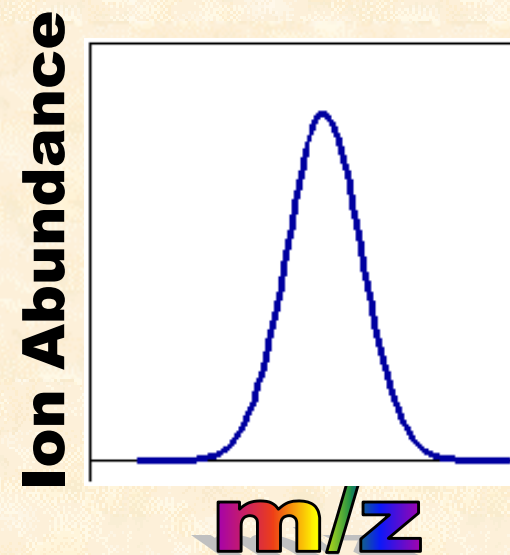
Jargon Review

Chromatographic Peak

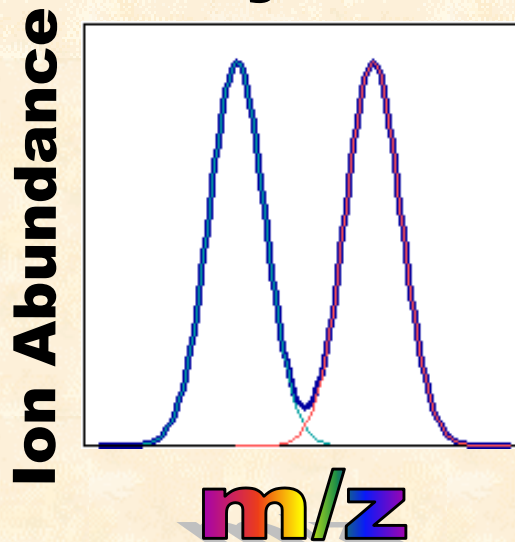


Total Ion
or
Single Ion
Chromatogram

Mass Peak Profile



10% valley



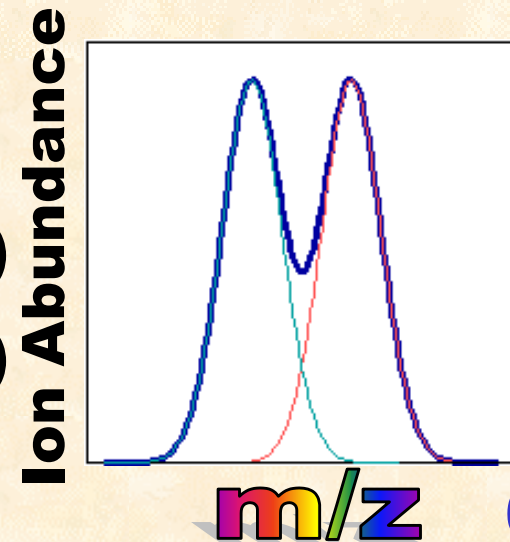
Mass Resolution

$$\bar{M}/\Delta M$$

10,000 (10%)

14,700 (50%)

50% valley



Click

What's the Problem, ICE Man?

Tentative Identification of organic compounds by LRMS:

Clean mass spectrum

Several mass peaks

Mass spectrum in the NIST or Wiley library

Limitations - No Tentative Identification:

Multiple library matches

No library matches

Liquid sample introduction – ESI or APCI

Soft ionization – few ions for comparison

No libraries of ESI or APCI mass spectra

Majority of Organic Compounds are not Identified by LRMS

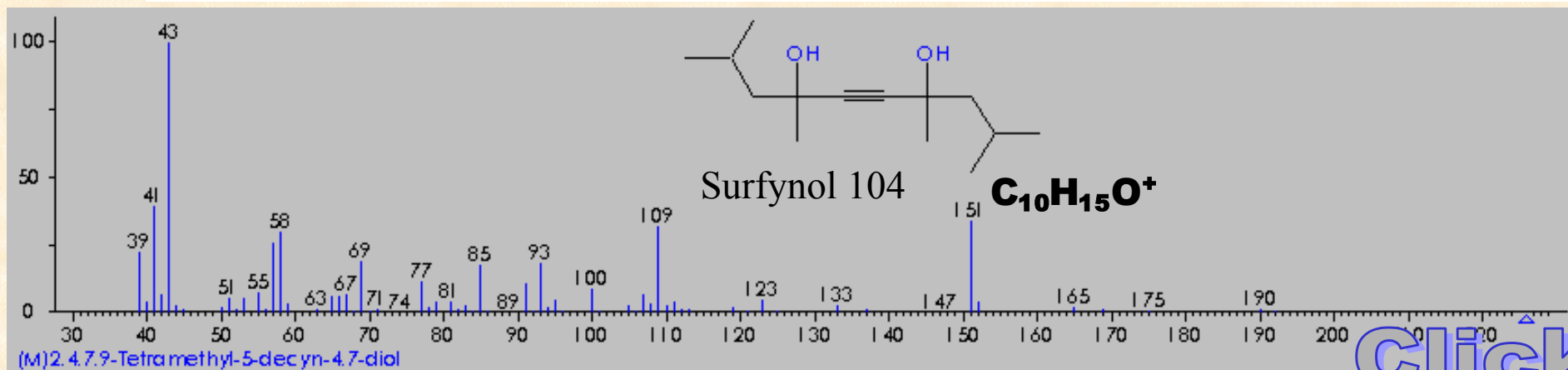
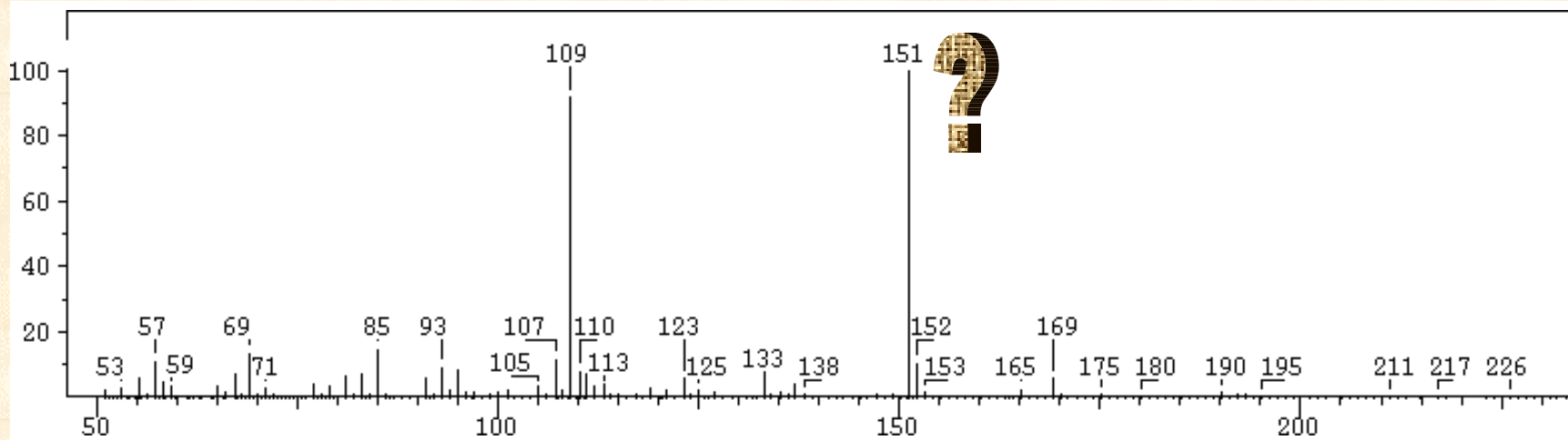
Click

Example

Multiple Matches



Acetaminophen

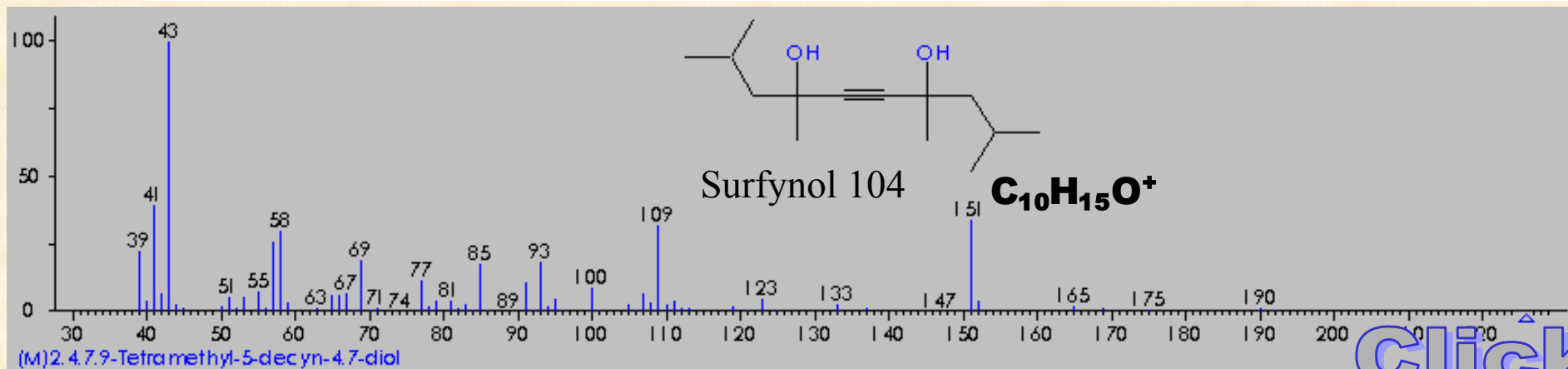
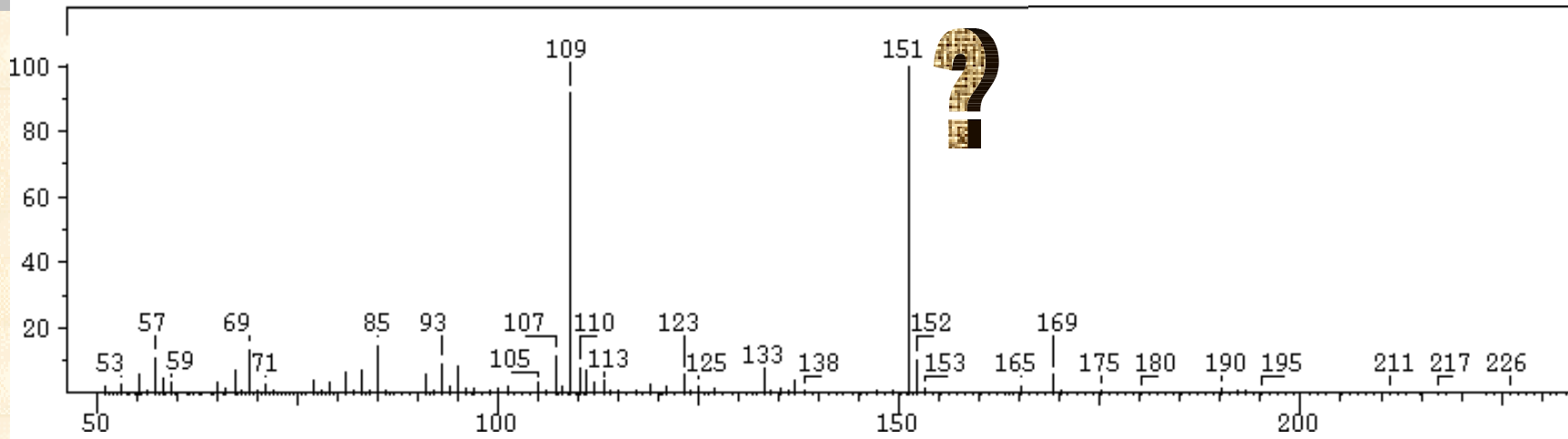
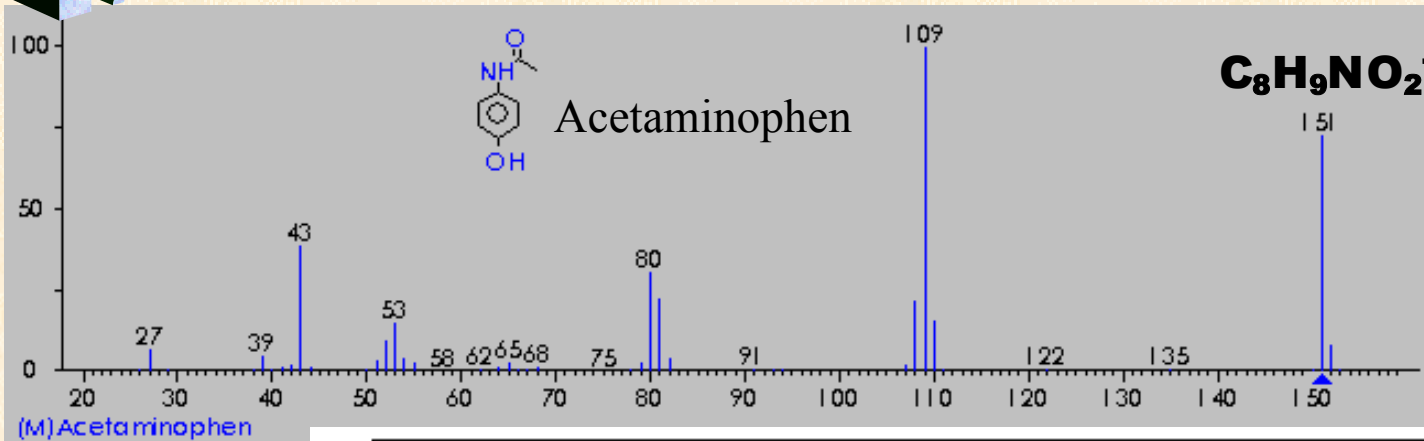


Click



Example

Multiple Matches



Click

What properties differ between these ions?

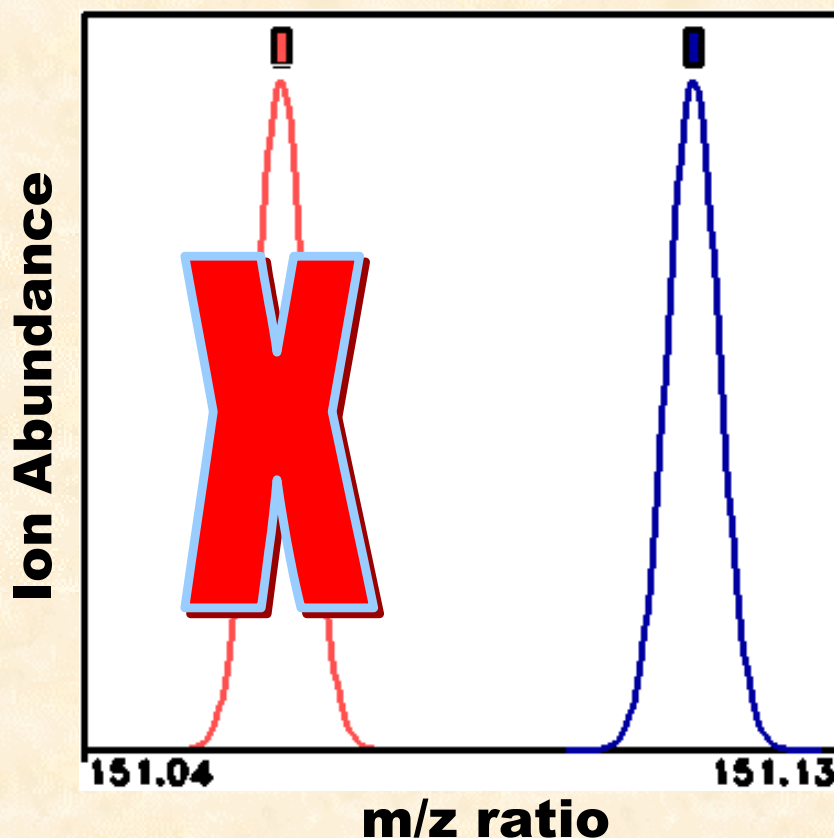


High Mass Resolution



8 x 12.00000
 9 x 1.00783
 1 x 14.00307
 2 x 15.99491
151.06333

10 x 12.00000
 15 x 1.00783
 1 x 15.99491
151.11229

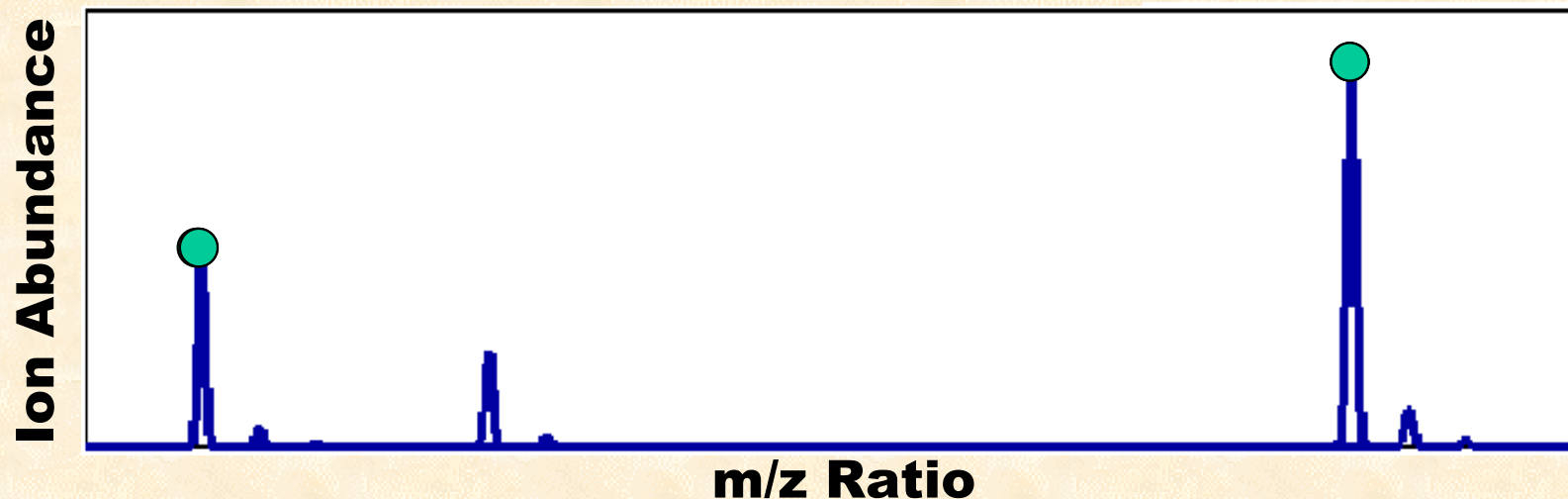


One property is Exact Mass.

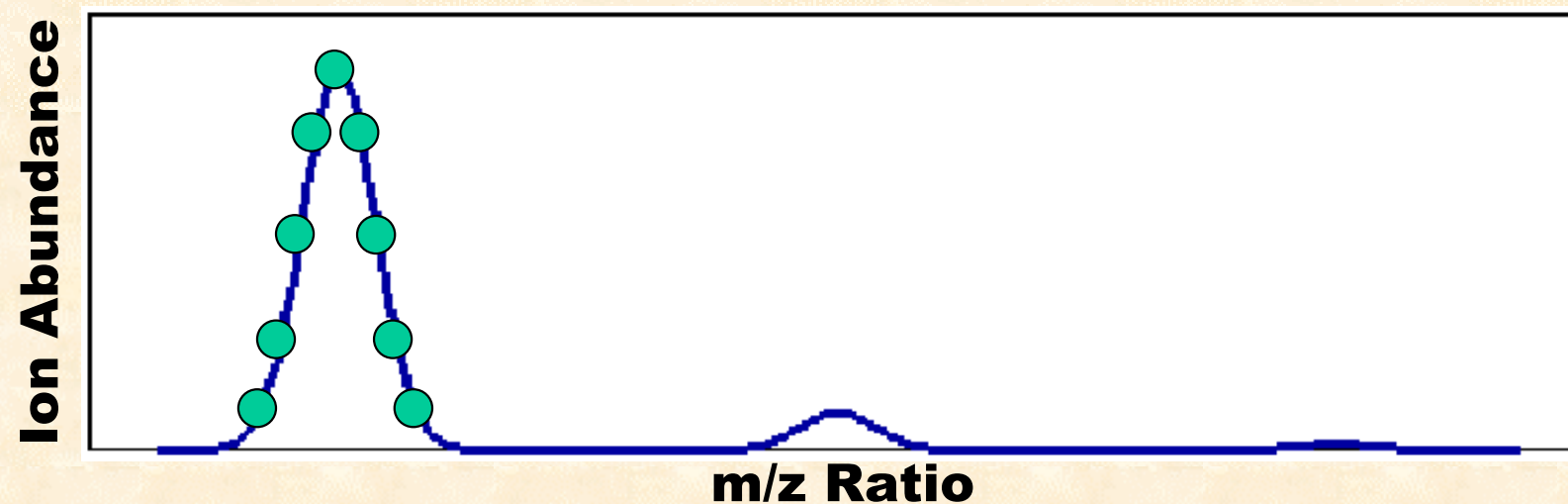
Click

Scan Modes

Selected Ion Recording

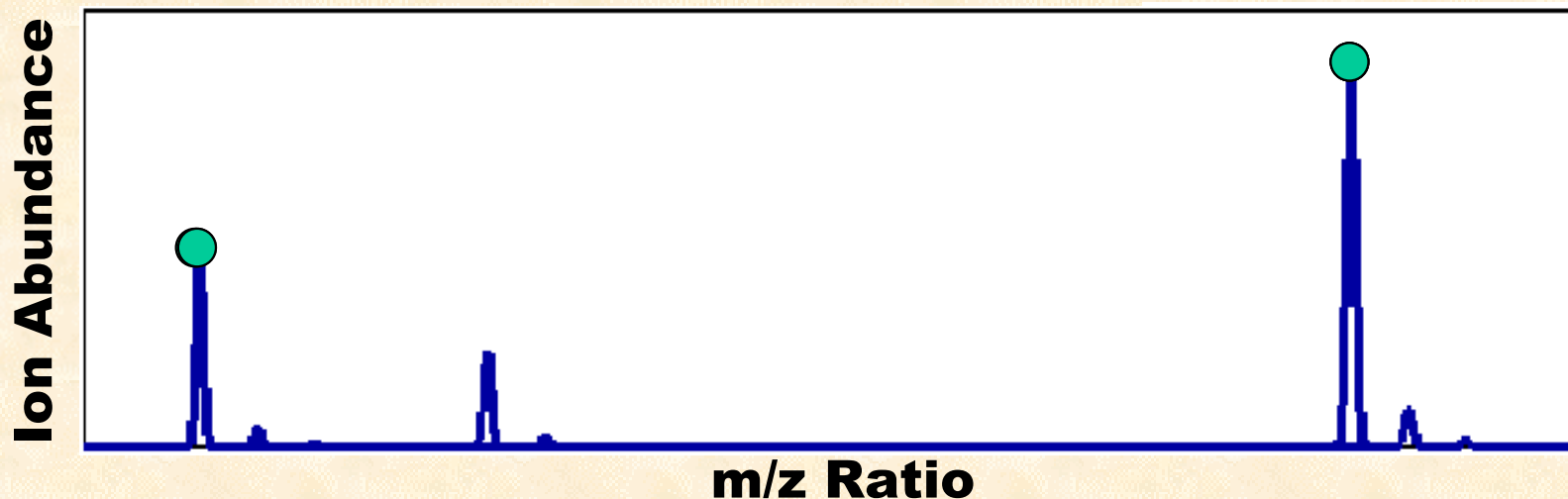


Hybrid Scan

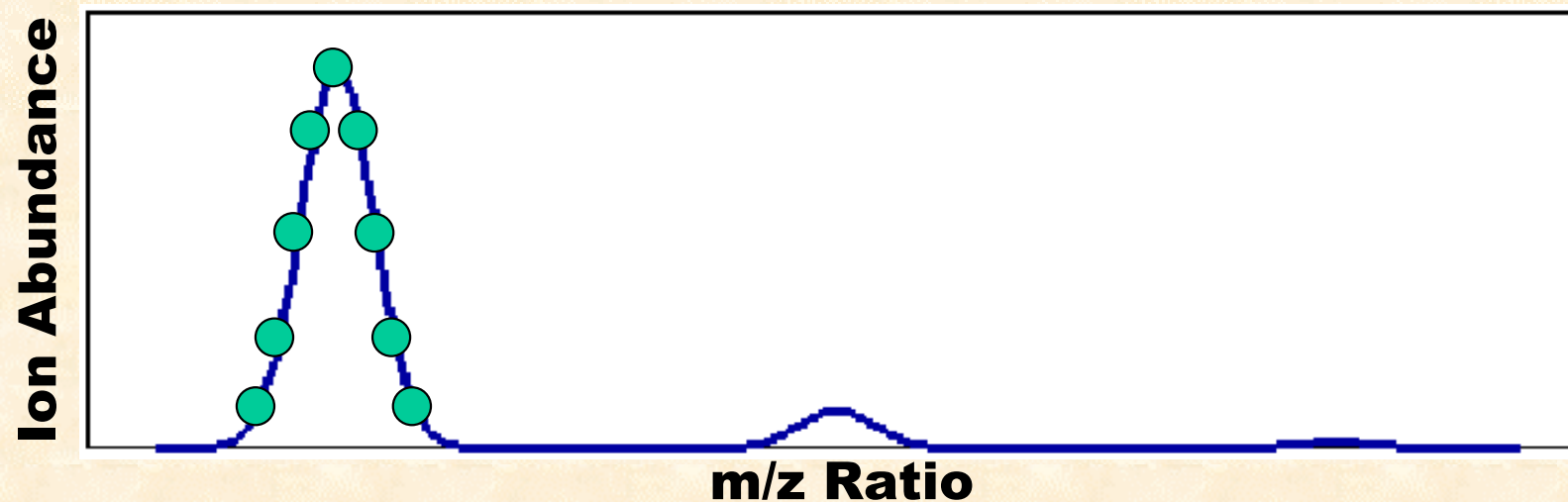


Scan Modes

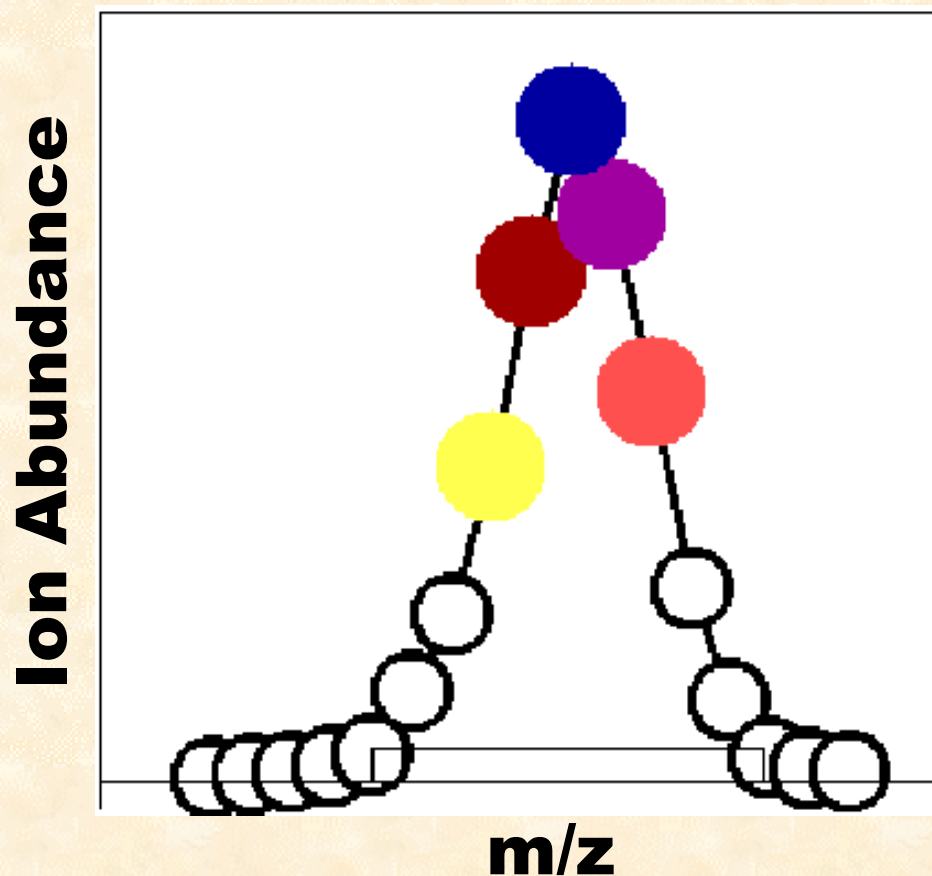
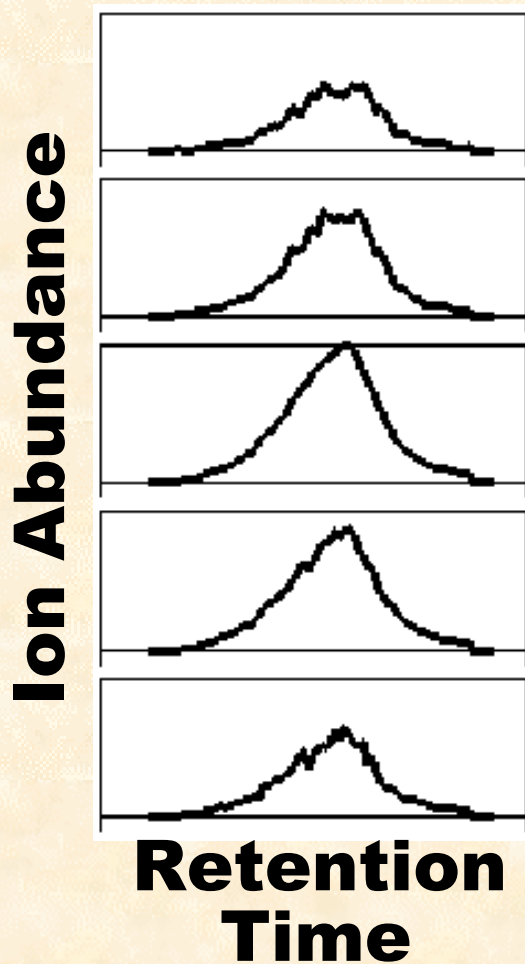
Selected Ion Recording



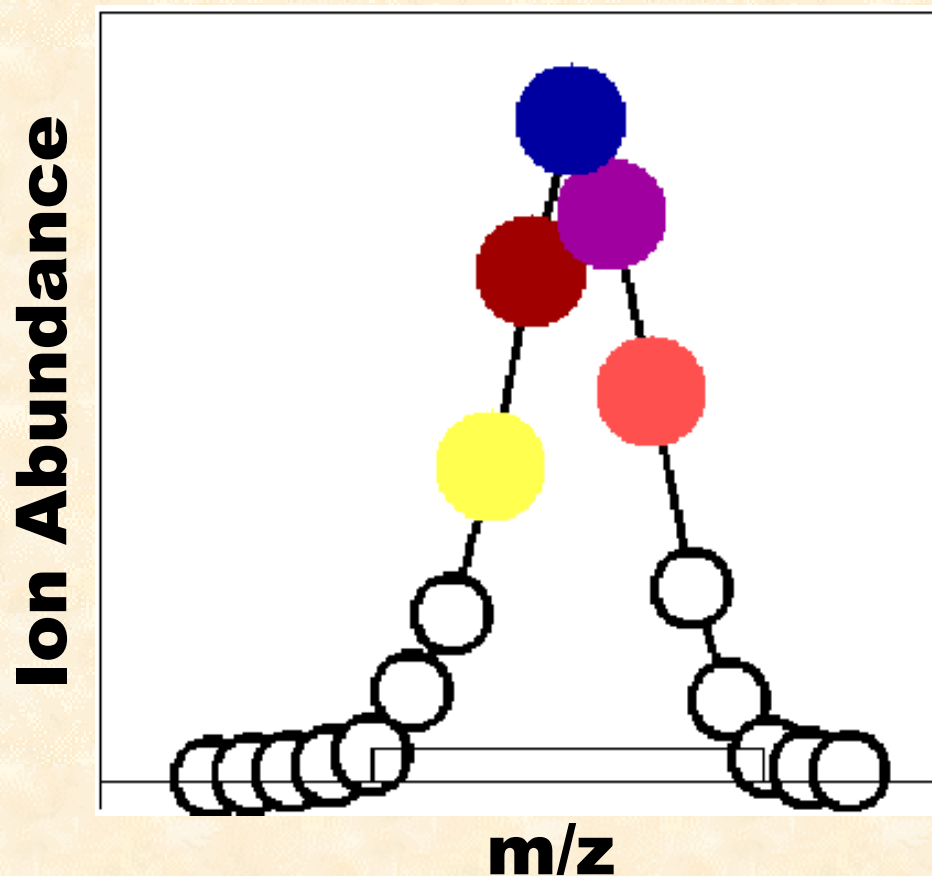
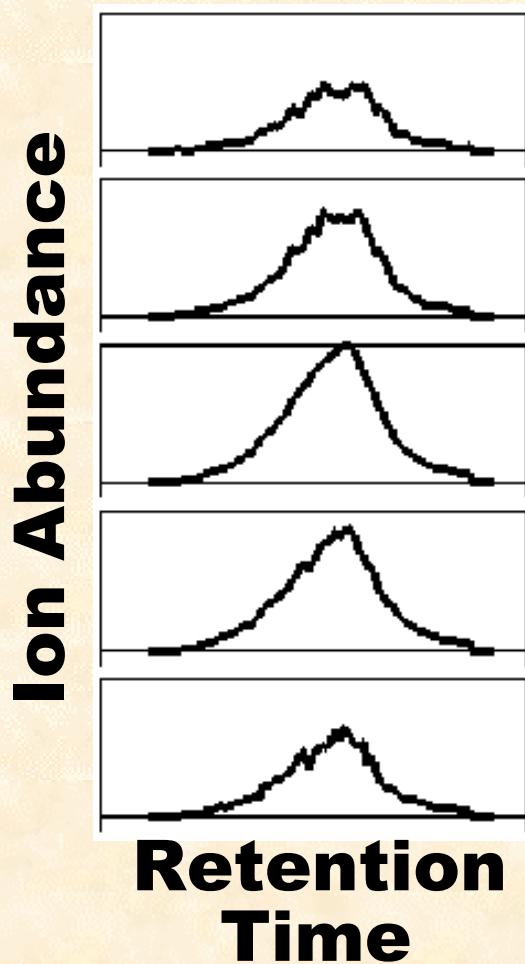
Hybrid Scan



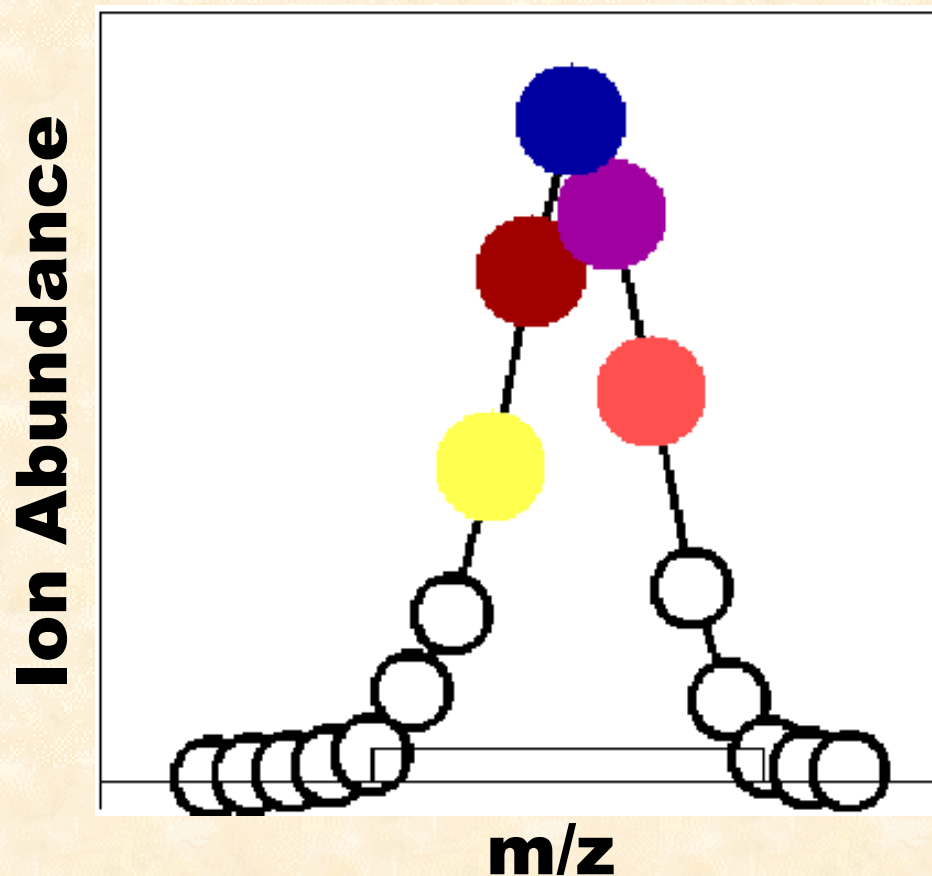
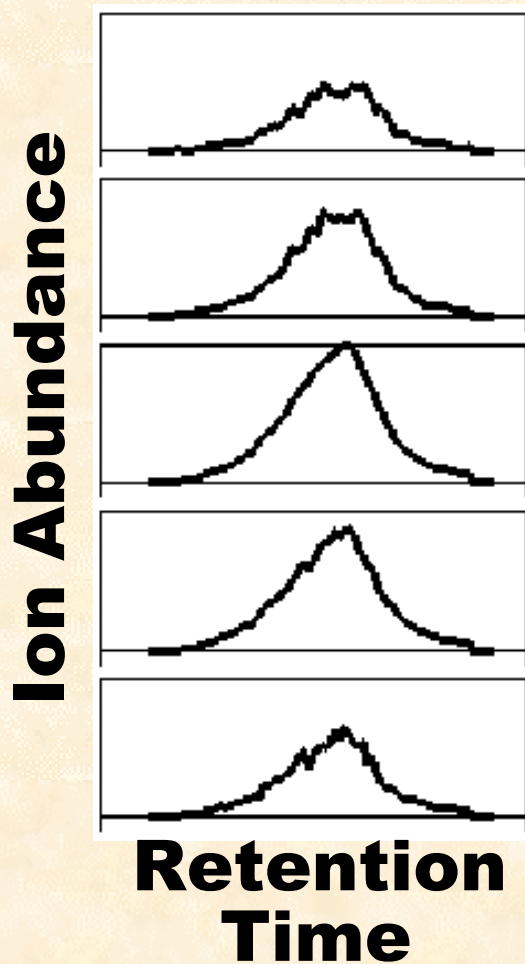
MPPSIRD Definition



MPPSIRD Definition



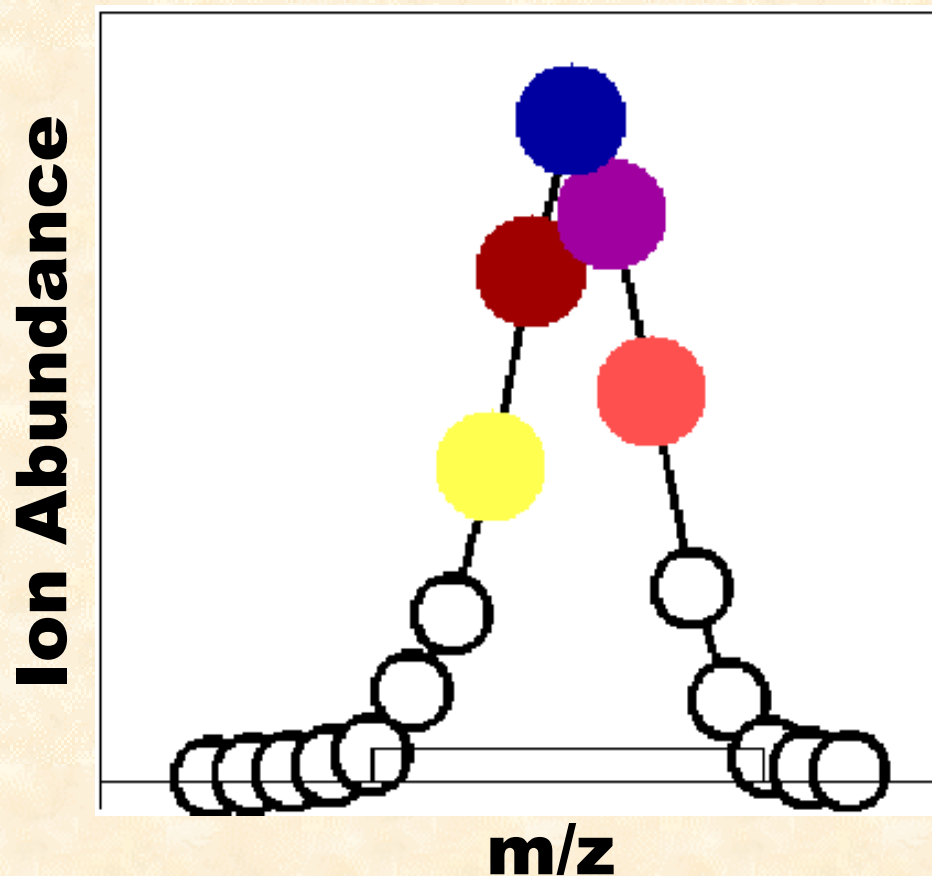
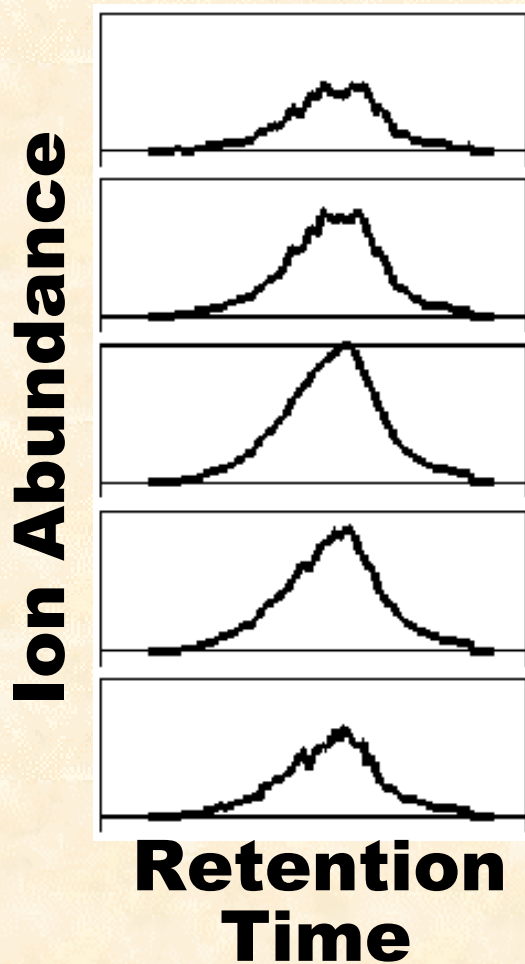
MPPSIRD Definition



Mass Peak Profiling from Selected Ion Recording Data

Click

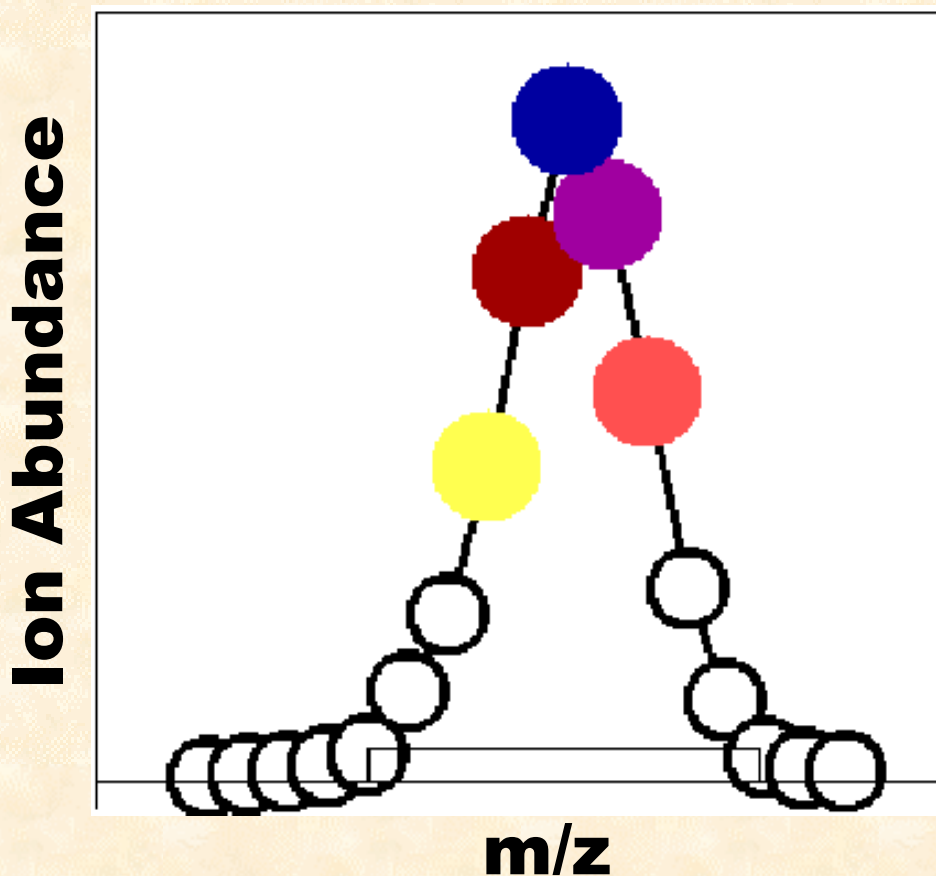
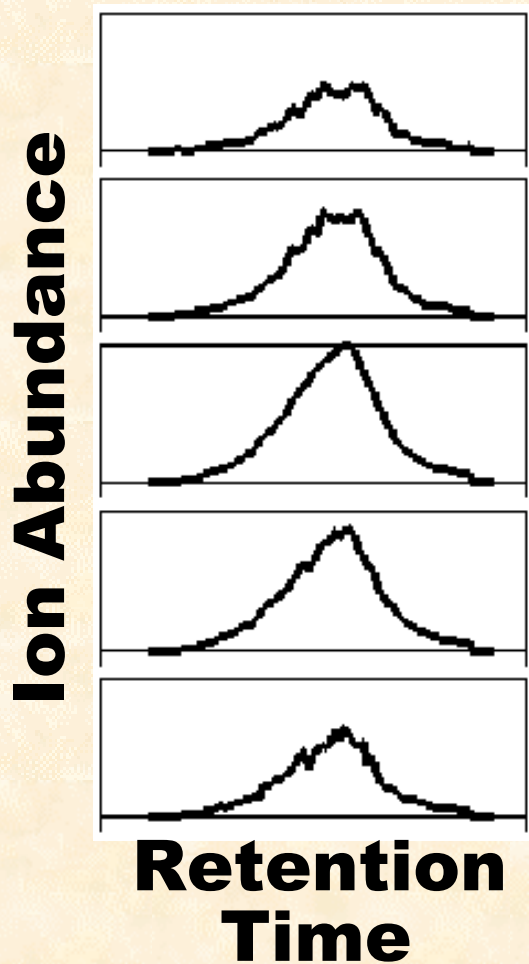
MPPSIRD Definition



Mass Peak Profiling from Selected Ion Recording Data

[Click](#)

MPPSIRD Definition



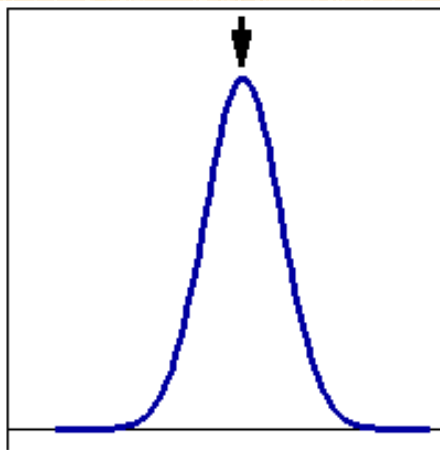
Mass Peak Profiling from Selected Ion Recording Data

Click

Calibration

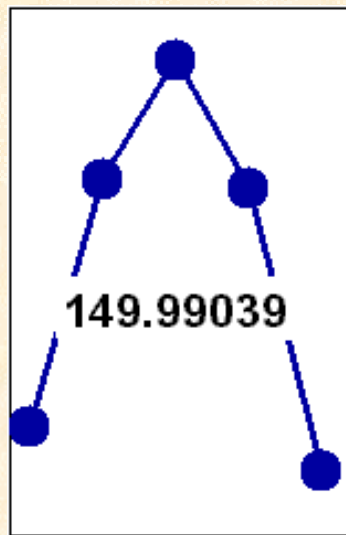
Recalibration each cycle

Maximum

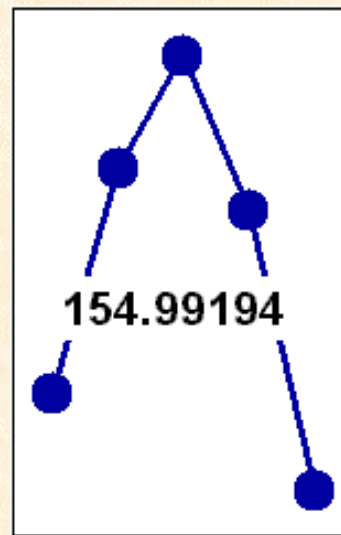


m/z Ratio

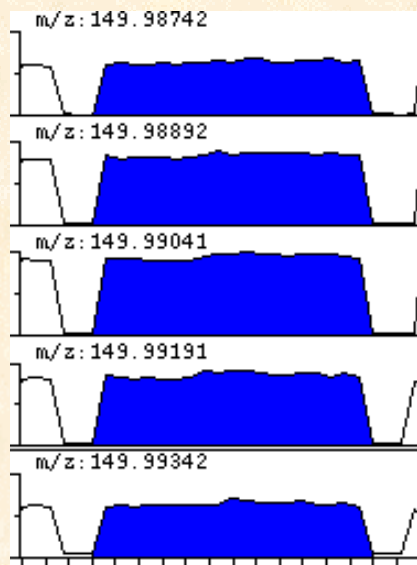
Lock Mass



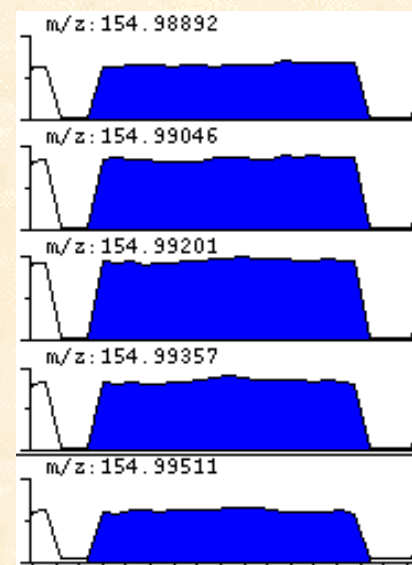
Calibration Mass



Ion Abundance



Time

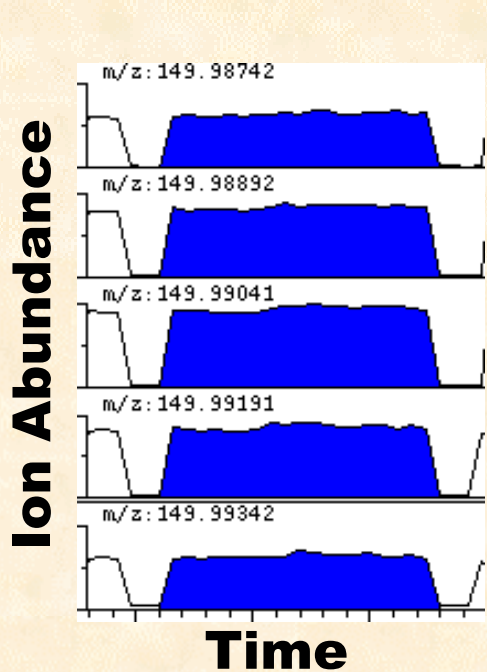
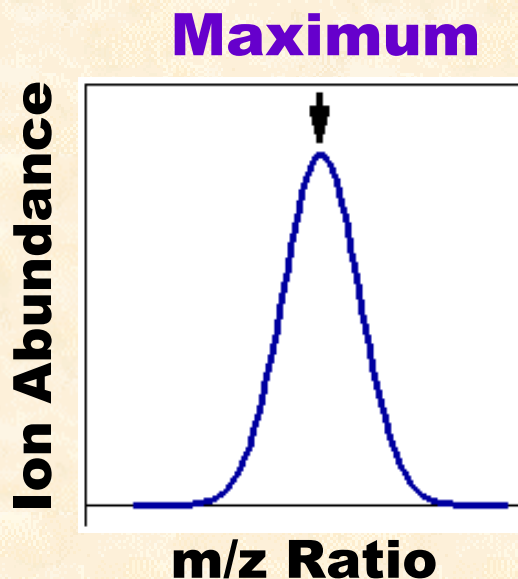


Time

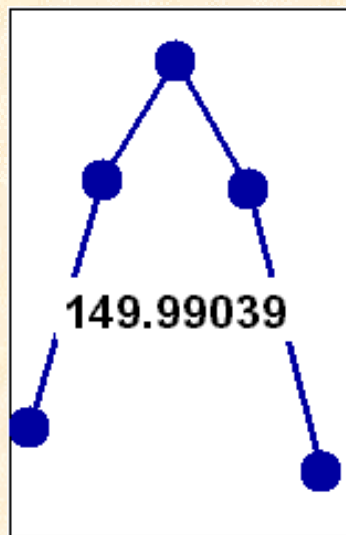
m/z Ratio

Calibration

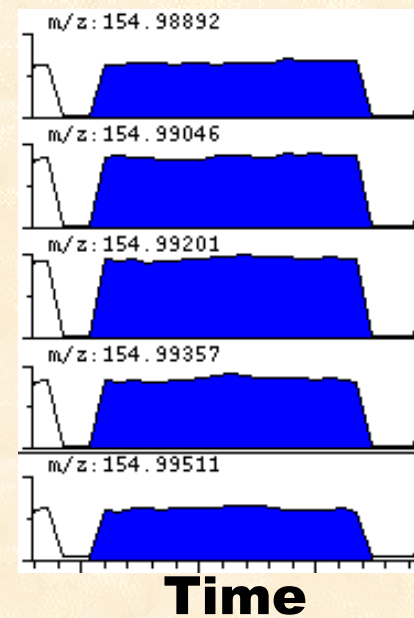
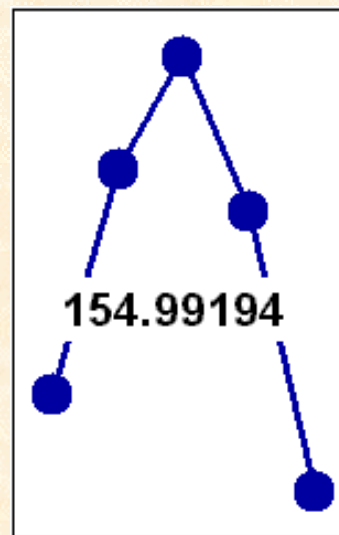
Recalibration each cycle



Lock Mass



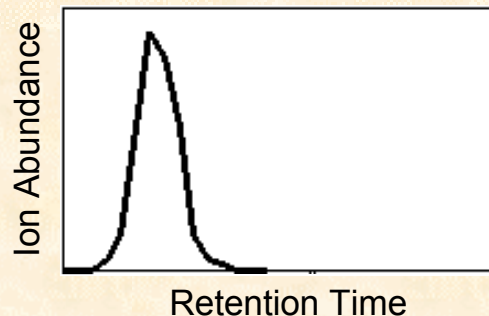
Calibration Mass



Instrumental Advantages of MPPSIRD

Delineate chromatographic peaks

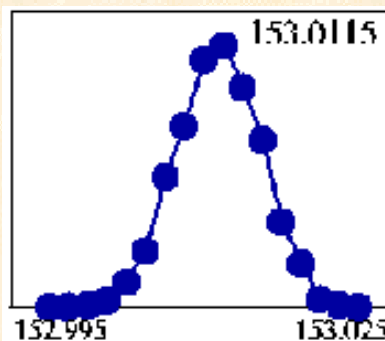
**For a single
m/z ratio**



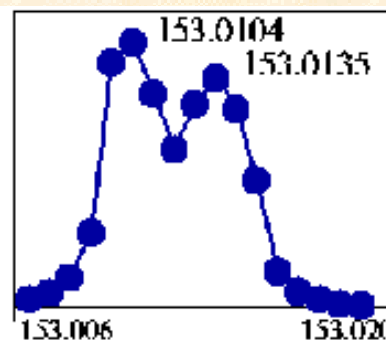
100-fold greater than full scans

Higher resolution feasible

**10,000
Resolution**



**24,000
Resolution**



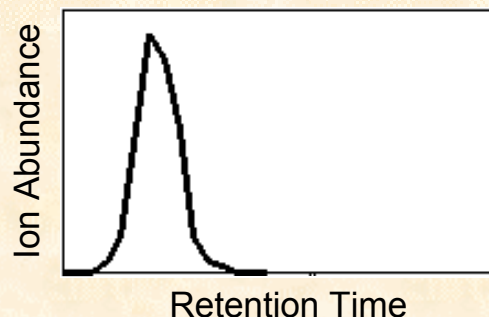
Lock mass recalibration each cycle

Instrumental Advantages of MPPSIRD

Speed

Delineate chromatographic peaks

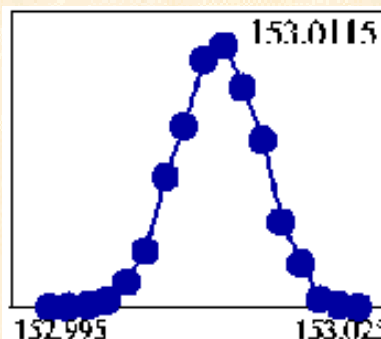
**For a single
m/z ratio**



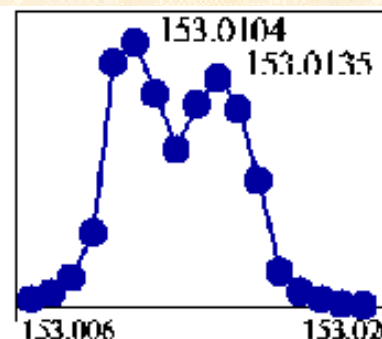
100-fold greater than full scans

Higher resolution feasible

**10,000
Resolution**



**24,000
Resolution**



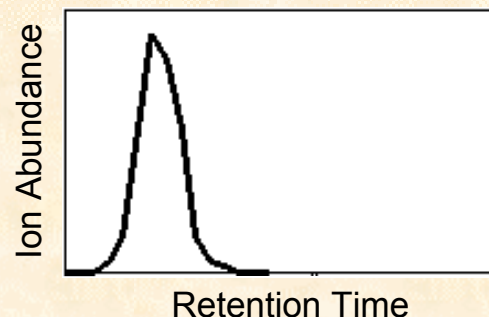
Lock mass recalibration each cycle

Instrumental Advantages of MPPSIRD

Speed

Delineate chromatographic peaks

**For a single
m/z ratio**

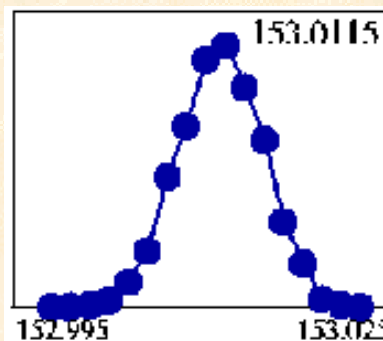


Sensitivity

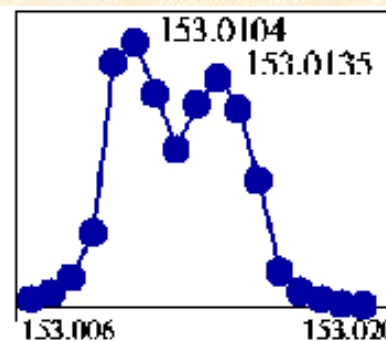
100-fold greater than full scans

Higher resolution feasible

**10,000
Resolution**



**24,000
Resolution**



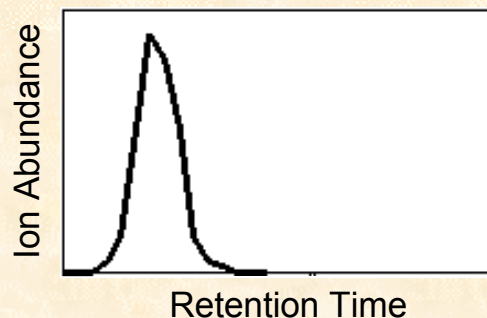
Lock mass recalibration each cycle

Instrumental Advantages of MPPSIRD

Speed

Delineate chromatographic peaks

**For a single
m/z ratio**



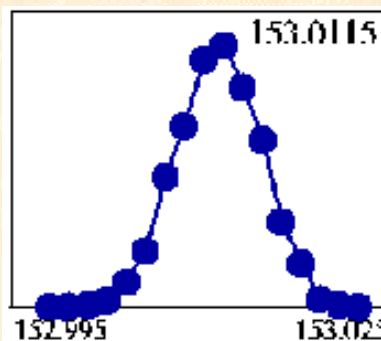
Sensitivity

100-fold greater than full scans

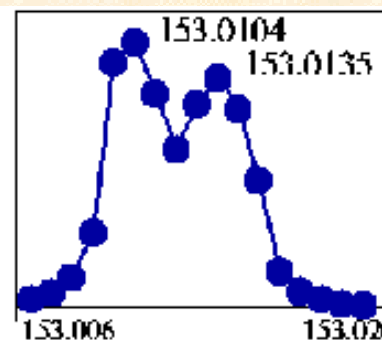
Selectivity

Higher resolution feasible

**10,000
Resolution**



**24,000
Resolution**



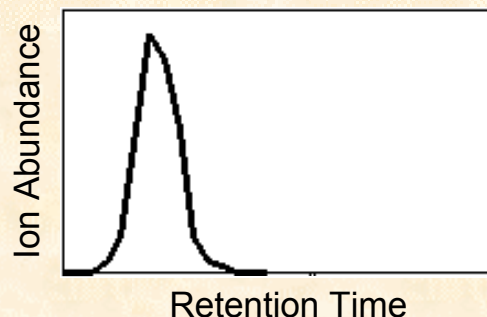
Lock mass recalibration each cycle

Instrumental Advantages of MPPSIRD

Speed

Delineate chromatographic peaks

**For a single
m/z ratio**



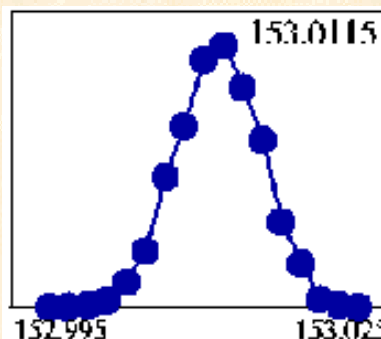
Sensitivity

100-fold greater than full scans

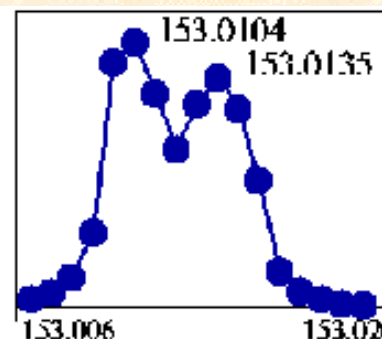
Selectivity

Higher resolution feasible

**10,000
Resolution**



**24,000
Resolution**



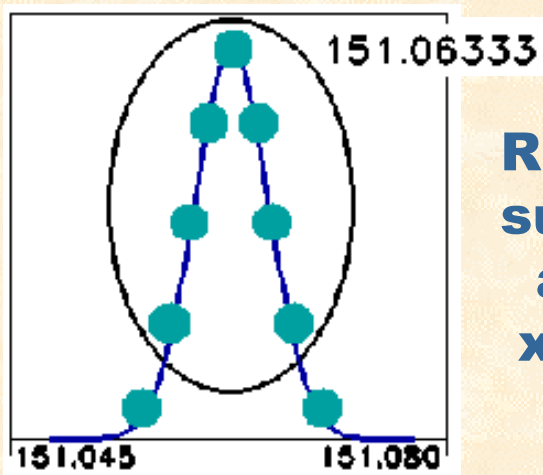
Stability

Lock mass recalibration each cycle

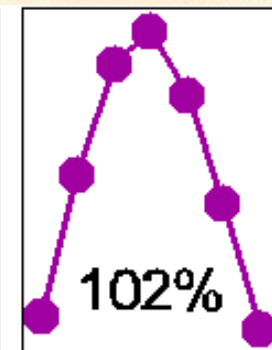
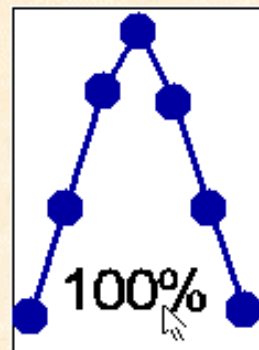
Measurement Advantages of MPPSIRD

Accurate Exact Masses & Relative Abundances

Weighted average of several points



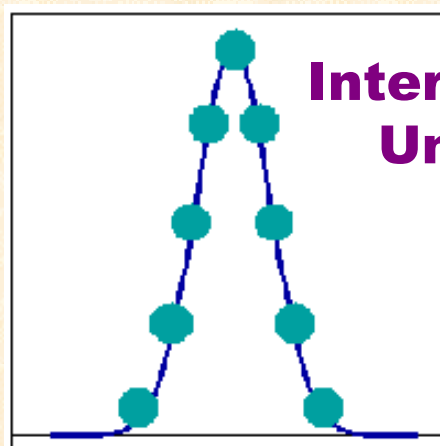
Ratios of summed areas x 100%



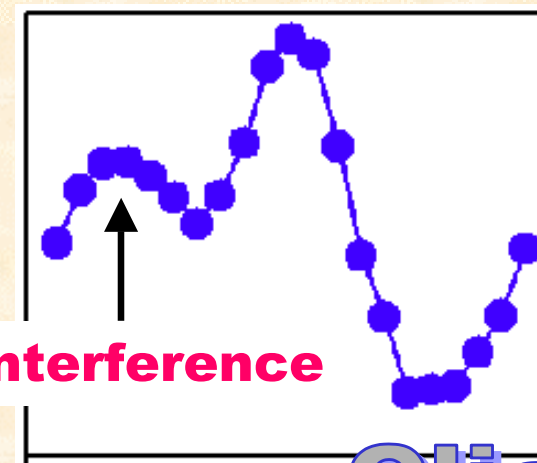
Quality Assurance Advantage of MPPSIRD

Interferences Revealed

Gaussian shape usually indicates no major Interferences



Interference Unlikely



Click

Limitations of MPPSIRD

Monitor four or fewer Analyte Profiles

1 Full Analyte Profile

2 Full Analyte Profiles

3 Partial Analyte Profiles

4 Partial Analyte Profiles

Multiple Experiments required

Double Focusing Mass Spectrometers
are expensive

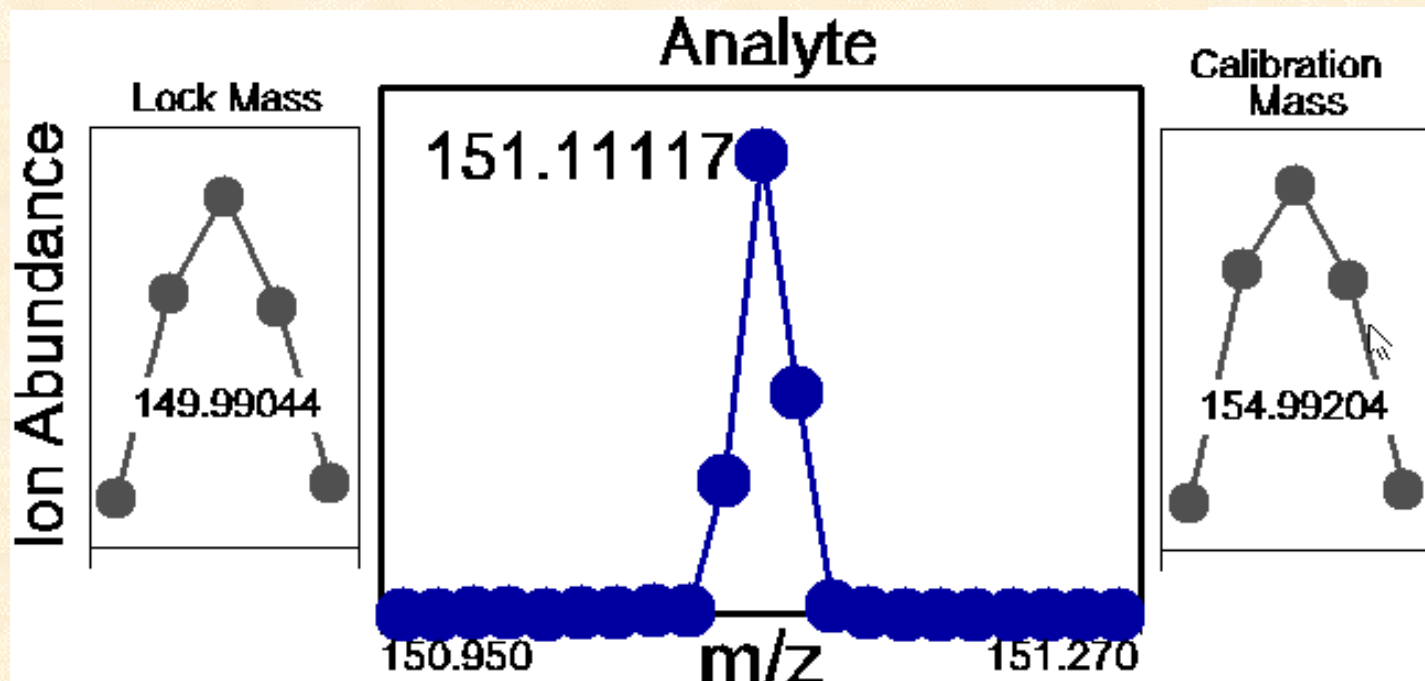
Ancillary DOS capable Computer required

Lotus 2.2, WordPerfect 5.1, QuickBasic 4.5

– Procurement inconvenient

+ Batch files supported, simple code

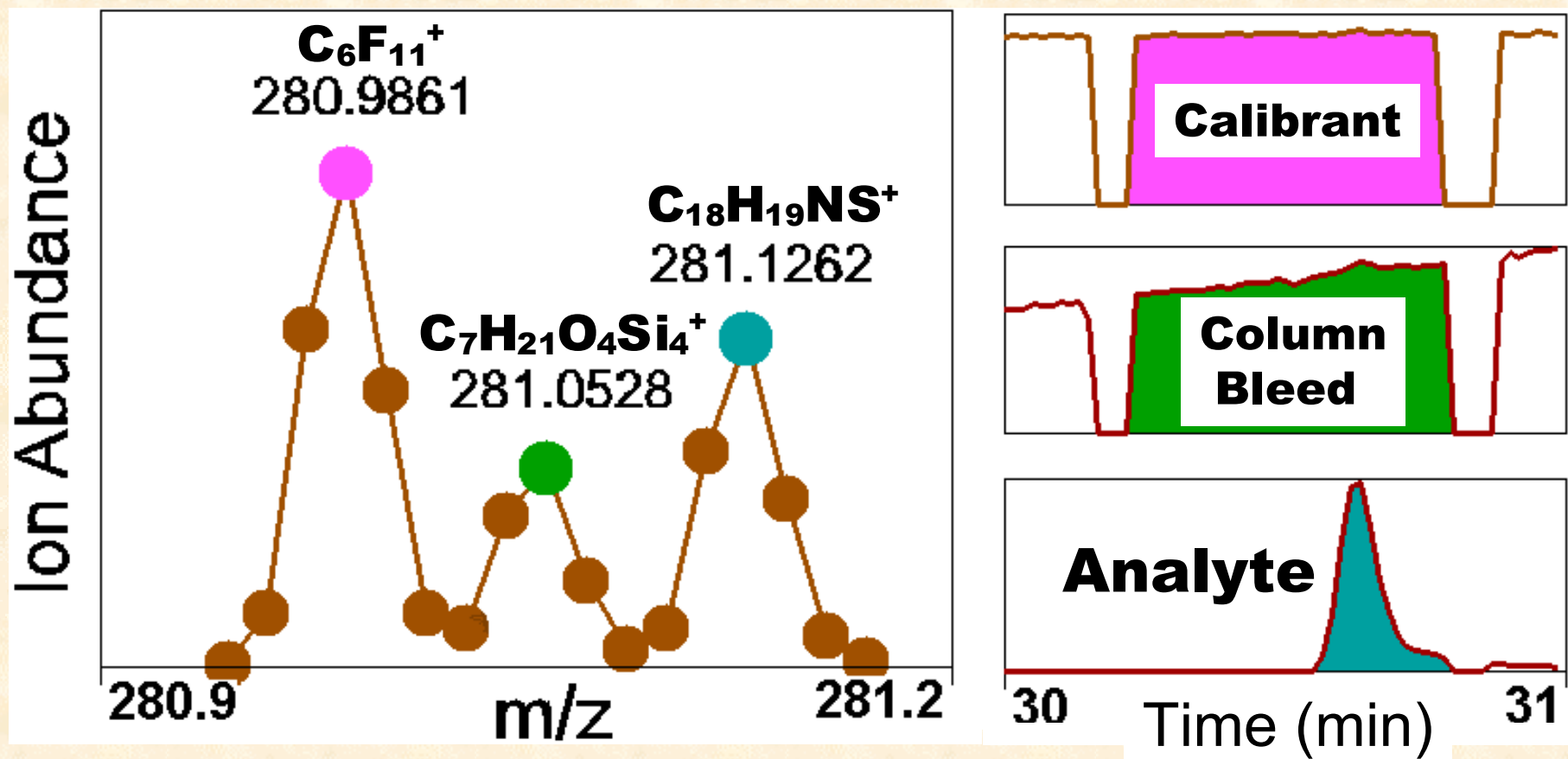
Survey Data



Wide mass range
3,000 mass resolution

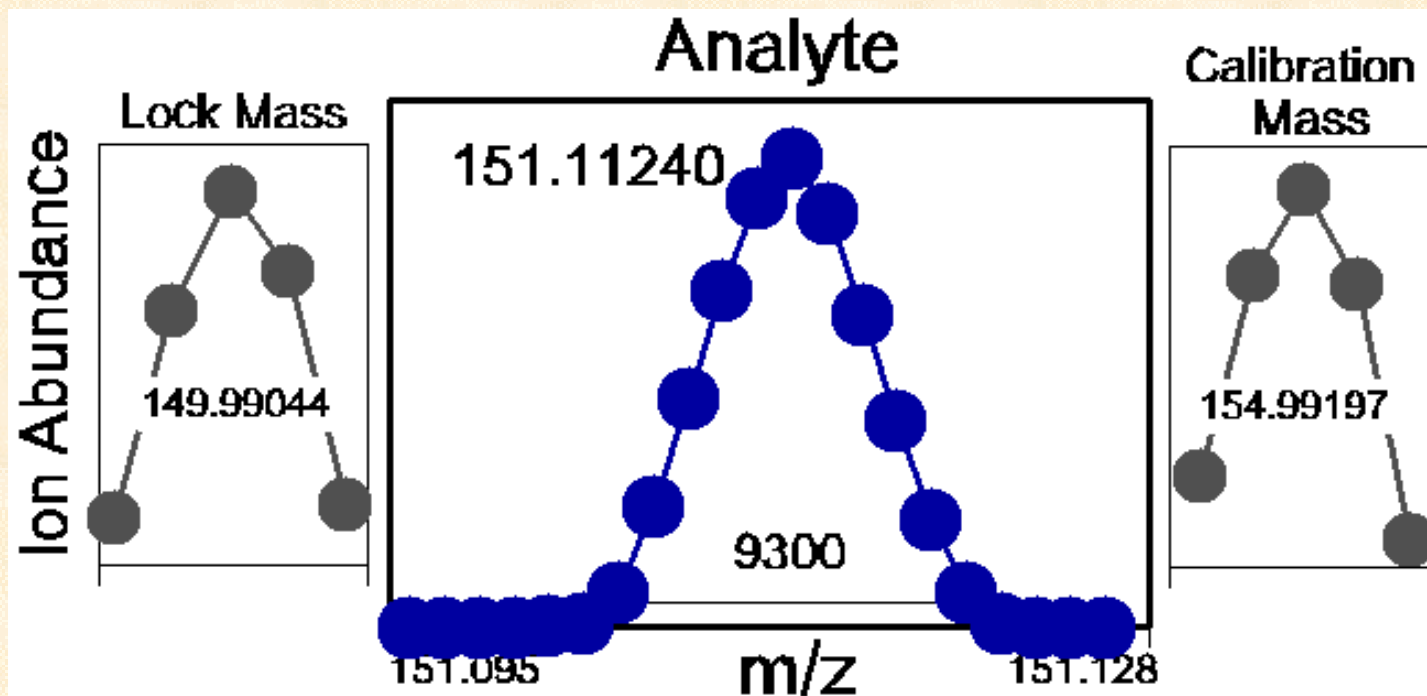
Coarse estimate of the exact mass
for the most abundant *Analyte* ion

Sources of Ions



Investigate the Analyte ion

Exact Mass of Analyte Ion



Elements Considered: C H N O F P S Si

m/z 151.11240 ± 6 ppm Resolution 10,000

PGM:

#	Err(mmu & ppm)	Composition
1	-0.3 -2.0	C5 H14 N3 O F
2	-0.1 -0.7	C10 H15 O

~~C8H9NO2~~ 151.06333 -325 ppm

Click

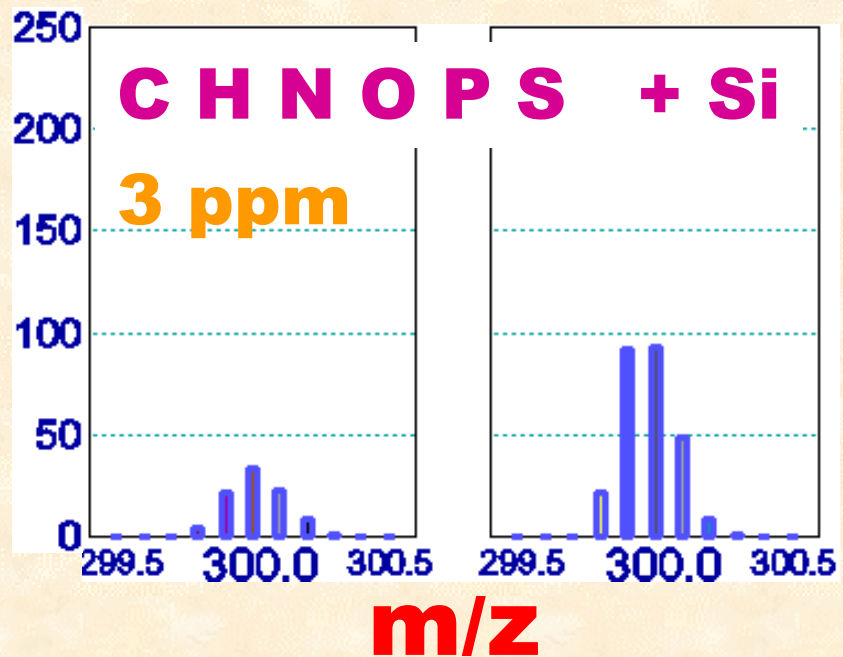
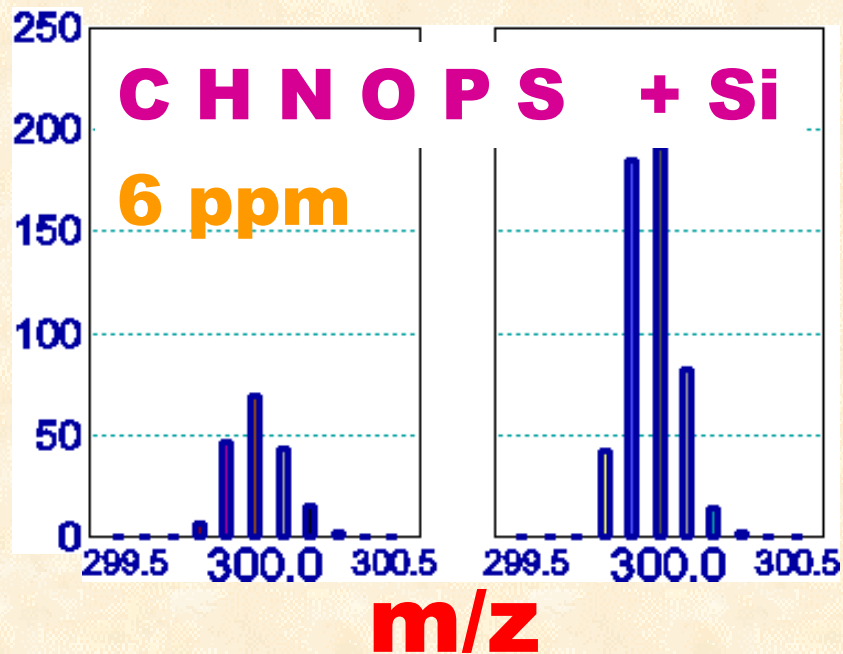
Number of Possible Compositions

3 Factors

m/z

Error Limit

Number of Elements

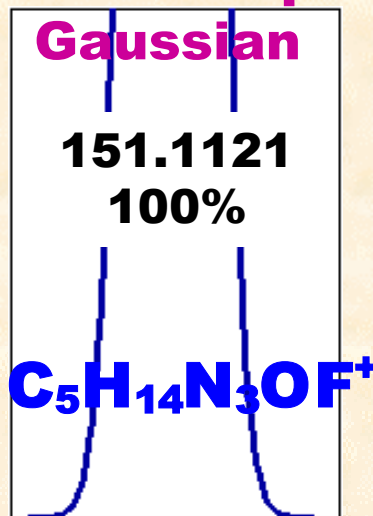


Isotopic Abundances

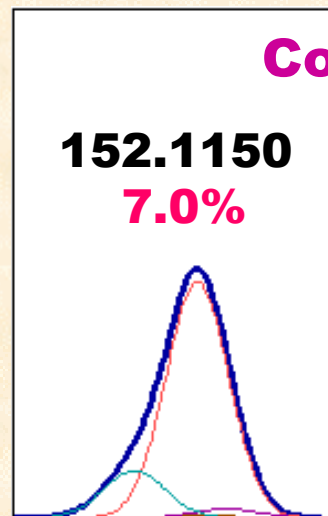
+1

¹³C 1.10%
²⁹Si 4.67%

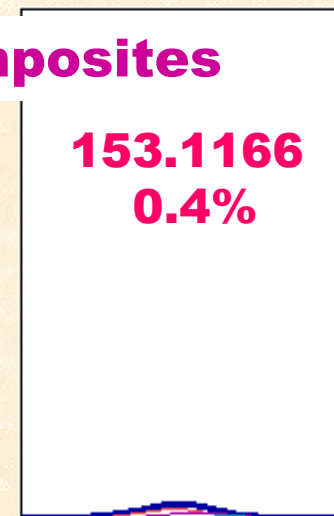
Monoisotopic



+1



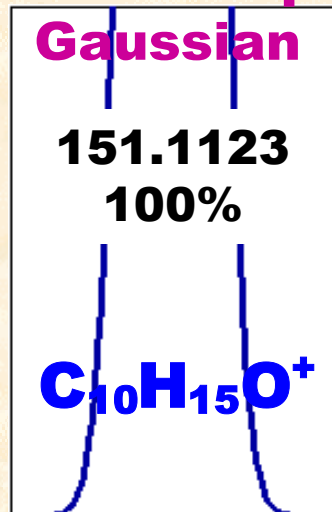
+2



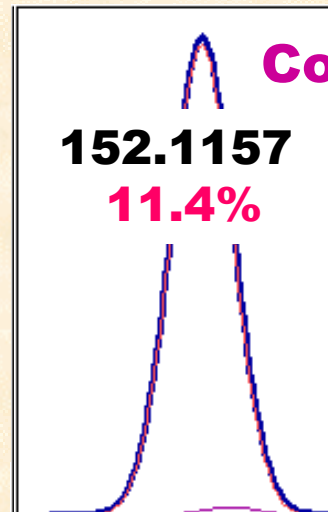
+2

³⁴S 4.21%
³⁰Si 3.10%
³⁷Cl 24.23%
⁸¹Br 49.31%

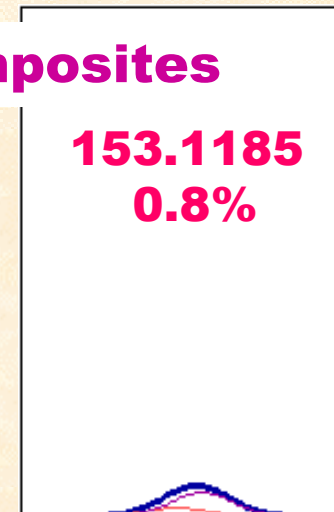
Monoisotopic



+1



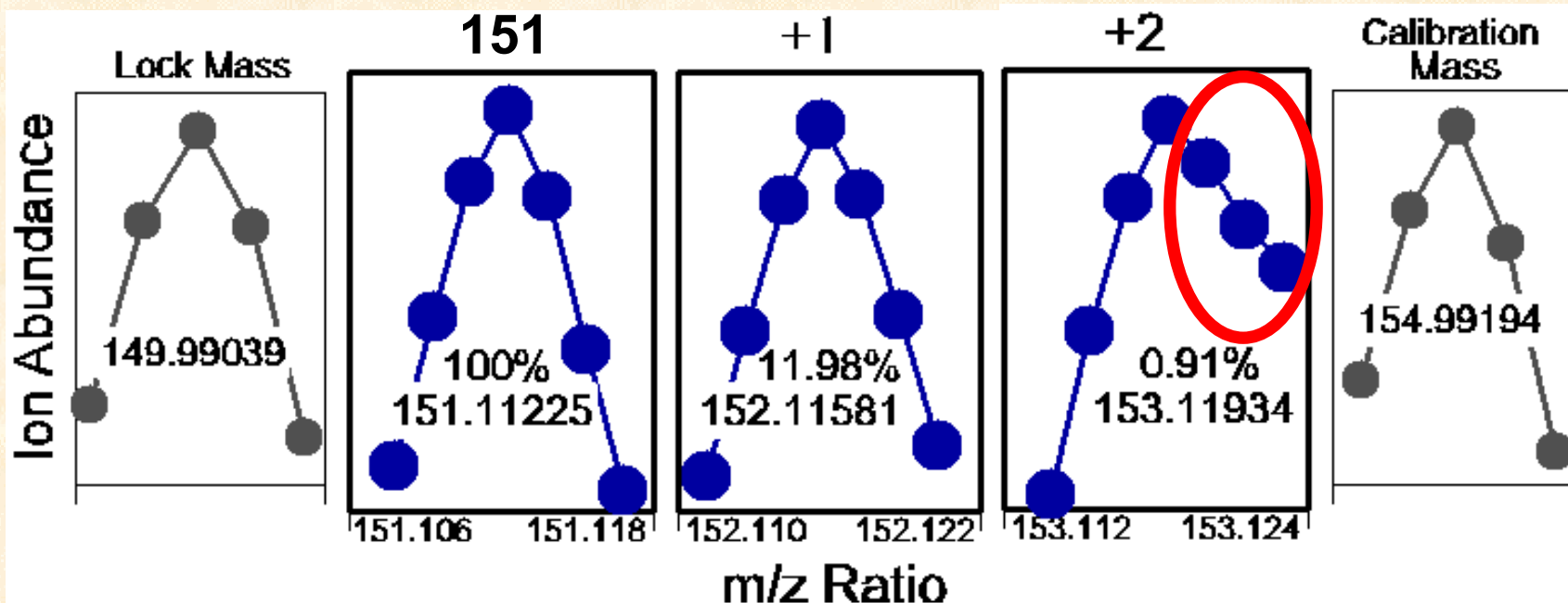
+2



10,000 Resolution (±6 ppm)

Click

Monitor Partial Profiles with MPPSIRD



PGM:

Elements Considered: C H N O F P S Si

m/z 151.11225 ± 6 ppm

Resolution 10,000

Mass Defects

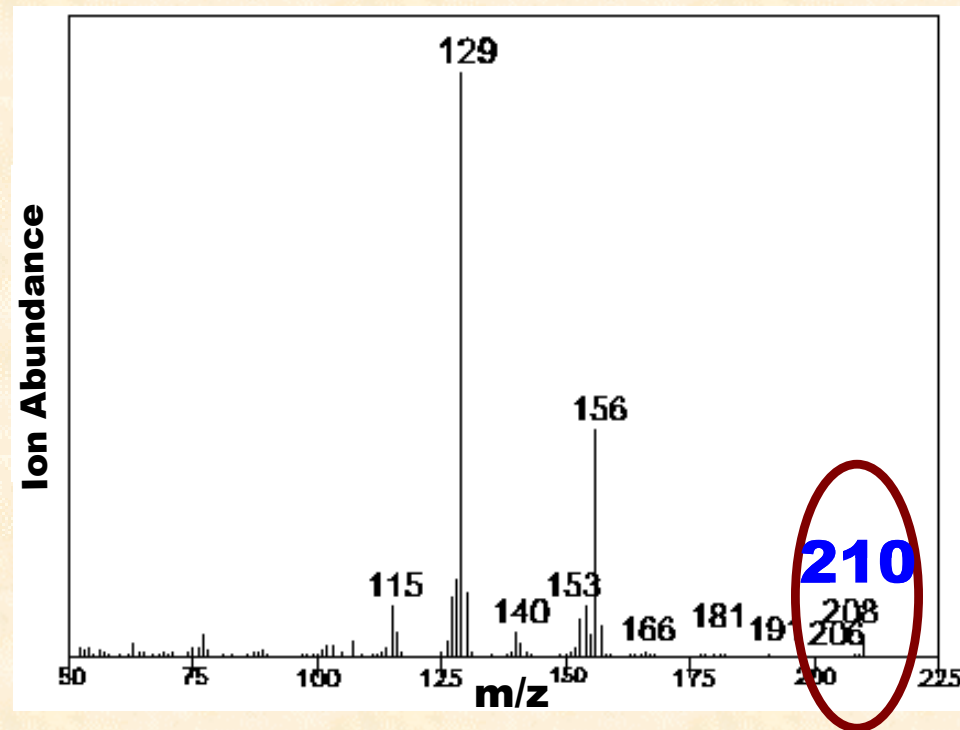
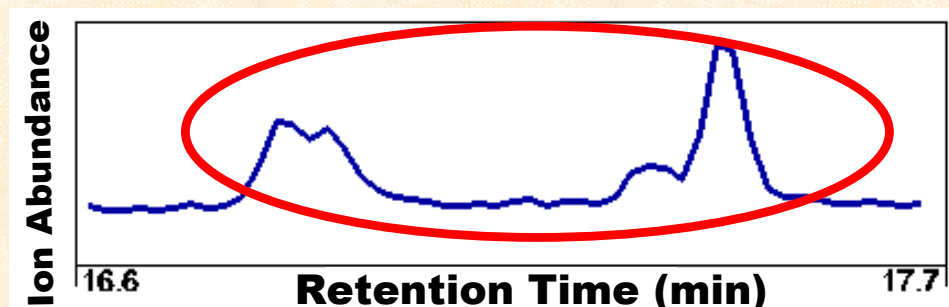
Relative Abundances

#	RDB	Composition	151	+1	+2	%+1(Range %+1)	%+2(Range %+2)
1	0.0	C5 H14 N3 O F	.11209	.11499	.11686 X	5.72(4.29- 7.23) X	0.20(0.09-0.33) X
2	3.5	C10 H15 O	.11229	.11570	.11848	11.32(9.50-13.14)	0.71(0.49-0.92)
Experimental Values:			.11225	.11581	.11934	11.98	0.91

Click

Toms River, NJ - Well Water Extract

This looks like a job for...



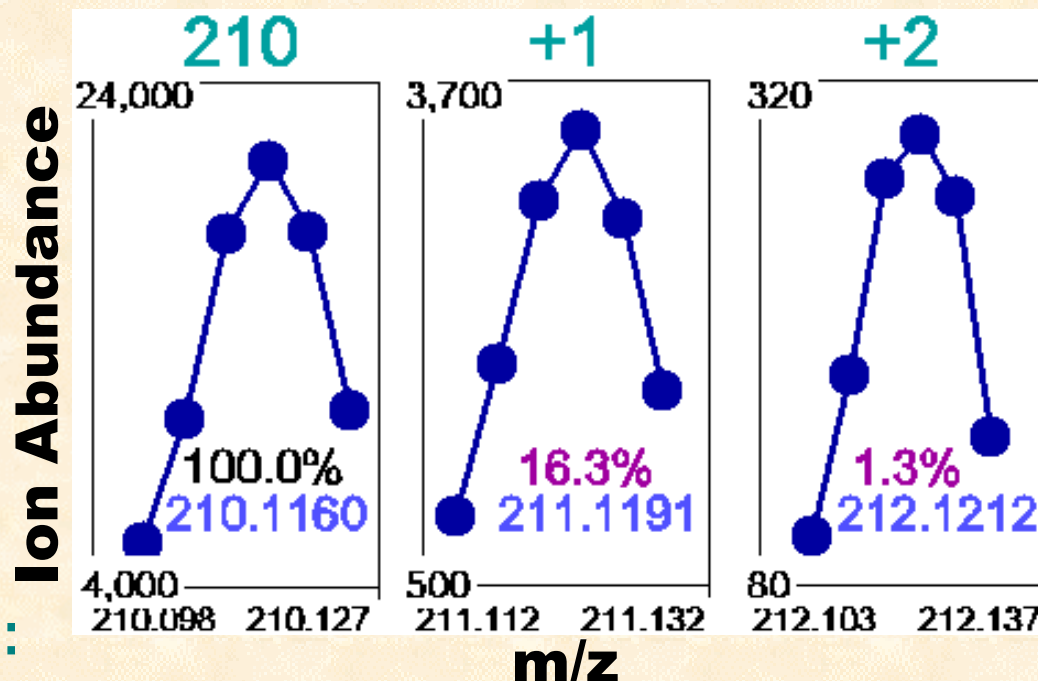
Not identified by conventional low or high resolution mass spectrometry

PGM:

Elements Considered:
C H N O F P S Si

m/z 210.1160 \pm 6 ppm
Resolution 10,000

Hypothetical Composition:



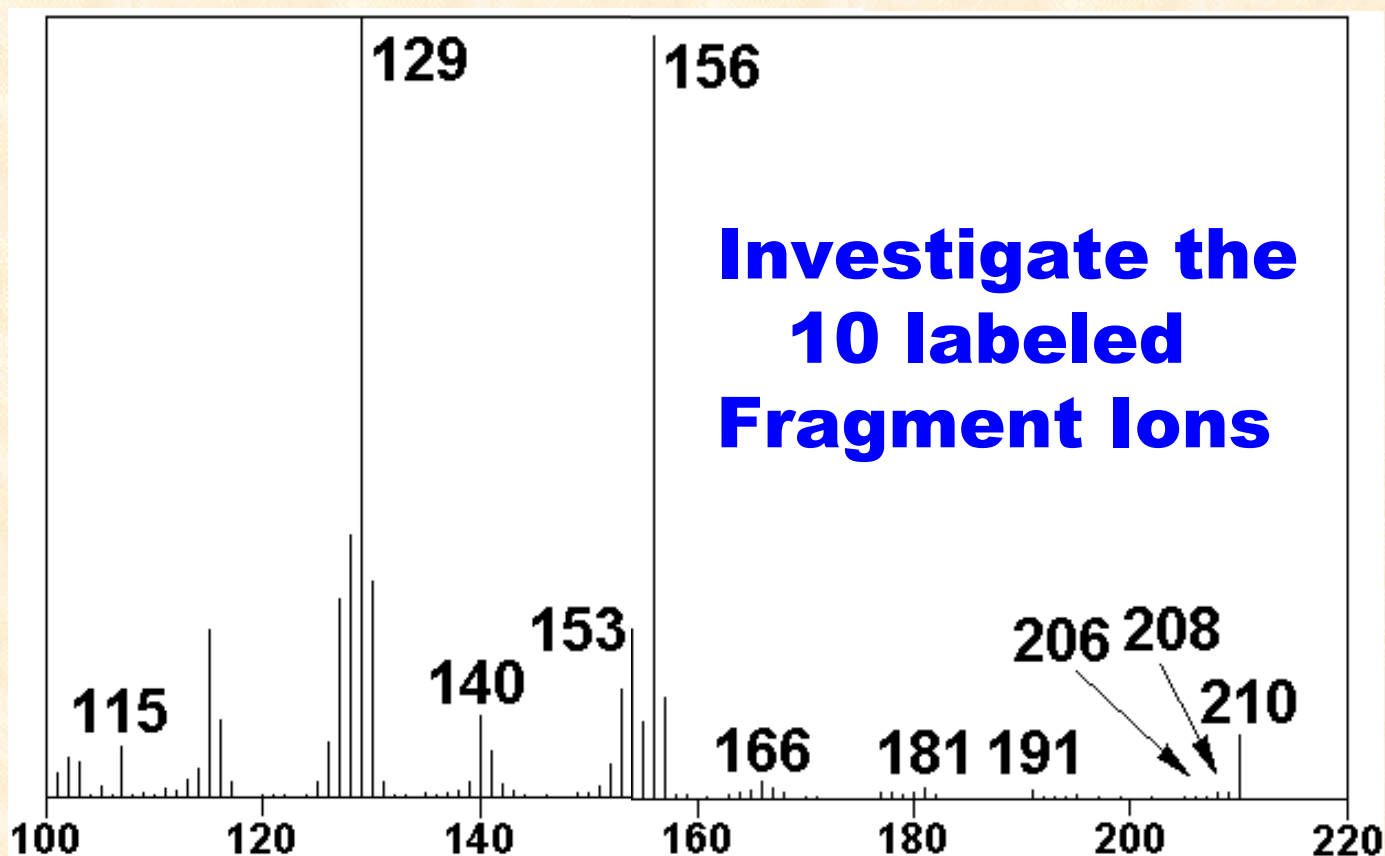
#	RDB Range	C ₁₄ H ₁₄ N ₂ Composition	Mass Defects			Relative Abundances	
			151	+1	+2	%+1(Range %+1)	%+2(Range %+2)
1	2.0	C₄H₁₂N₆F₂	.11530	.11638 X	.11697 X	5.08(3.39- 6.93) X	0.11(0.06-0.18) X
2	0.0 1.0	C₅H₁₆N₄O₃Si	.11482	.11598 X	.11286 X	7.95(5.15-10.84) X	0.32(0.03-0.76) X
3	1.0	C₅H₁₆N₆F₂	.11581	.11770 X	.11941 X	6.54(4.78- 8.40) X	0.21(0.14-0.28) X
4	0.0	C₆H₂₀N₄F₂	.11632	.11886	.12138	7.90(6.23- 9.66) X	0.28(0.22-0.34) X
5	0.0 1.0	C₆H₁₈N₄O₂S	.11505	.11731 X	.11148 X	7.87(6.16- 9.61) X	0.18(0.00-0.53) X
6	1.5	C₆H₁₄N₅O₂F₂	.11664	.11894	.12089	8.21(6.32-10.24) X	0.50(0.37-0.64) X
7	-0.5 0.5	C₇H₂₀N₆Si	.11616	.11805	.11476 X	12.39(9.21-15.67) X	1.01(0.34-2.03)
8	0.5	C₇H₁₈N₅O₂F₂	.11715	.11999	.12217	8.88(7.48-10.34) X	0.55(0.44-0.66) X
9	-0.5 1.5	C₈H₂₀N₆S	.11639	.11939	.11298 X	10.22(8.58-11.89) X	0.64(0.11-1.47)
10	5.5	C₉H₁₈N₅F₂	.11550	.11811	.12078	10.77(8.47-13.11) X	0.59(0.48-0.71) X
11	4.5	C₁₀H₁₇N₅F₂	.11601	.11899	.12210	12.02(10.17-13.90) X	0.65(0.51-0.81) X
12	5.0	C₁₁H₁₅N₂O₂F₂	.11684	.11998	.12266 X	12.88(11.06-14.74) X	0.92(0.71-1.12) X
13	9.0	C₁₄ H₁₄ N₂	.11570	.11888	.12203	16.22(13.91-18.57)	1.20(0.89-1.52)
Experimental Values:			.1160	.1191	.1212	16.3	1.3

Click

Limiting Possible Compounds

The number of possible compounds was greatly reduced, but further reduction is required.

Determine fragment ion compositions from full profiles with 10,000 resolution – 0-14 C, 0-14 H, and 0-2 N are the elemental limits.





Exact Masses Determined for 10 Fragment Ions from the Isomers

Experimental Mass	0 N	Error (mmu)	1 N	Error (mmu)	2 N	Error (mmu)
208.1001					C₁₄H₁₂N₂	+0.1
206.0846					C₁₄H₁₀N₂	+0.2
191.0607			C ₁₄ H ₉ N	- 12.8	C₁₃H₇N₂	- 0.2
181.0887	C₁₄H₁₃	-12.6	C₁₃H₁₁N	- 0.4	C₁₂H₉N₂	+12.5
166.0661	C ₁₃ H ₁₀	-12.2	C₁₂H₈N	+0.4	C ₁₁ H ₆ N ₂	+13.0
156.0816	C ₁₂ H ₁₂	-12.3	C₁₁H₁₀N	+0.3	C ₁₀ H ₈ N ₂	+12.9
153.0578	C ₁₂ H ₉	-12.6	C₁₁H₇N	0.0	C ₁₀ H ₅ N ₂	+12.5
140.0501	C ₁₁ H ₈	-12.5	C₁₀H₆N	+0.1	C ₉ H ₄ N ₂	+12.7
129.0707	C₁₀H₉	+0.3	C ₉ H ₇ N	+12.9	C ₈ H ₅ N ₂	+25.4
115.0548	C₉H₇	0.0	C ₈ H ₅ N	+12.6	C ₇ H ₃ N ₂	+25.2

ICE is Nice A.H. Grange ORD, NERL, ESD, ECB

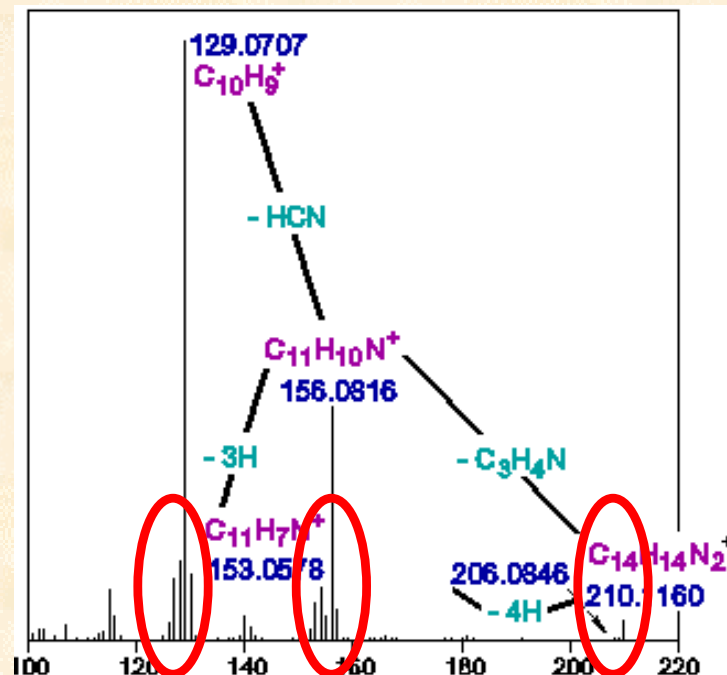
Exact Masses of Composite Neutral Losses Determined as the Mass Differences Between the Molecular and Fragment Ions

Experimental Mass	0 N	Error (mmu)	1 N	Error (mmu)	2 N	Error (mmu)
2.0159	H₂	+0.2				
4.0314	H₄	+0.1				
19.0553	CH₇	+0.5	NH ₅	+13.1		
29.0273	C ₂ H ₅	- 11.8	CH₃N	+0.8	N ₂ H	+13.3
44.0499	C ₃ H ₈	- 12.7	C₂H₆N	- 0.1	CH ₄ N ₂	+12.5
54.0344	C ₄ H ₆	- 12.6	C₃H₄N	0.0	C ₂ H ₂ N ₂	+12.6
57.0582	C ₄ H ₉	- 12.2	C₃H₇N	+0.4	C ₂ H ₅ N ₂	+12.9
70.0659	C ₅ H ₁₀	- 12.4	C₄H₈N	+0.2	C ₃ H ₆ N ₂	+12.8
81.0453	C ₆ H ₉	- 25.1	C ₅ H ₇ N	- 25.1	C₄H₅N₂	0.0
95.0612	C ₇ H ₁₁	- 24.9	C ₆ H ₉ N	- 24.9	C₅H₇N₂	+0.3

A limited number of possible isomers

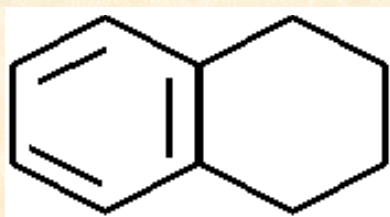
A core portion loses several H atoms

C₁₀H₉ is characteristic of Tetralin, which loses multiple H atoms to increase aromaticity

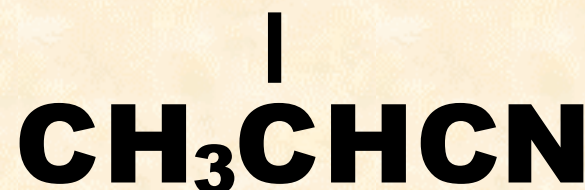


Two N atoms are external to the rings
Two CN groups account for 4 RDB

Possible isomers contain:



Tetralin

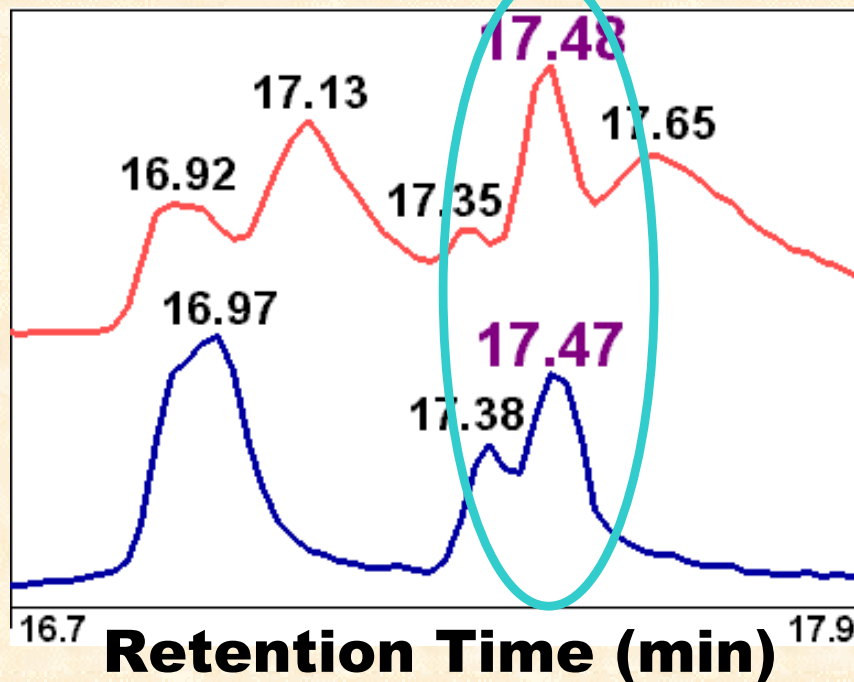


OR

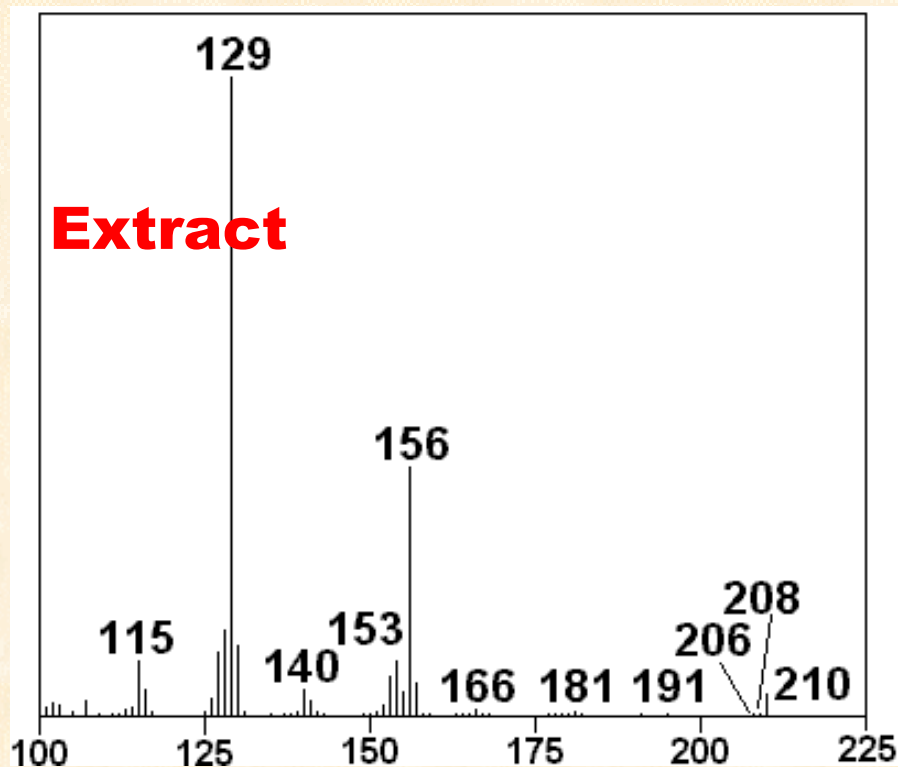


Confirmation

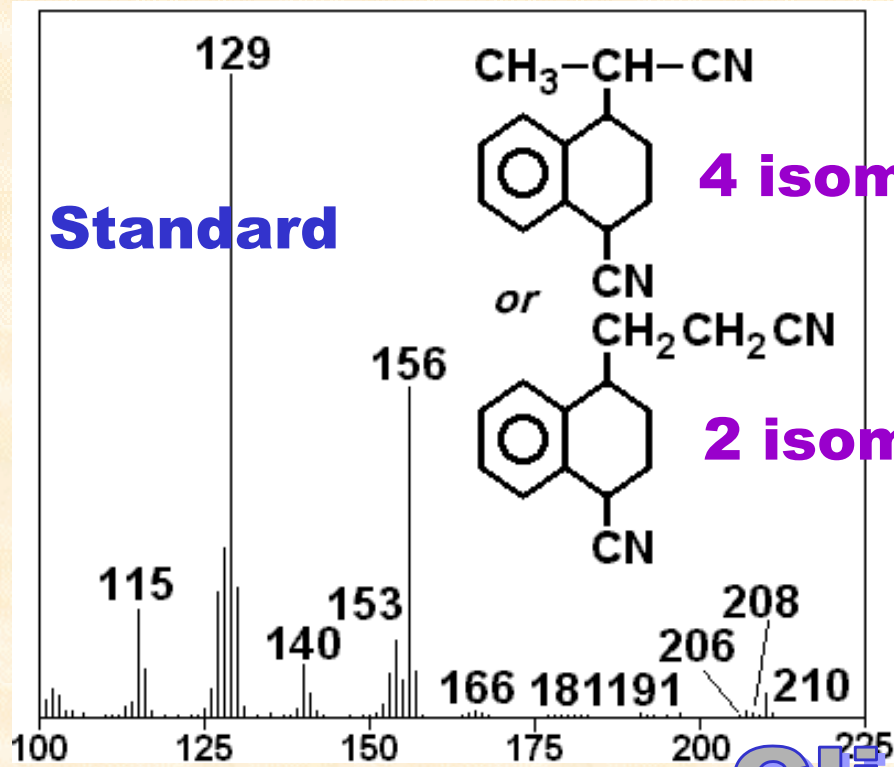
Ion Abundance



Ion Abundance



Standard



m/z

Click

Legal Proceedings

**Compound Identification is
1 link in the chain of evidence**

ICE provides a Preponderance of Evidence:

**Exacts masses of molecular and fragment ions
Exact masses, relative abundances, and shapes
of +1 and +2 profiles**

**Rejection of all but one composition for each ion
Tables of fragment ion and composite
neutral loss compositions**

Logical fragmentation pattern

**Superimposed ion chromatograms obtained
with high mass resolution**

**Opposing Council – Attack a Weaker Link,
e.g. the Transport Model**

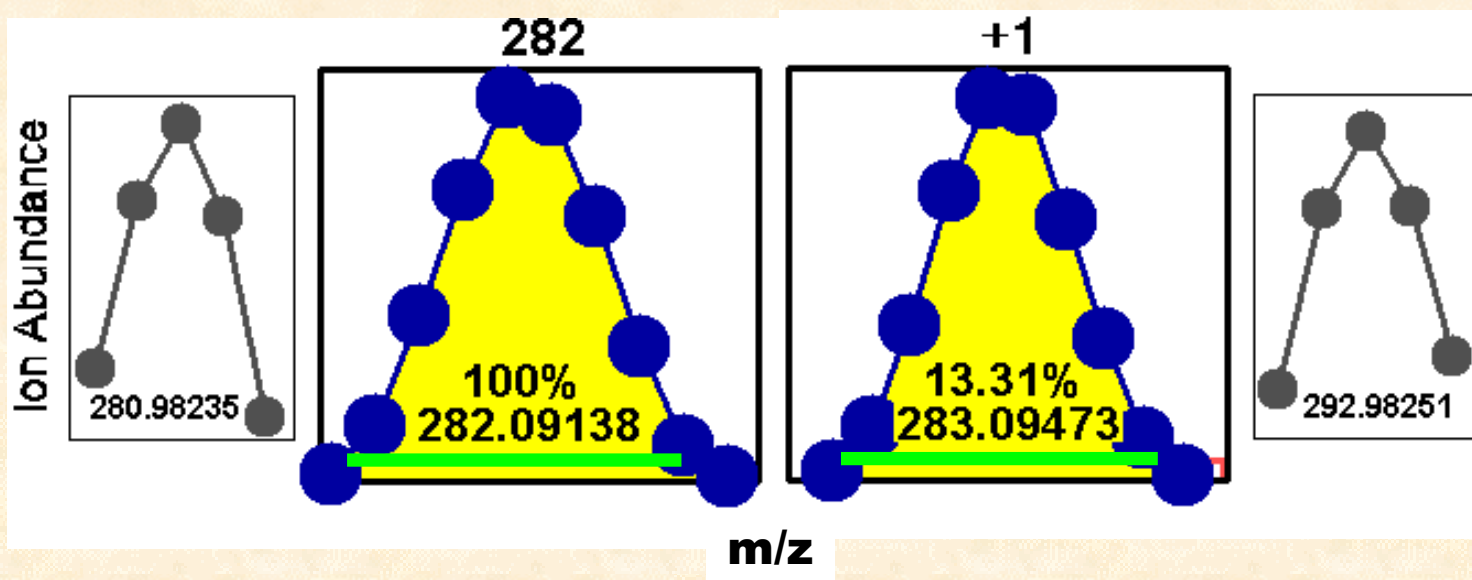
Simplicity

Errors:

Variation in Isotopic Abundances
Instrumental Precision

Partial Profile Errors:

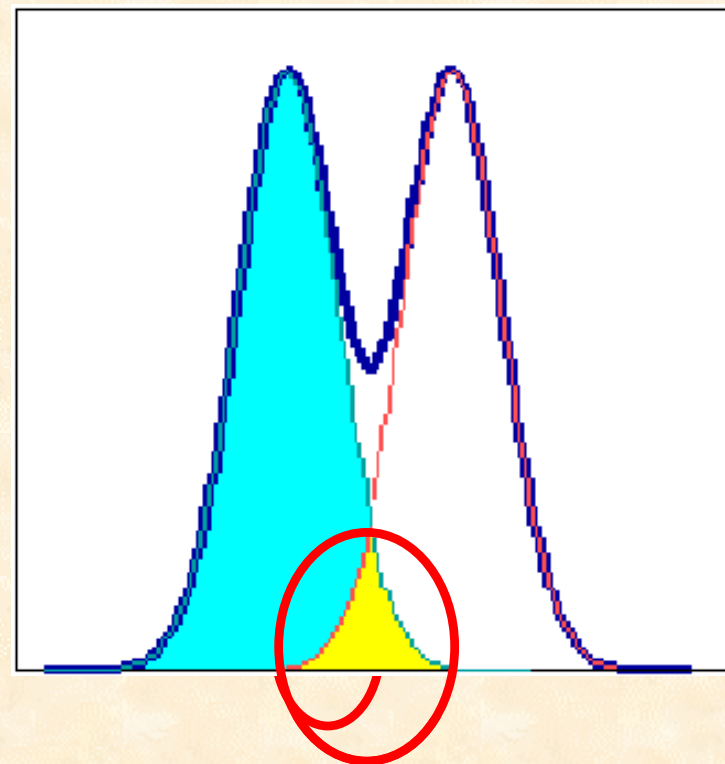
Center Mass Offsets for Other Compositions
Up to 1 mass increment experimental offsets
Up to 10% mass resolution error



Partial or Full Profiles?

Partial profile advantages:

- ★ **Five measurements –
3 exact masses &
2 relative abundances**
- ★ **Less profile overlap
with interferences**

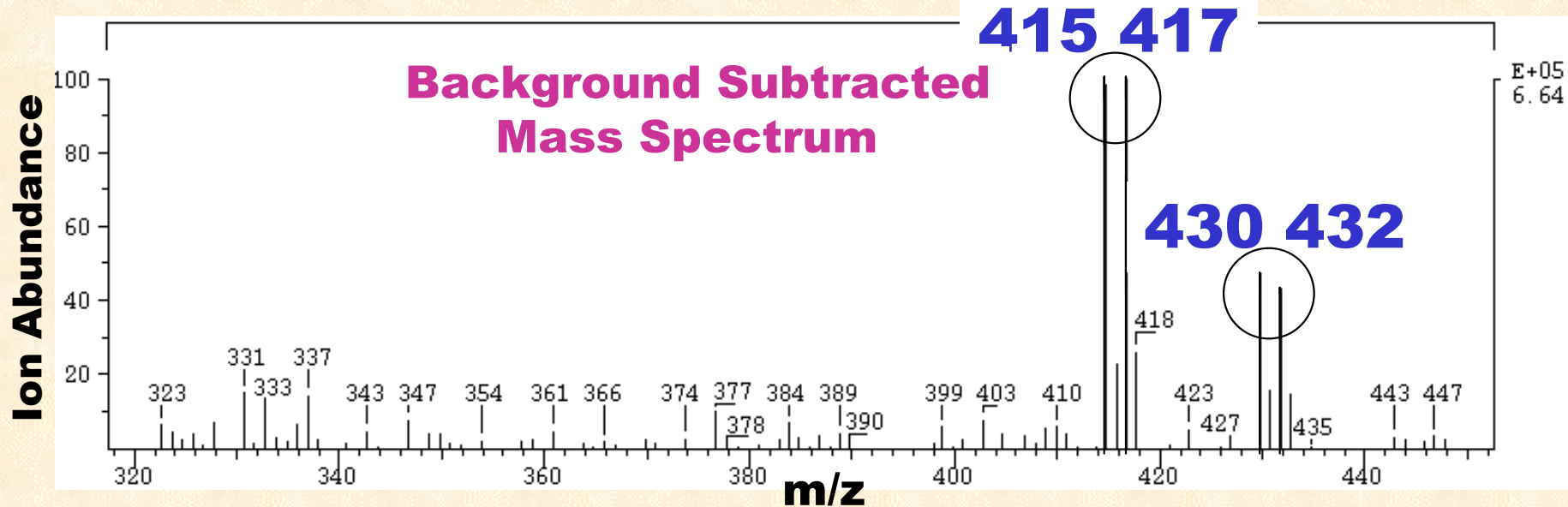


Full profile advantages:

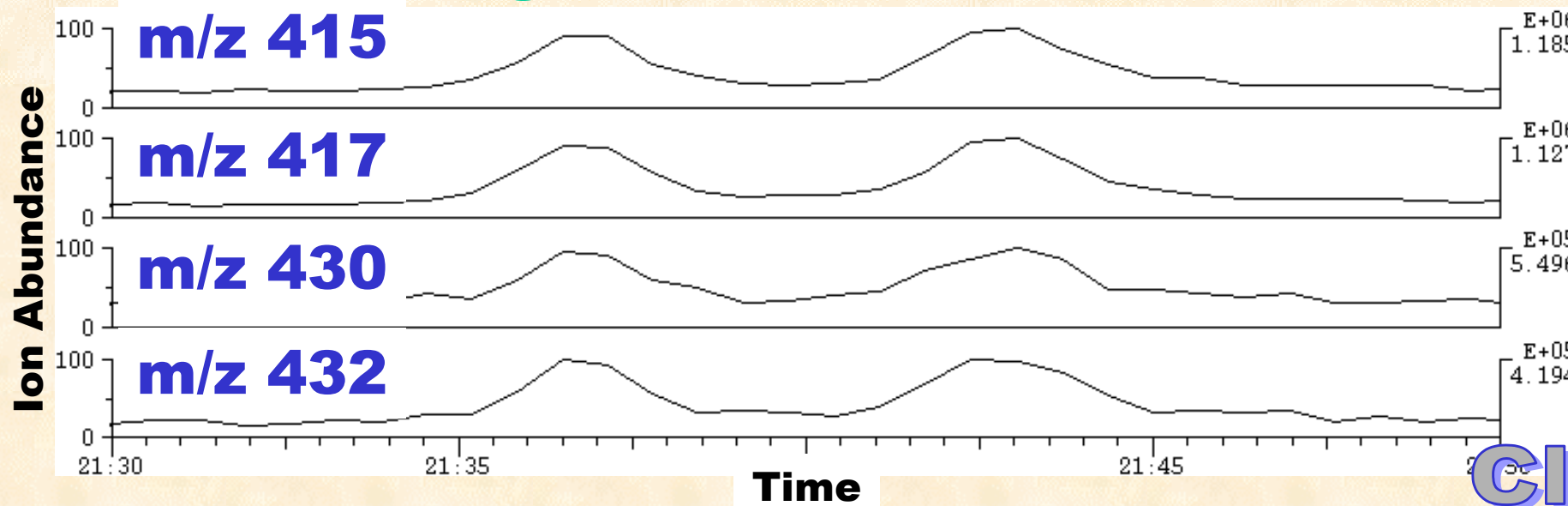
- ★ **Fewer errors –
narrower relative abundance ranges**
- ★ **Simpler to explain in legal proceedings**

Utility of Limited ICE Information

Extract of chlorine-disinfected drinking water



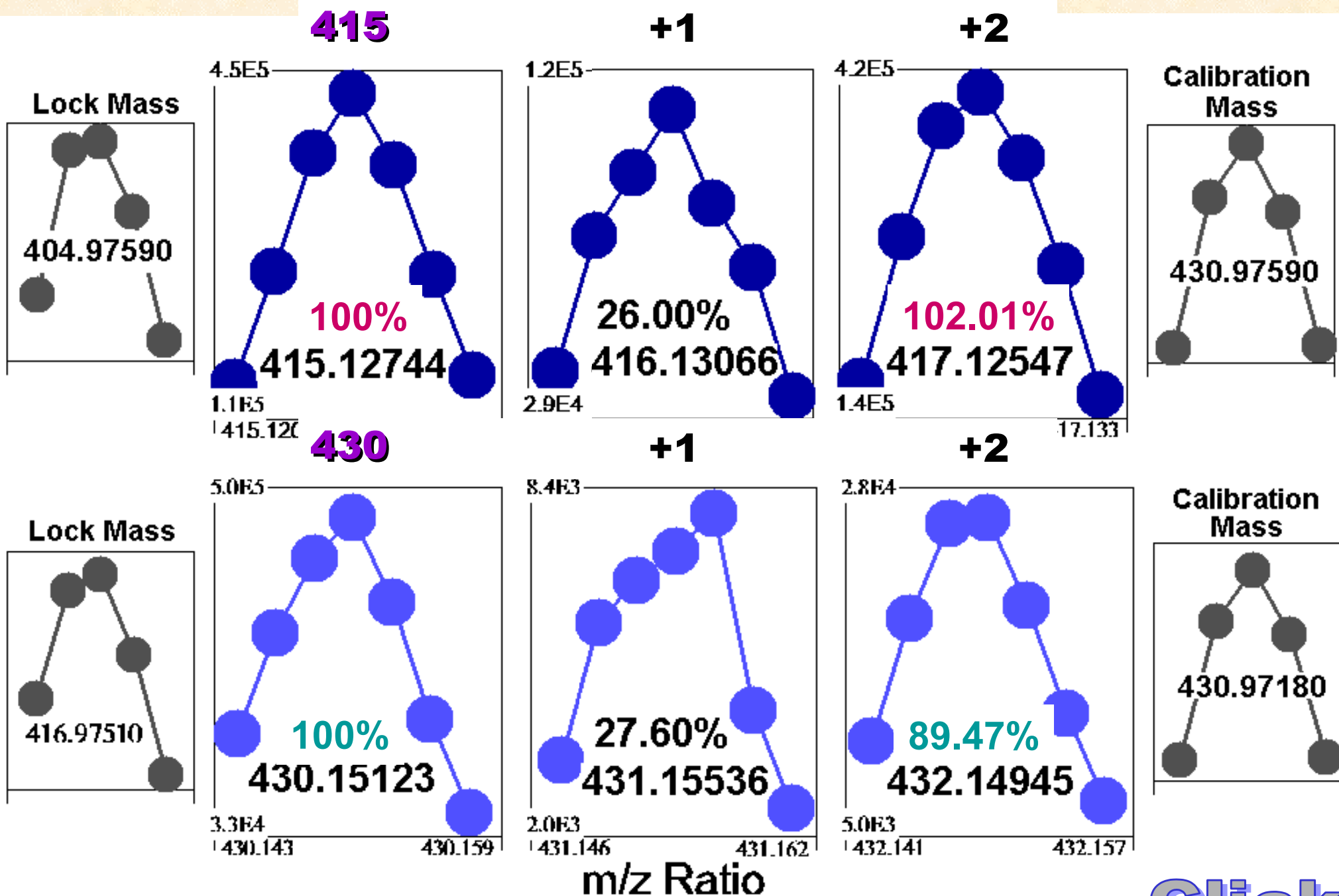
Ion Chromatograms



Click

Partial Profiles for m/z 415 Fragment Ion and m/z 430 Molecular Ion

Ion Abundance





m/z = 415.12744 ± 3 ppm

Elements: C H N O F P S Cl Br

ICE is Nice

A.H. Grange

ORD, NERL, ESD, ECB

Resolution: 20000

#	ROB Range	Composition	415	+1	+2	%+1 (Range +1)	%+2 (Range+2)
1	4.5	C19 H25 F5 S CL	.12857	.13184	.12561	22.11 (19.03-25.22)	37.71 (28.31- 48.09)
2	5.5	C19 H22 O F6 CL	.12634	.12974	.12358	21.70 (18.25-25.22)	32.27 (25.25- 40.01)
3	6.5 7.5	C19 H31 O2 P4	.12745	.13087	.13391	21.58 (18.12-25.05)	1.01 (0.24- 1.98)
4	5.0 6.0	C19 H31 N O2 P BR	.12758	.13092	.12567	21.79 (18.26-25.33)	98.23 (85.51-111.10)
5	8.0 9.0	C19 H25 N O3 F2 P2	.12777	.13110	.13393	21.79 (18.74-24.87)	1.11 (0.29- 2.13)
6	8.0 10.0	C19 H23 N O5 F2 S	.12650	.12971	.12559	22.52 (19.32-25.78)	5.83 (4.62- 7.36)
7	7.5	C19 H27 N2 O F P2 CL	.12712	.13037	.12438	21.98 (18.87-25.15)	32.63 (25.51- 40.49)
8	6.5 8.5	C19 H28 N2 O2 S2 CL	.12807	.13109	.12504	23.47 (19.74-27.26)	42.11 (31.83- 53.28)
9	9.5 11.5	C19 H19 N2 O4 F4	.12810	.13134	.13399	21.95 (18.86-25.09)	1.23 (0.36- 2.29)
10	9.0 10.0	C19 H21 N3 O2 F3 CL	.12744	.13060	.12473	22.14 (18.99-25.37)	32.73 (24.87- 41.33)
11	8.5	C19 H23 N4 F2 CL2	.12678	.12987	.12403	22.37 (19.14-25.71)	63.74 (48.92- 79.67)
12	12.5	C19 H21 N6 F P S	.12701	.12983	.12496	23.35 (19.78-27.01)	5.52 (4.58- 6.70)
13	12.5 13.5	C19 H20 N6 O3 CL	.12854	.13148	.12588	23.03 (19.47-26.71)	33.89 (25.77- 42.90)

43	12.5	C24 H22 O2 F2 CL	.12764	.13103	.12512	27.01 (22.68-31.34)	33.14 (26.27- 40.93)
44	12.0	C24 H24 N F CL2	.12698	.13031	.12413	27.24 (23.44-31.07)	64.12 (48.92- 80.59)
45	16.0	C24 H22 N3 P S	.12721	.13031	.12683	28.32 (24.28-32.47)	5.84 (4.55- 7.51)
46	16.5 17.5	C25 H20 N2 O F S	.12804	.13121	.12849	29.19 (25.06-33.37)	5.80 (4.53- 7.48)
47	15.5 16.5	C26 H24 O P S	.12855	.13185	.12975	29.92 (25.76-34.10)	5.76 (4.63- 7.27)
48	16.5 17.5	C26 H21 O2 F P	.12632	.12971	.13288	29.59 (24.89-34.39)	2.14 (0.59- 4.11)
49	16.5	C27 H21 O F CL	.12650	.12988	.12389	30.35 (26.16-34.55)	32.78 (25.22- 41.25)
50	20.5	C28 H19 N2 S	.12689	.13008	.12888	32.50 (27.91-37.17)	6.34 (4.71- 8.44)
16	5.5	C20 H29 O3 F BR	.12841	.13182	.12652	22.51 (18.86-26.12)	97.84 (85.25-110.56)
39	9.5	C23 H28 O2 BR	.12727	.13067	.12541	26.04 (22.43-29.65)	98.59 (86.48-110.97)

Experimental Values: .12744 .13066 .12547 26.00 102.01

m/z = 430.15123 ± 3 ppm

Elements: C H N O F P S Cl Br

Resolution: 20000

31	5.0	C21 H32 O3 F BR	.15188	.15530	.15001	24.11 (19.75-28.57)	98.91 (86.86-111.21)
54	9.0	C24 H31 O2 BR	.15074	.15415	.14891	26.73 (21.79-31.62)	98.66 (86.59-111.01)

Experimental Values: .15123 .15536 .14945 27.60 89.47

PGM:

430.15123

- 415.12744

15.02379

15.02348

CH₃

Click

ICE Utilizes:

Reject incorrect compositions mechanically:

Sums of Atomic Masses

Sums of Isotopic Abundances

Valences of Elements

**For multiple remaining compositions, invoke
chemical and commercial arguments**

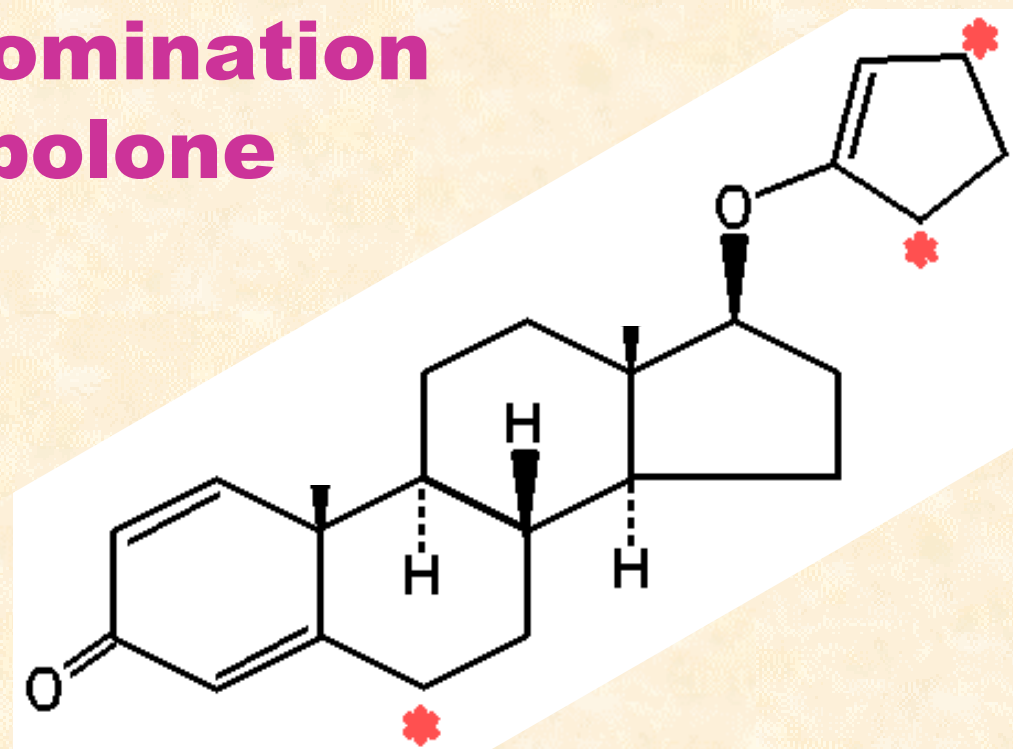
Commercial argument:

**Anabolic steroids could be used to enhance
cattle growth in a nearby feedlot.**

* Possible Allylic Bromination Sites for Quinbolone

Multiple Isomers

Next Steps:



Purchase Quinbolone

Add to well water

Chlorinate

Extract products

Obtain mass spectra and retention times
for comparison



Click

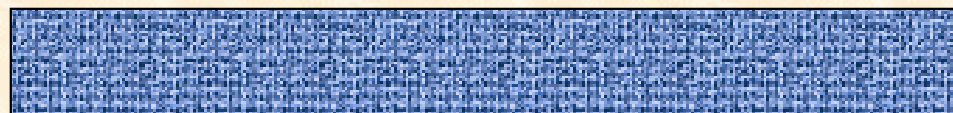
Characterization or Identification

Analysis & Data

Number of Possible Compositions

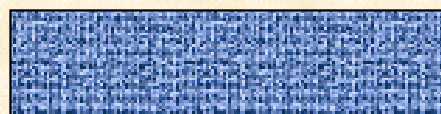
Low Resolution MS

Nominal Mass and
No Library Matches



Conventional High Res MS

Exact Mass of
Apparent Molecular Ion



ICE

Ion Composition of
Apparent Molecular Ion



Ion Composition of
Multiple Fragment Ions



Characterization

Identification

Chemical Literature
Commercial Literature



**Single
Compound**
Click

Selected ICE Publications and Posters

Grange, A.H.; Donnelly, J.R.; Brumley, W.C.; Billets, S.; Sovocool, G.W.
*Mass Measurement by an Accurate and Sensitive
Selected-Ion-Recording Technique*
Anal. Chem., 1994, 66, 4416-4421

Grange, A.H.; Donnelly, J.R.; Brumley, W.C.; Sovocool, G.W.
*Determination of Elemental Compositions from Mass Peak
Profiles of the Molecular (M), M+1 and M+2 Ions*
Anal. Chem., 1996, 553-560

Grange, A.H.; Brumley, W.C.
*A Mass Peak Profile Generation Model to Facilitate Determination
of Elemental Compositions of Ions Based on Exact Masses and
Isotopic Abundances*
J. Amer. Soc. for Mass Spectrum., 1997, 8, 170-182

Grange, A.H.; Sovocool, G.W.; Donnelly, J.R.; Genicola, F.A.; Gurka, D.F.
*Identification of Pollutants in a Municipal Well Using
High Resolution Mass Spectrometry*
Rapid Commun. Mass Spectrom., 1998, 12, 1161-1169

6 Posters - <http://www.epa.gov/crdlvweb/chemistry/ecb-posters.htm>

The End