Mass Accuracy and Mass Resolution in TOF MS

October 2011

What will we discuss?

- What is mass resolution and mass accuracy
- Why and when they are important
- How to use resolution and mass accuracy for practical analysis

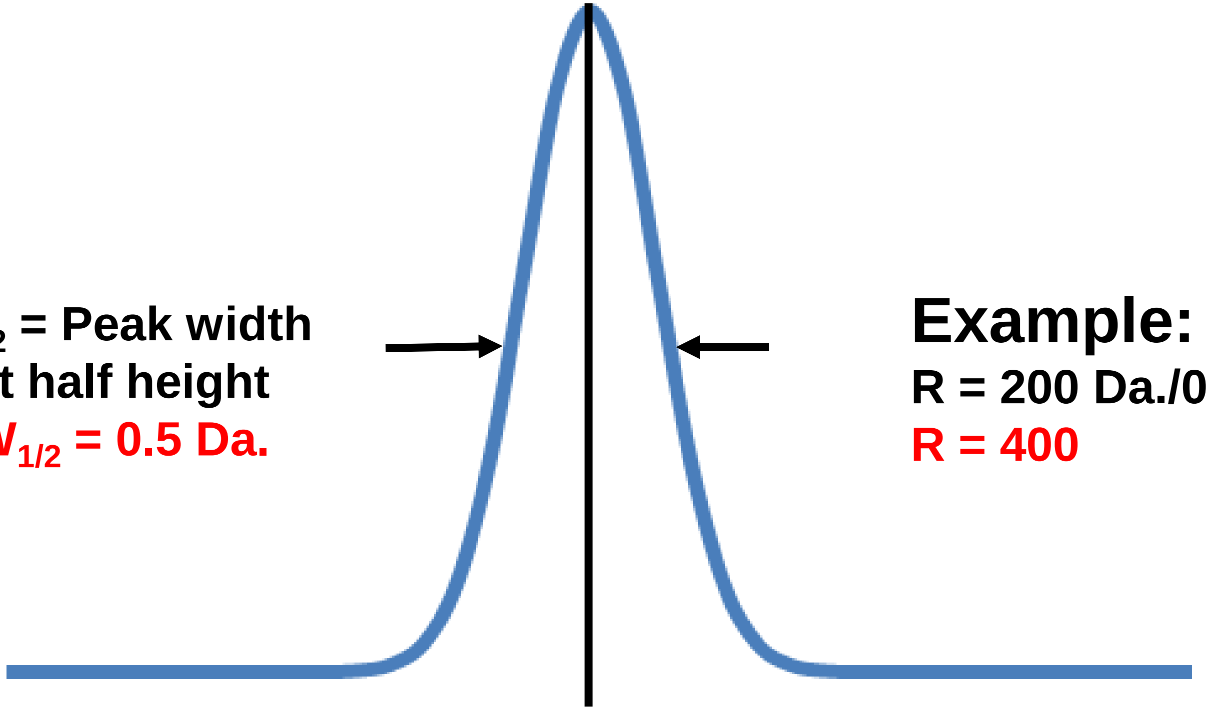
Mass resolution

What is it?

Definition:

Mass resolution = (ion mass)/(mass peak width)

$R = (m/z) / W_{1/2}$



$W_{1/2}$ = Peak width at half height

$W_{1/2} = 0.5$ Da.

Example:

R = 200 Da./0.5 Da.

R = 400

m/z = 200 Da.

Mass resolution

Older definition – peaks of equal heights

Definition:

Mass resolution = (ion mass)/(mass peak separation)

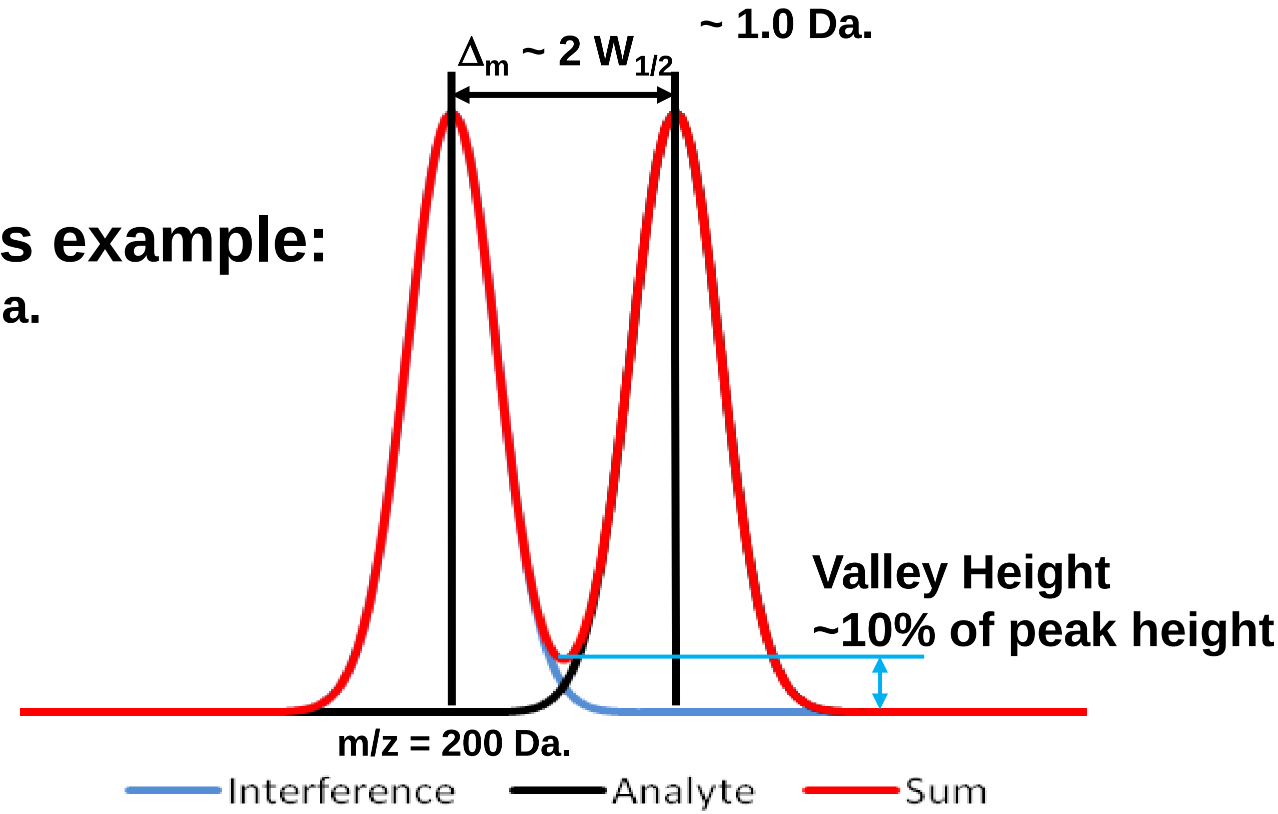
$$R = (m/z) / \Delta_m$$

From previous example:

$R = 200$ Da. / 1.0 Da.

$R_{10\%} = 200$

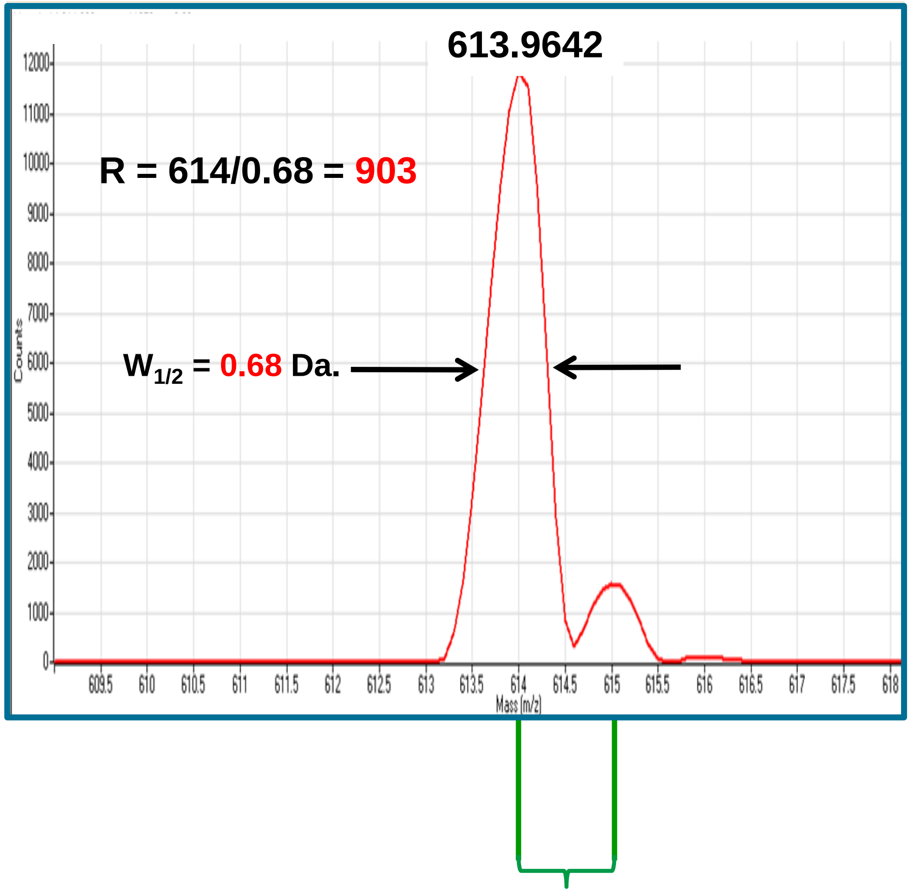
$R_{W1/2} = 400$



Resolving power & mass accuracy

m/z = 613.964203

SQ, TQ, IT



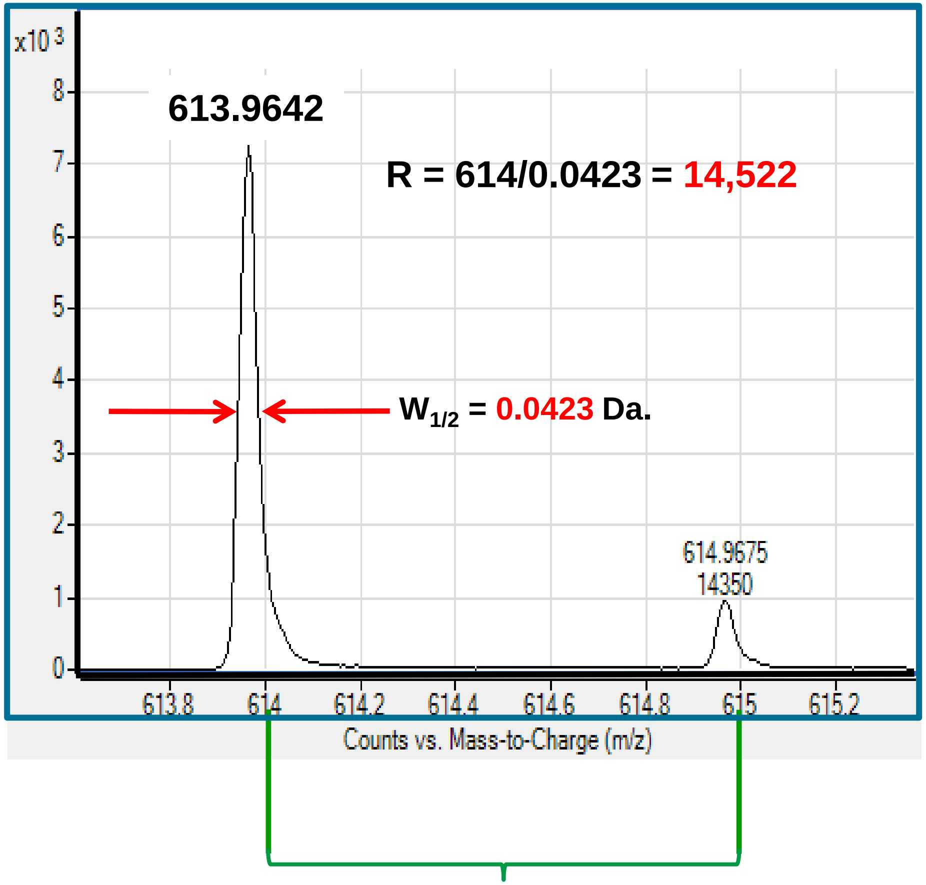
613.9642

R = 614/0.68 = 903

$W_{1/2}$ = 0.68 Da.

1 Da.

TOF, Q-TOF



613.9642

R = 614/0.0423 = 14,522

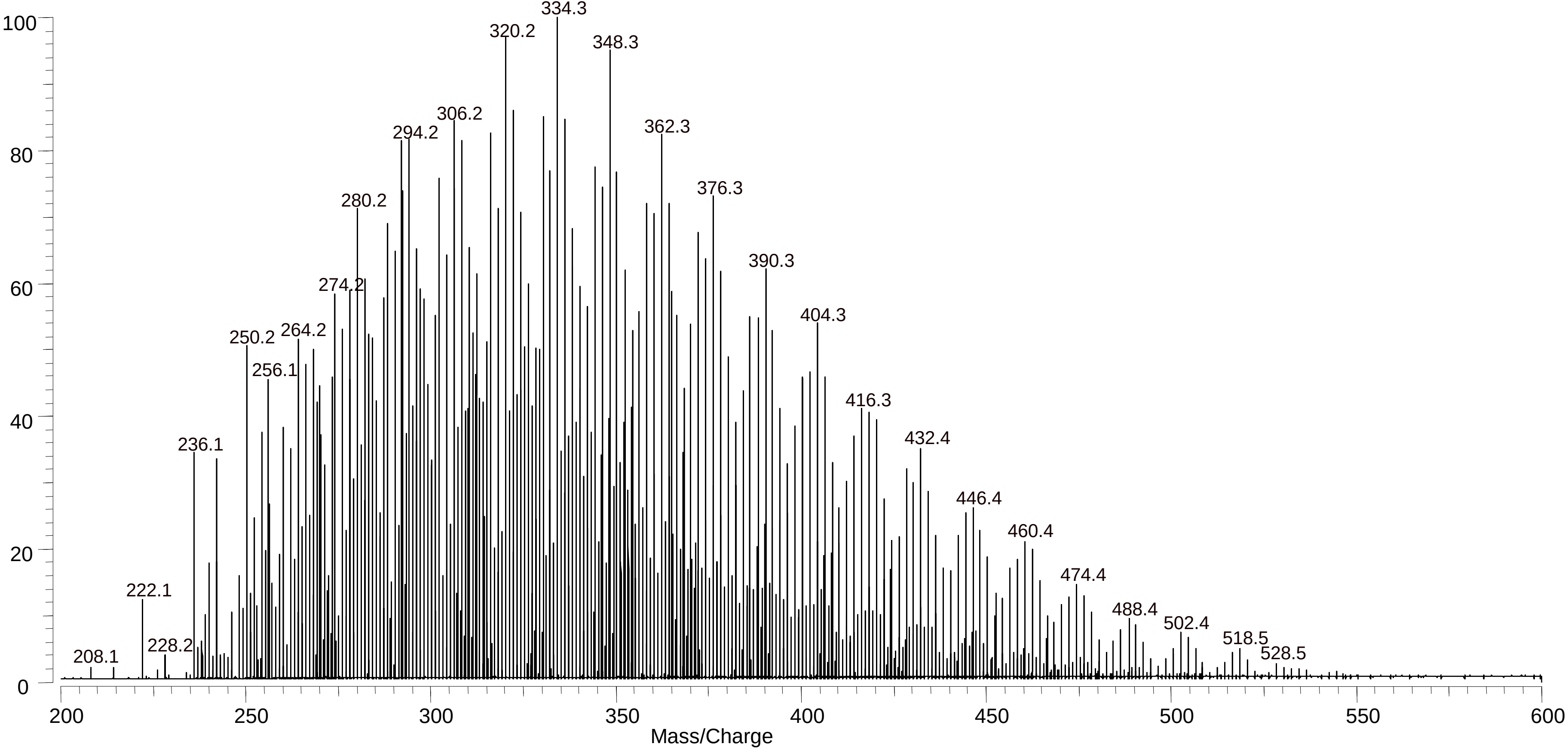
$W_{1/2}$ = 0.0423 Da.

1 Da.

Why is resolution important?

Complex sample or matrix

Crude Oil
FTMS

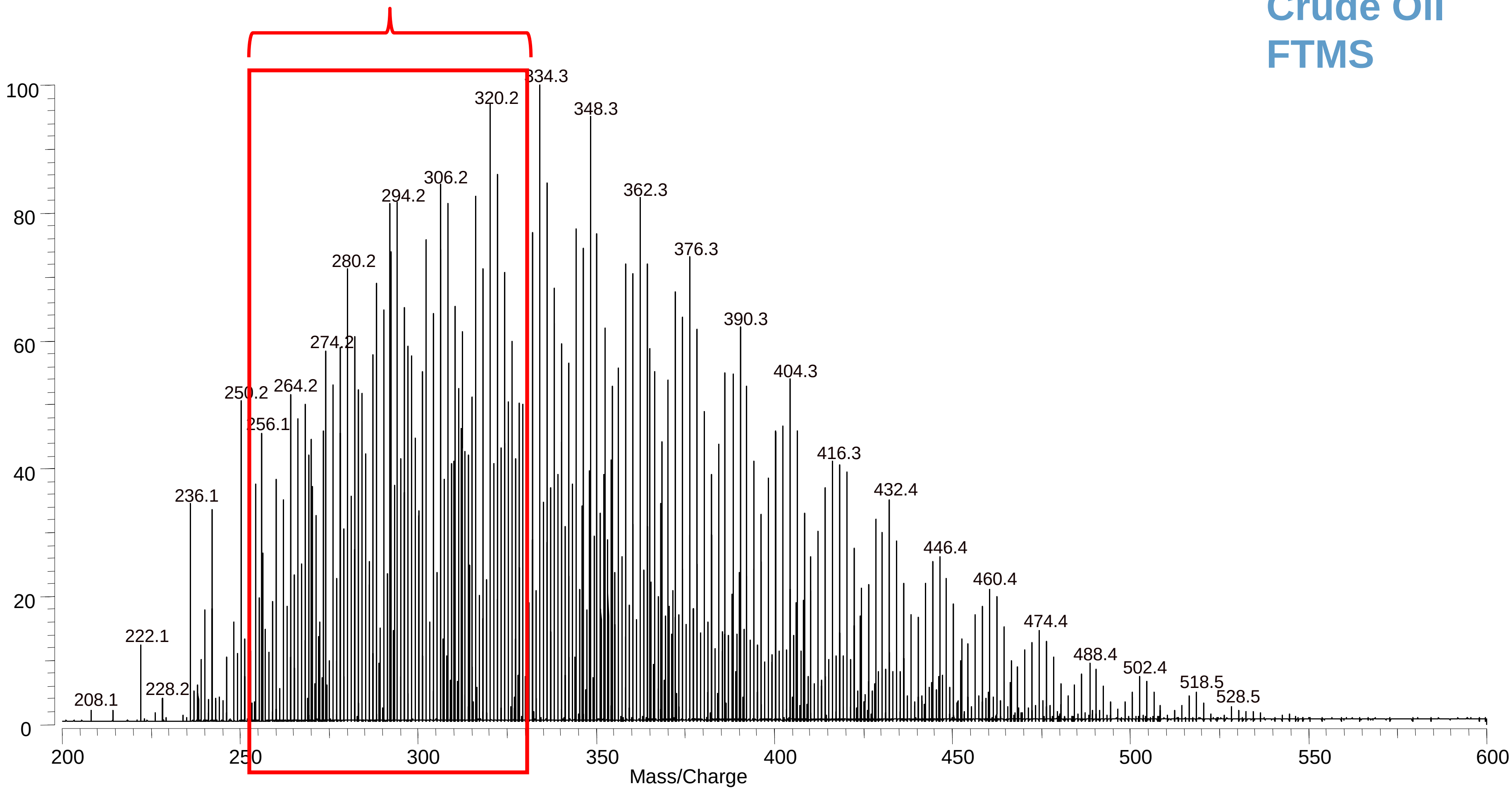


Why is resolution important?

Complex sample or matrix – take a closer look

***m/z* 200 - 600** **m/z = 250 - 325**

Crude Oil
FTMS



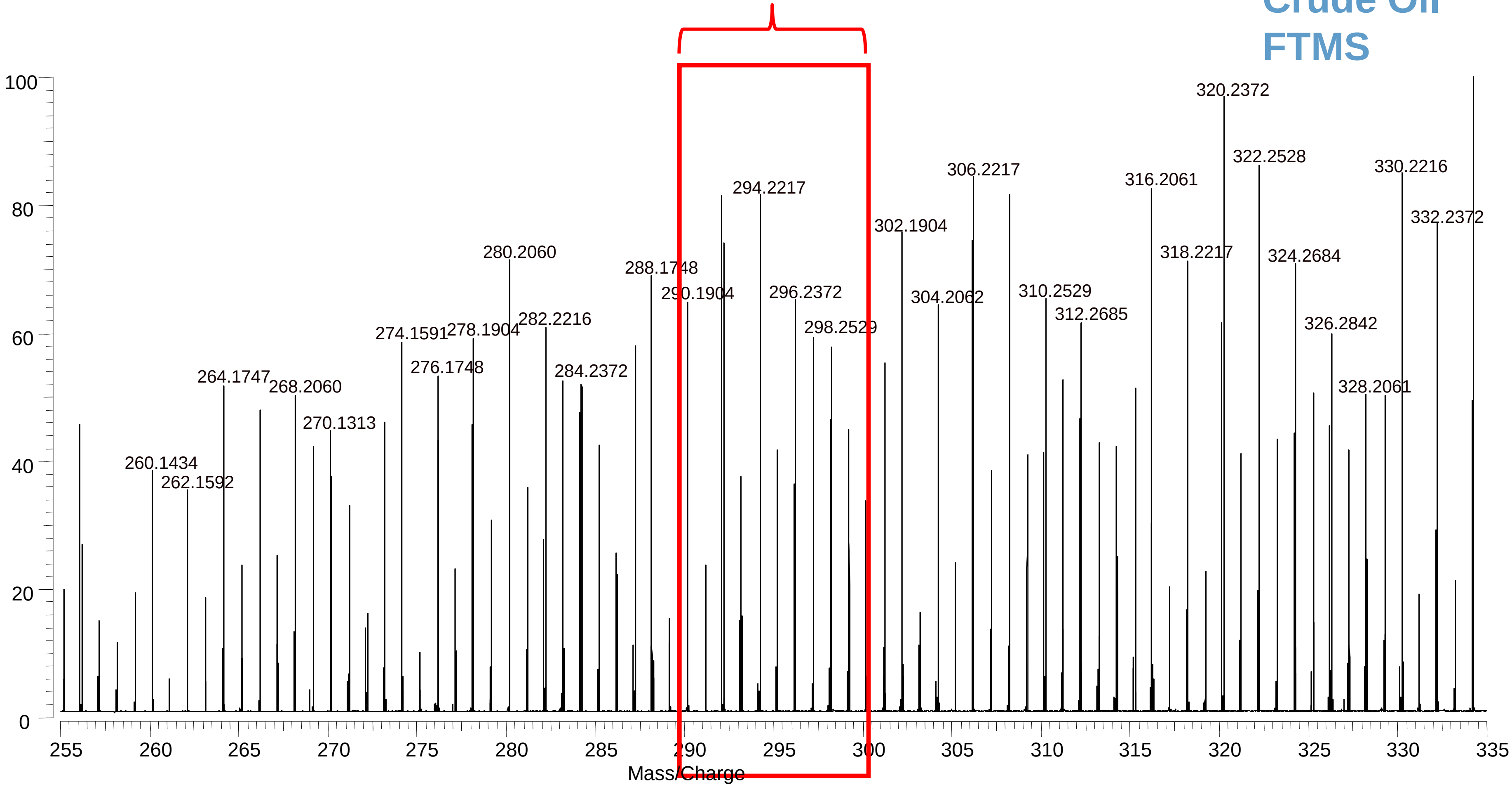
Why is resolution important?

Complex sample or matrix – take a closer look

5X zoom → *m/z* 255 - 335

m/z = 290 - 300

Crude Oil FTMS



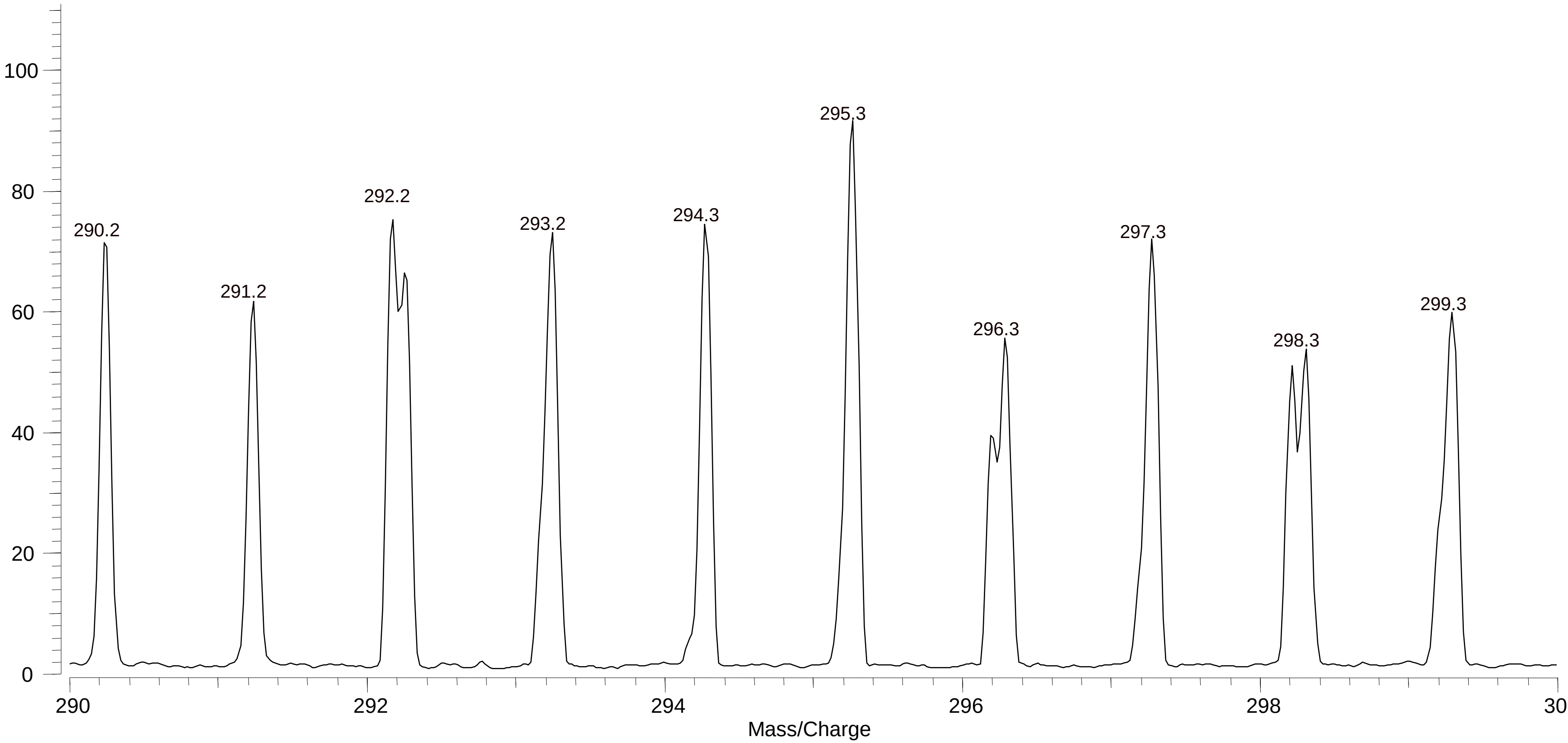
Why is resolution important?

Complex sample or matrix – take a closer look

40X zoom → *m/z* 290 - 300

Resolution → 5000

Crude Oil FTMS



Why is resolution important?

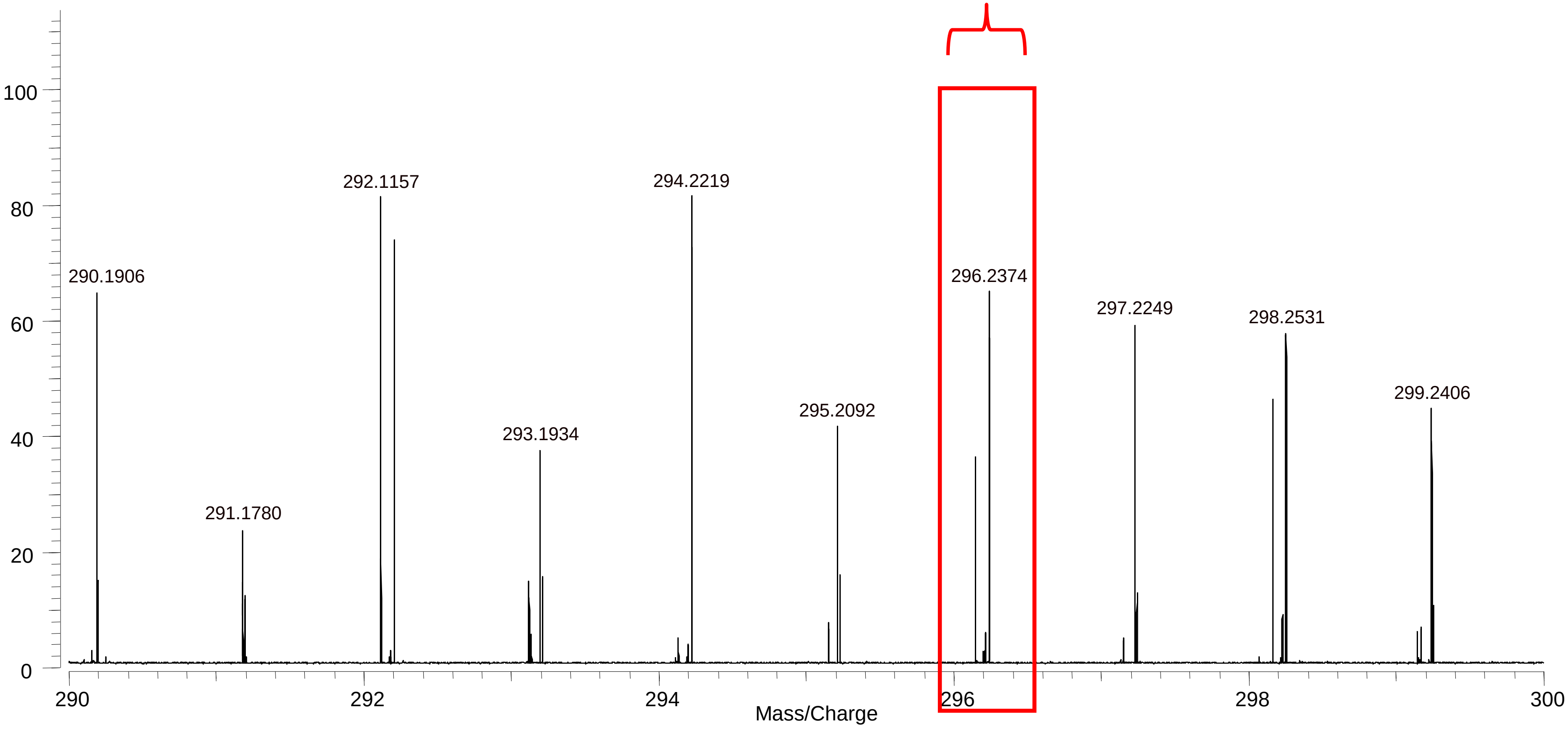
Complex sample or matrix – take a closer look

40X zoom → *m/z* 290 - 300

Resolution → 237,000

Crude Oil
FTMS

m/z = 296.14 - 296.24



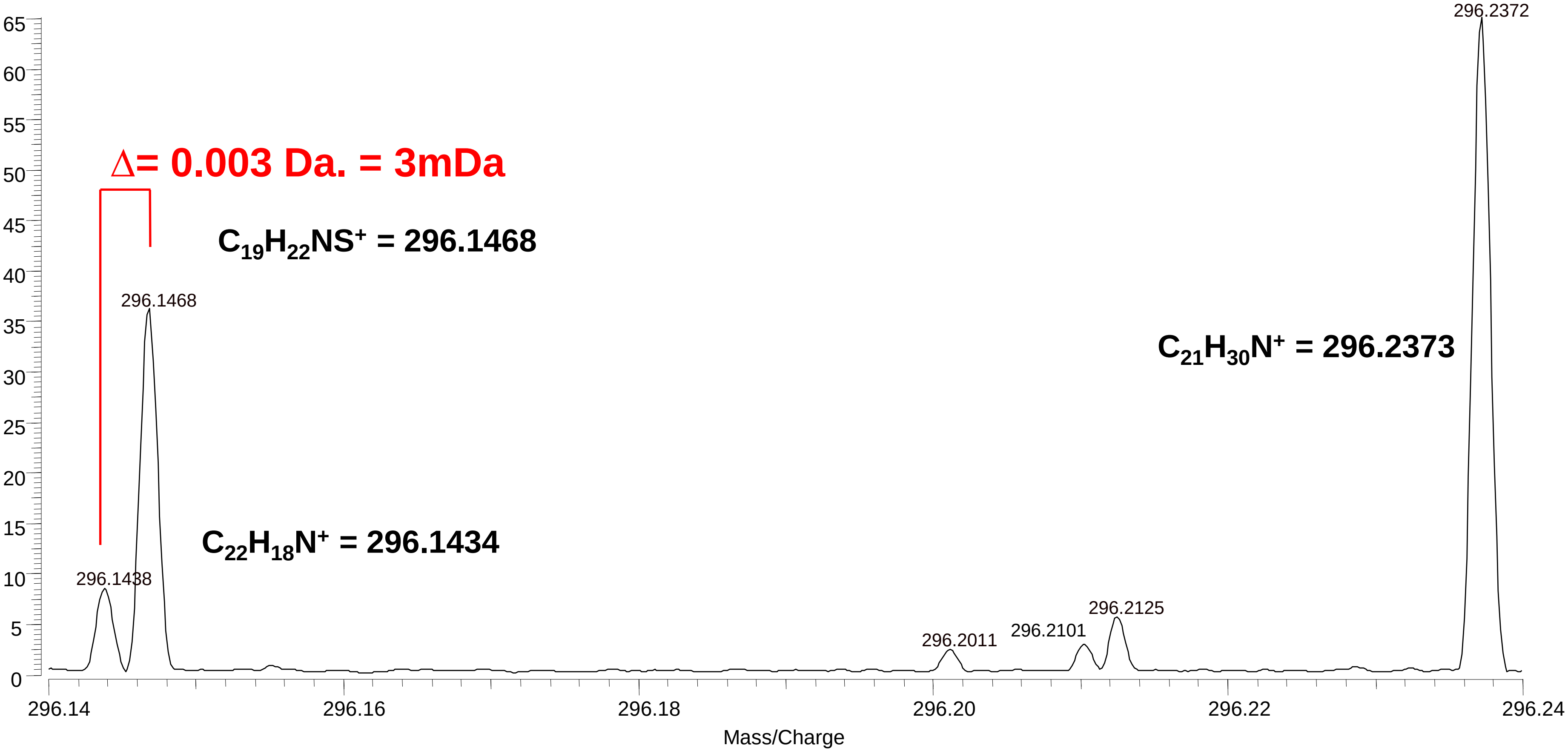
Why is resolution important?

Complex sample or matrix – take a closer look

4000X zoom → *m/z* 295.14 - 295.24

Resolution → 237,000

Crude Oil
FTMS



Δ= 0.003 Da. = 3mDa

$C_{19}H_{22}NS^+$ = 296.1468

$C_{22}H_{18}N^+$ = 296.1434

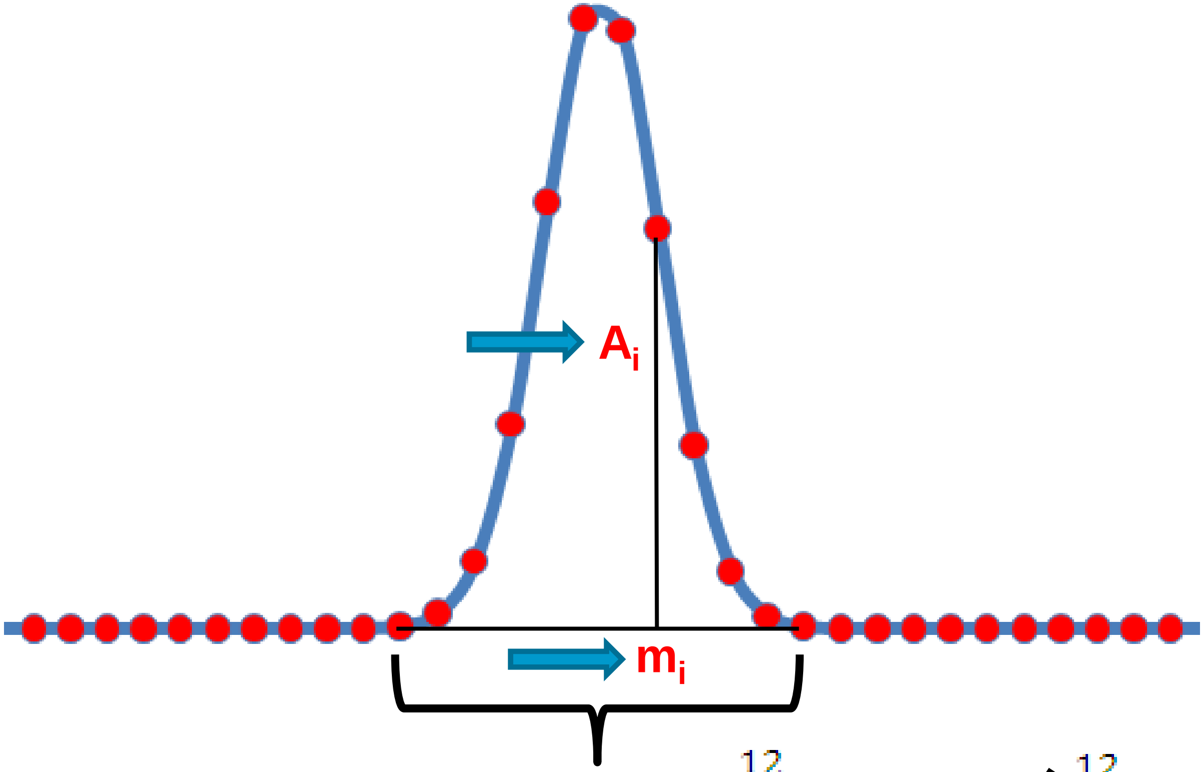
$C_{21}H_{30}N^+$ = 296.2373

How much resolution is required?

- The resolution required to solve a given analytical problem depends on the sample and matrix
- Sample preparation reduces potential chemical interferences and therefore the resolution requirements
- Most applications require a resolution of 10,000
- For some sample/matrix combinations however, there may never be enough resolution

How the mass determined - mass centroid

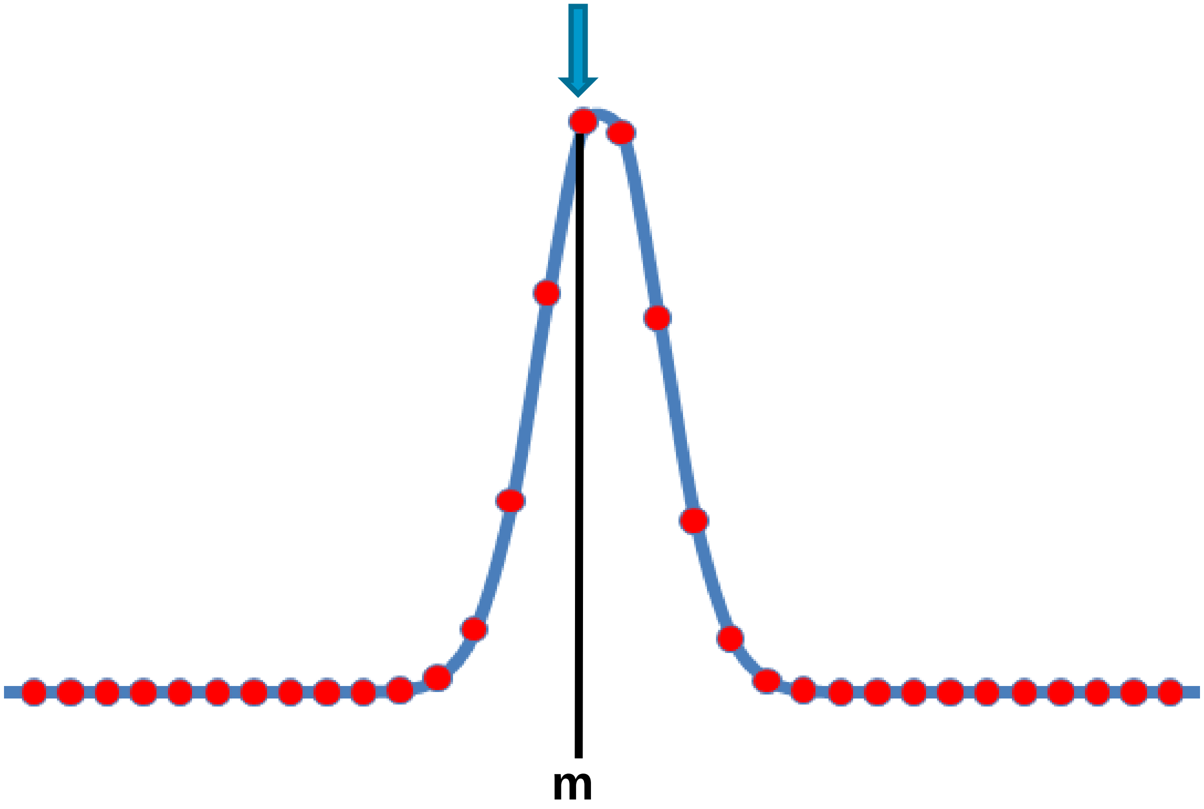
Definition: – “center of mass” of the peak = 1st moment



Mass centroid $= \bar{m} = \sum_{i=0}^{12} m_i \ A_i \Big/ \sum_{i=0}^{12} A_i$

Mass centroid

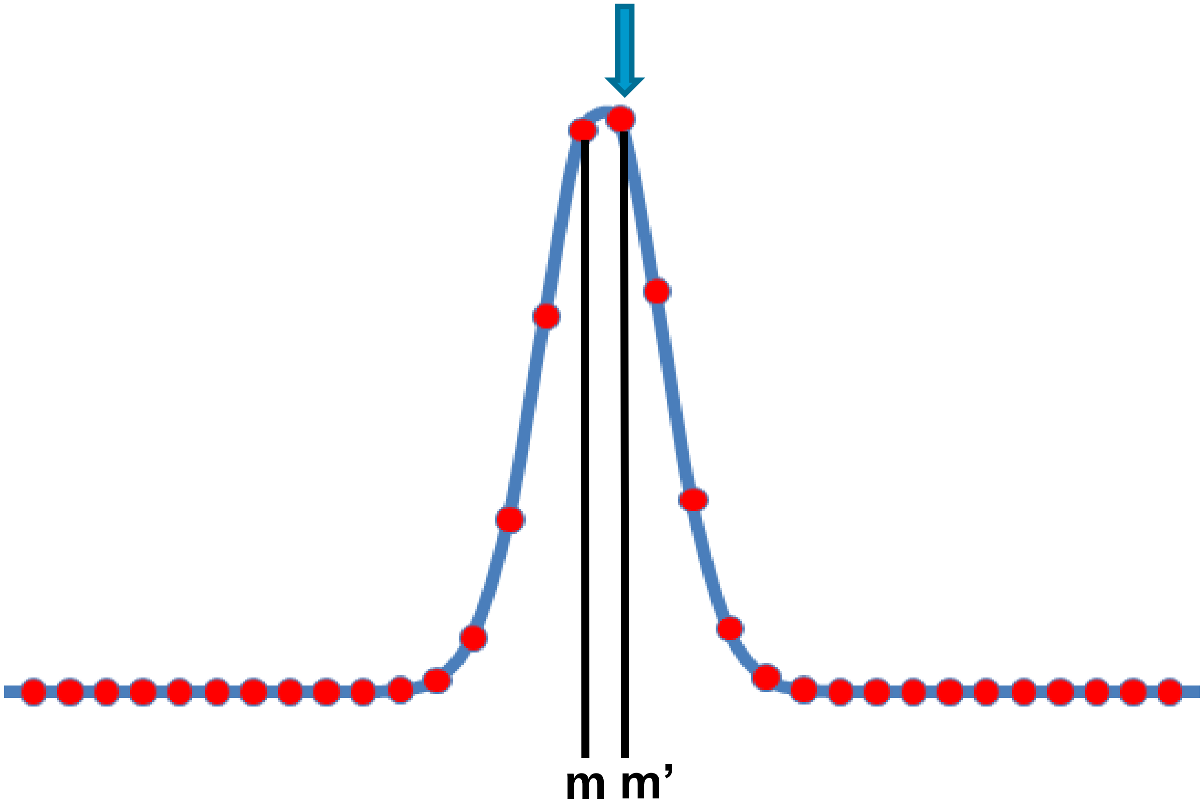
Why centroid and not apex?



Small changes in amplitude can change where the apex is located

Mass centroid

Why centroid and not apex?



Variation in mass measurement equals the mass spacing of data points

Centroid mass accuracy is greater than a single point measurement

Exact mass and accurate mass

- **Accurate mass** is the experimentally measured mass value
- **Exact mass** is the calculated mass based on adding up the masses of each atom in the molecule
- **Atomic mass** of each element is determined relative to Carbon having a mass of exactly 12.0000
- **Mass defect** is the difference between the mass of the individual components of the nucleus alone, and the mass of the bound nucleus

Mass error

- Mass error = (exact mass) – (accurate mass)
- Mass error in parts per million (ppm) =

$$\frac{\text{(mass error)}}{\text{(exact mass)}} \quad \text{X } 10^{6}$$

Accurate mass makes mass defect important

Element	Symbol	Integer Mass	Exact Mass	Abundance	Mass Defect
Hydrogen	H	1	1.0078	99.99	0.0078
	D or ^{2}H	2	2.0141	0.01	0.0141
Carbon	^{12}C	12	12	98.91	0
	^{13}C	13	13.0034	1.1	0.0034
Nitrogen	^{14}N	14	14.0031	99.6	0.0031
	^{15}N	15	15.0001	0.4	0.0001
Oxygen	^{16}O	16	15.9949	99.76	-0.0051
	^{17}O	17	16.9991	0.04	-0.0009
	^{18}O	18	17.9992	0.2	-0.0008
Fluorine	F	19	18.9984	100	-0.0016
Silicon	^{28}Si	28	27.9769	92.2	-0.0231
	^{29}Si	29	28.9765	4.7	-0.0235
	^{30}Si	30	29.9738	3.1	-0.0262
Phosphorus	P	31	30.9738	100	-0.0262
Sulfur	^{32}S	32	31.9721	95.02	-0.0279
	^{33}S	33	32.9715	0.76	-0.0285
	^{34}S	34	33.9679	4.22	-0.0321
Chlorine	^{35}Cl	35	34.9689	75.77	-0.0311
	^{37}Cl	37	36.9659	24.23	-0.0341
Bromine	^{79}Br	79	78.9183	50.5	-0.0817
	^{81}Br	81	80.9163	49.5	-0.0837
Iodine	I	127	126.9045	100	-0.0955

Why is mass defect important?

Many defects are large enough to be measurable by TOF MS

Element	Symbol	Integer Mass	Exact Mass	Abundance	Mass Defect
Hydrogen	H	1	1.0078	99.99	0.0078
	D or ^{2}H	2	2.0141	0.01	0.0141
Carbon	^{12}C	12	12	98.91	0
	^{13}C	13	13.0034	1.1	0.0034
Nitrogen	^{14}N	14	14.0031	99.6	0.0031
	^{15}N	15	15.0001	0.4	0.0001
Oxygen	^{16}O	16	15.9949	99.76	-0.0051
	^{17}O	17	16.9991	0.04	-0.0009
	^{18}O	18	17.9992	0.2	-0.0008
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	^{37}Cl	37	36.9659	24.23	-0.0341

One ^{1}H
+ 13 ppm

One ^{16}O
- 8 ppm

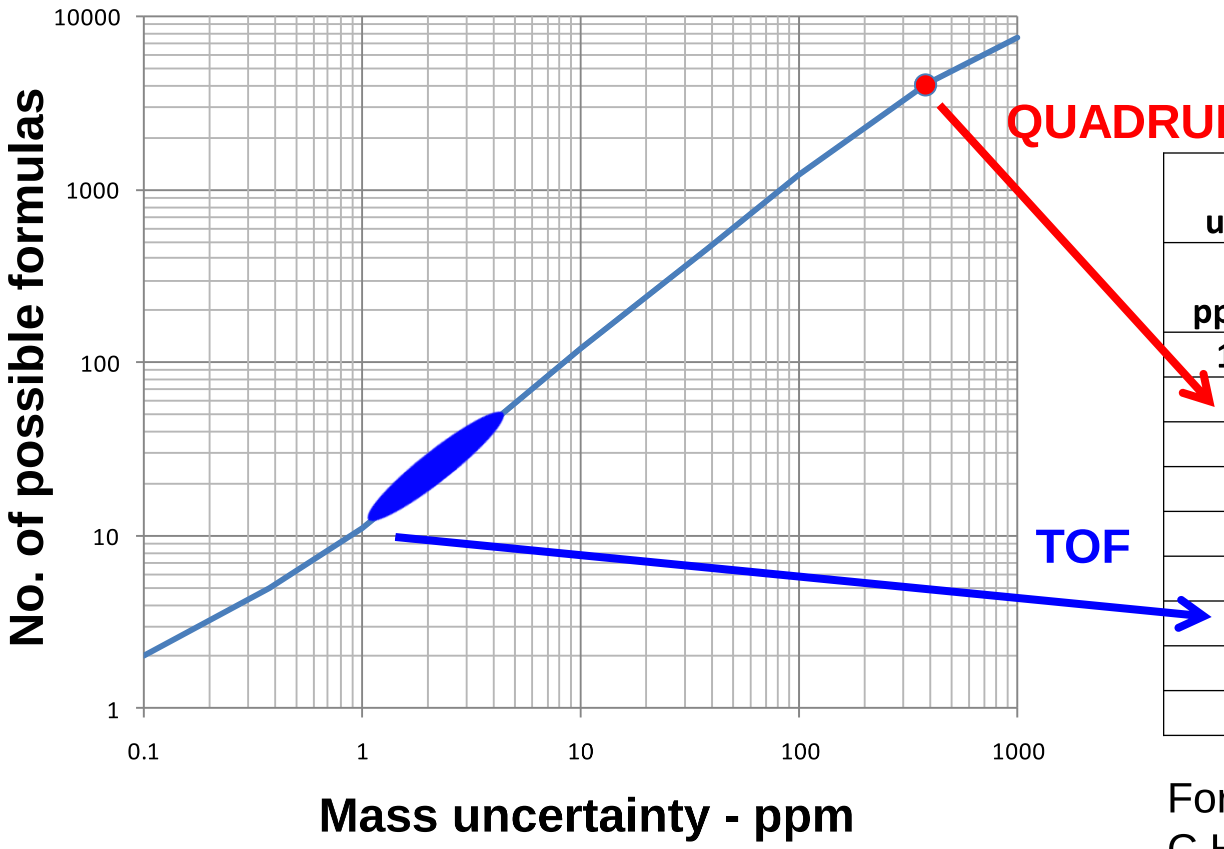
One ^{35}Cl
- 51 ppm

TOF capable of < 5 ppm measurement routinely

Many possible formulas with an MSD or IT

But only a few with TOF

Possible chemical formulas for m/z = $C_{10}F_8$ = 271.98667



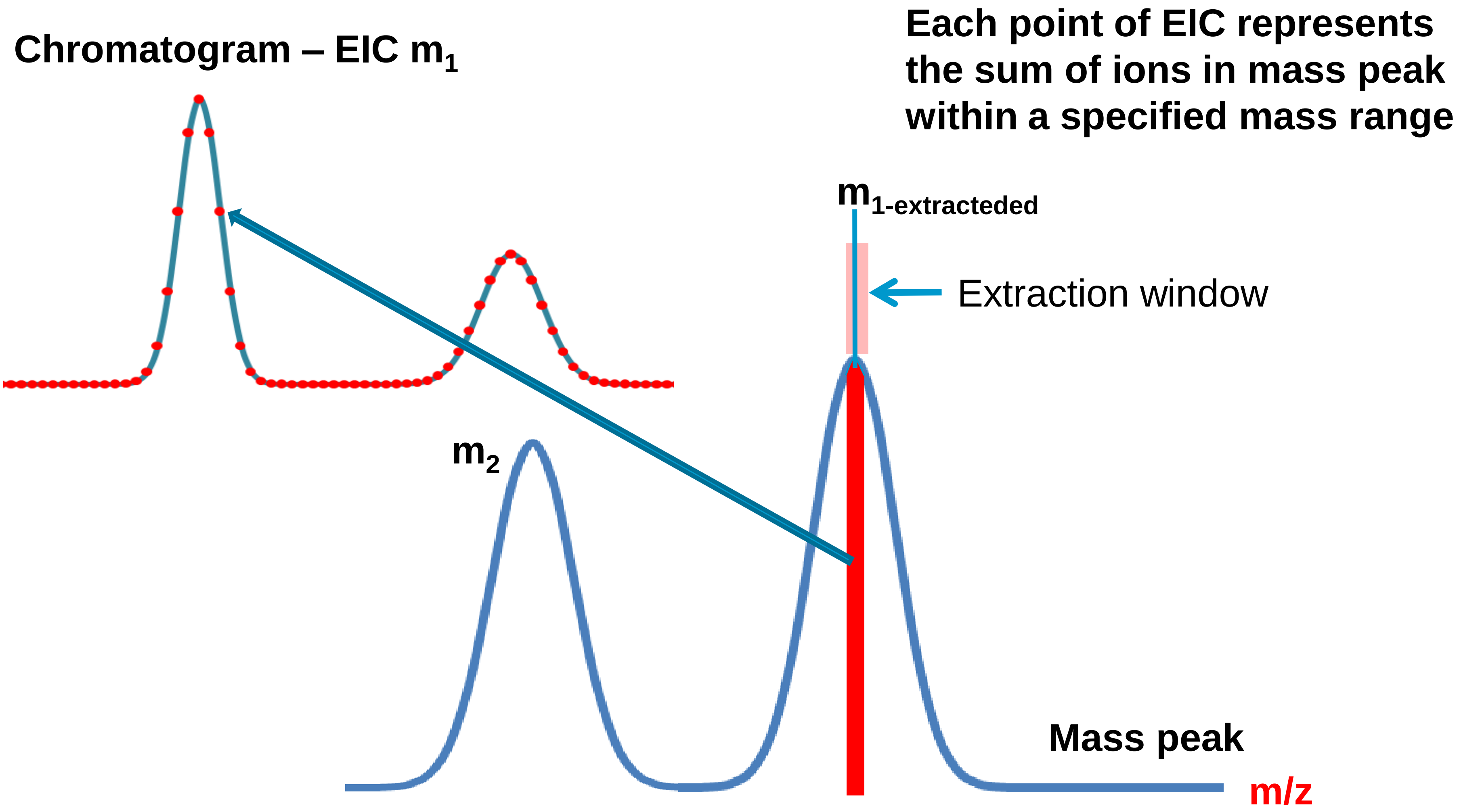
mass uncertainty		
ppm	amu	# of Possible Formulas
1000	0.3	7657
368	0.1	4050
100	0.03	1223
37	0.01	466
10	0.003	120
4	0.001	43
1	0.0003	11
0.4	0.0001	5
0.1	0.00003	2

Formulas made of:
C,H,N,O,F, & Cl

Isotopic abundances can further reduce the number of possible formulas

How is accurate mass used?

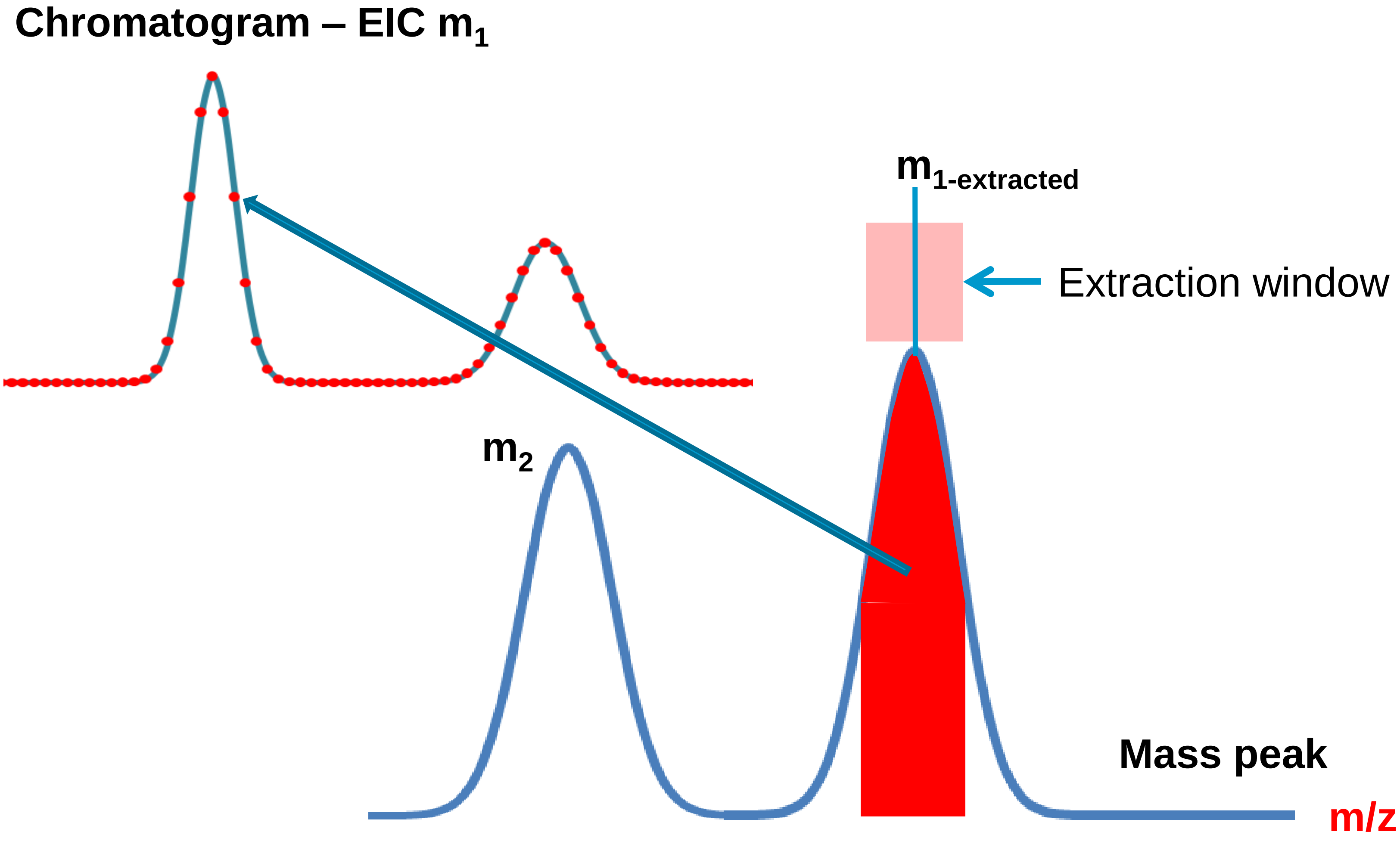
Extracted ion chromatograms - EIC



Each point of EIC represents the sum of ions in mass peak within a specified mass range

Extraction window

Wide extraction window measures more ions = more sensitivity



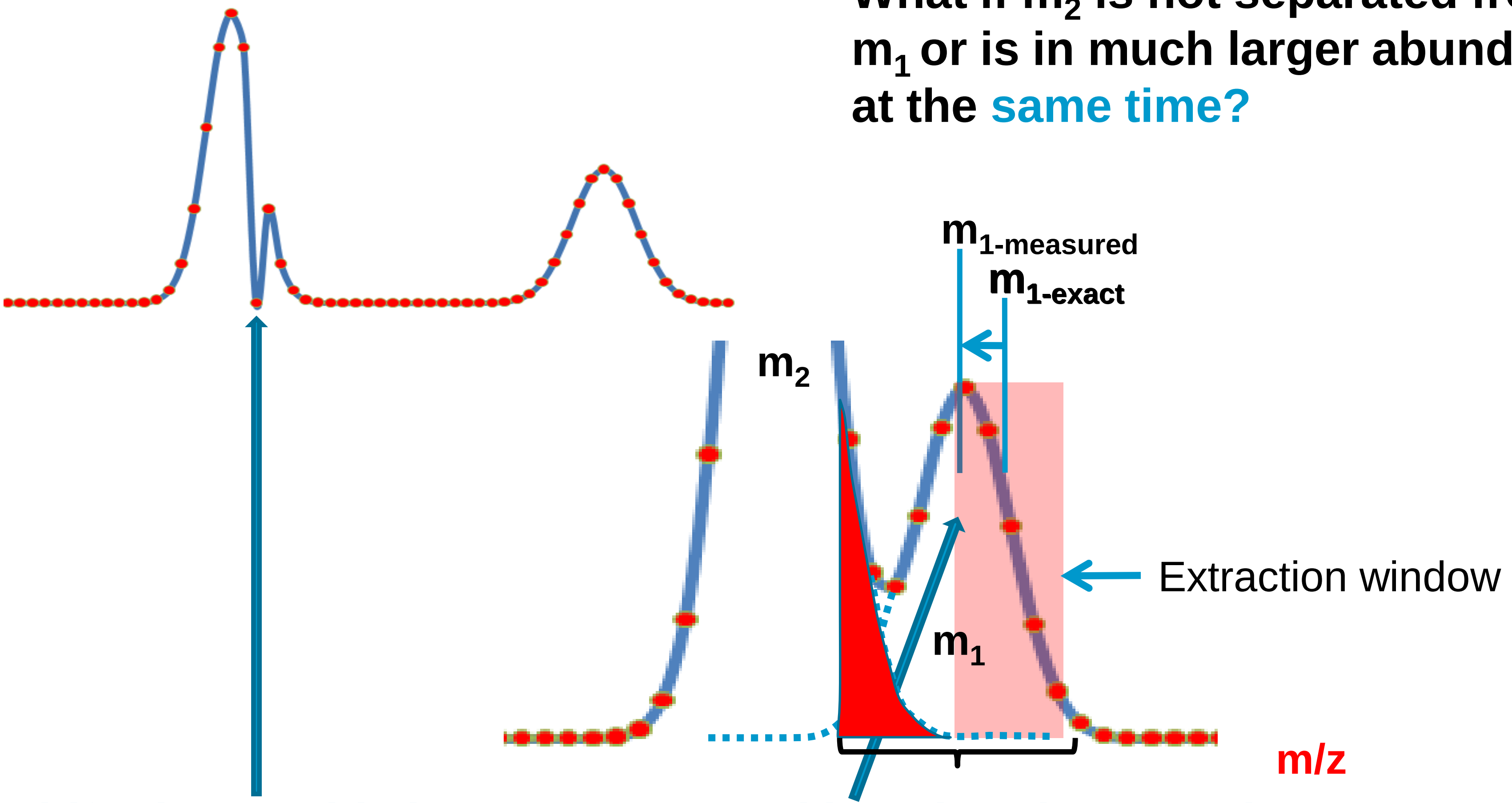
Good results if m_1 is well separated from m_2 and comparable abundance

Why is resolution important?

Ions from m_2 are added to m_1 EIC thus shifting the m_1 centroid

Chromatogram – EIC m_1

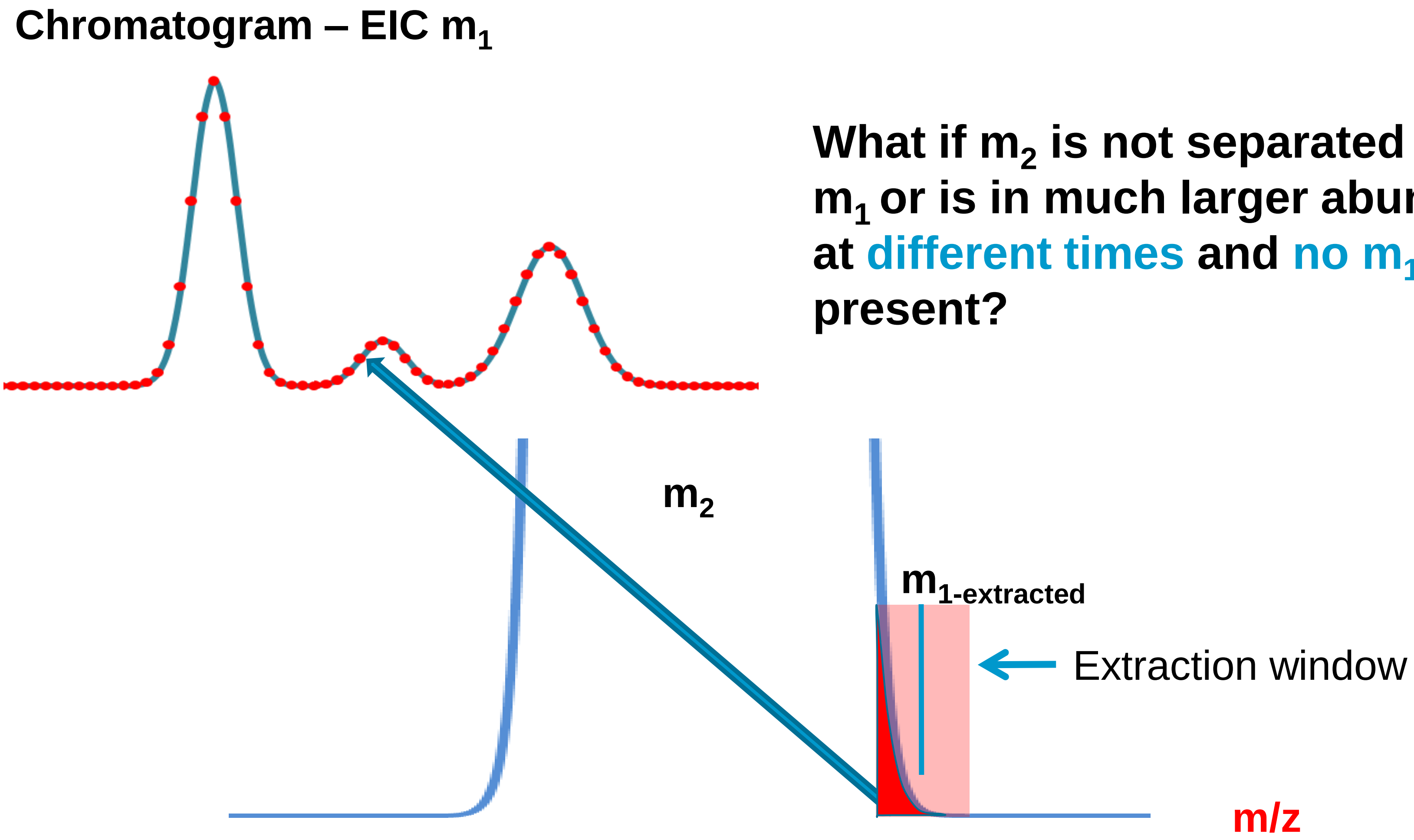
What if m_2 is not separated from m_1 or is in much larger abundance at the same time?



Shifted centroid changes measured ion abundance and mass accuracy

Why is resolution important?

Wide extraction window will add in ions from adjacent mass



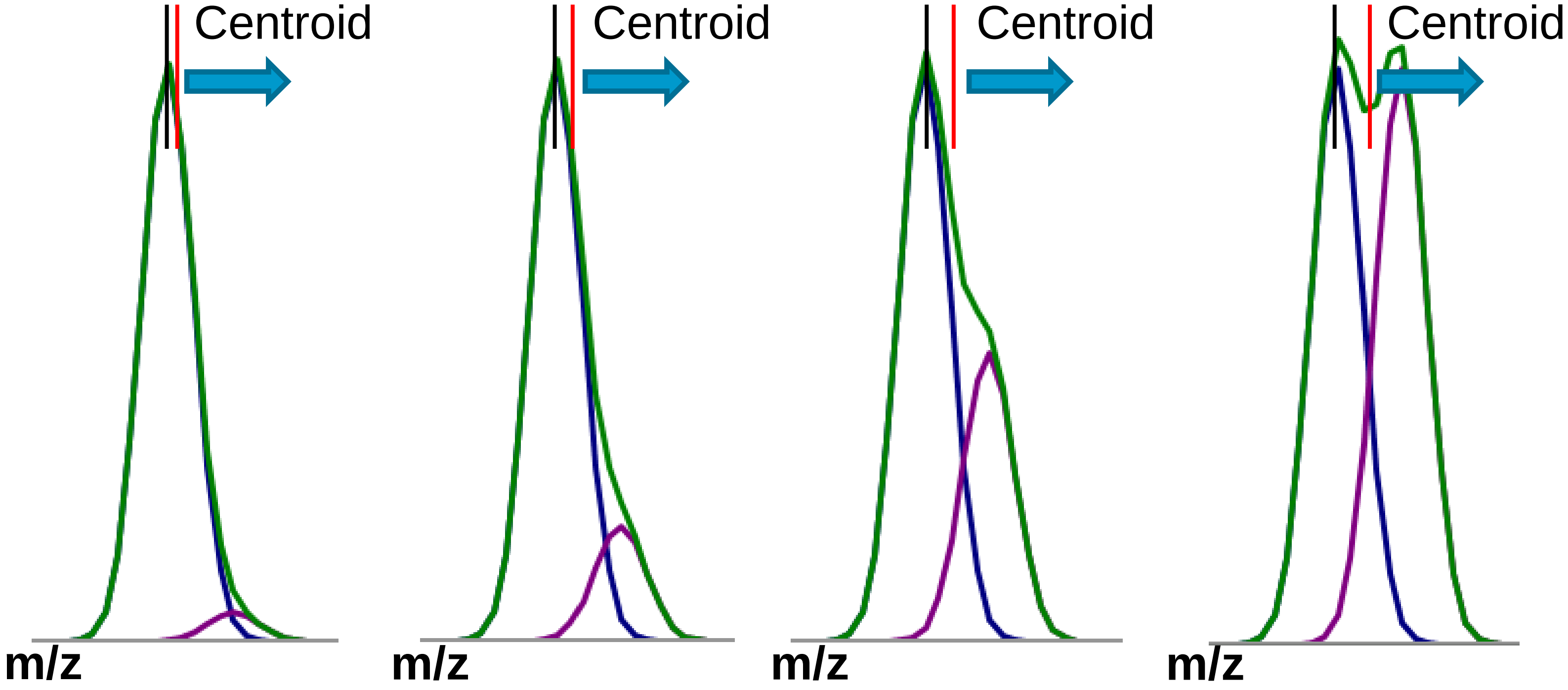
What if m_2 is not separated from m_1 or is in much larger abundance at different times and no m_1 is present?

Ions from m_2 are added into m_1 EIC thus displaying a false m_1 response

Mass centroid

Relative intensity affects the result

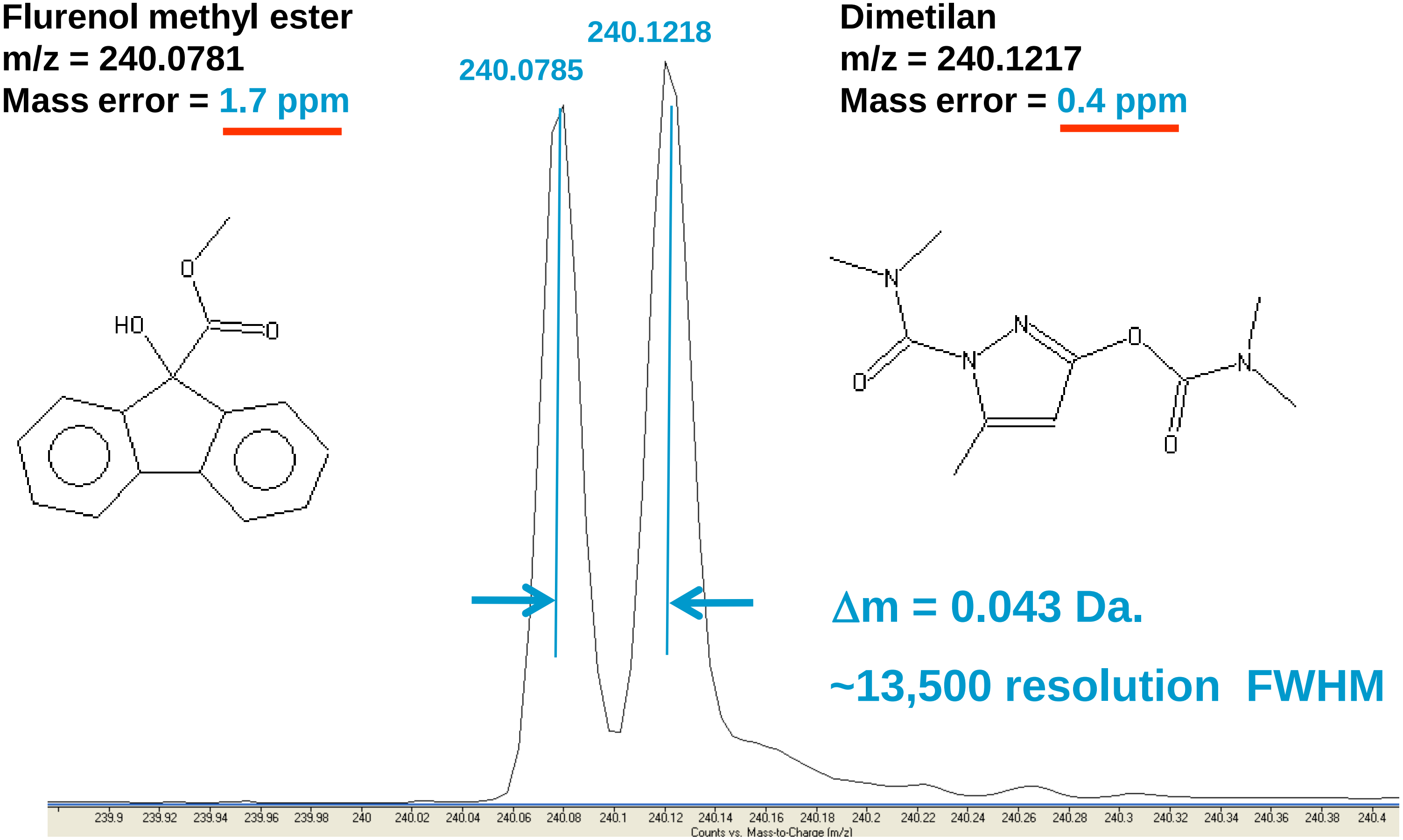
Profile view of mass peaks



Centroid view of mass peaks obscures this fact

How much resolution is enough?

Relative intensity affects the result



Flurenol methyl ester
m/z = 240.0781
Mass error = 1.7 ppm

240.0785

240.1218

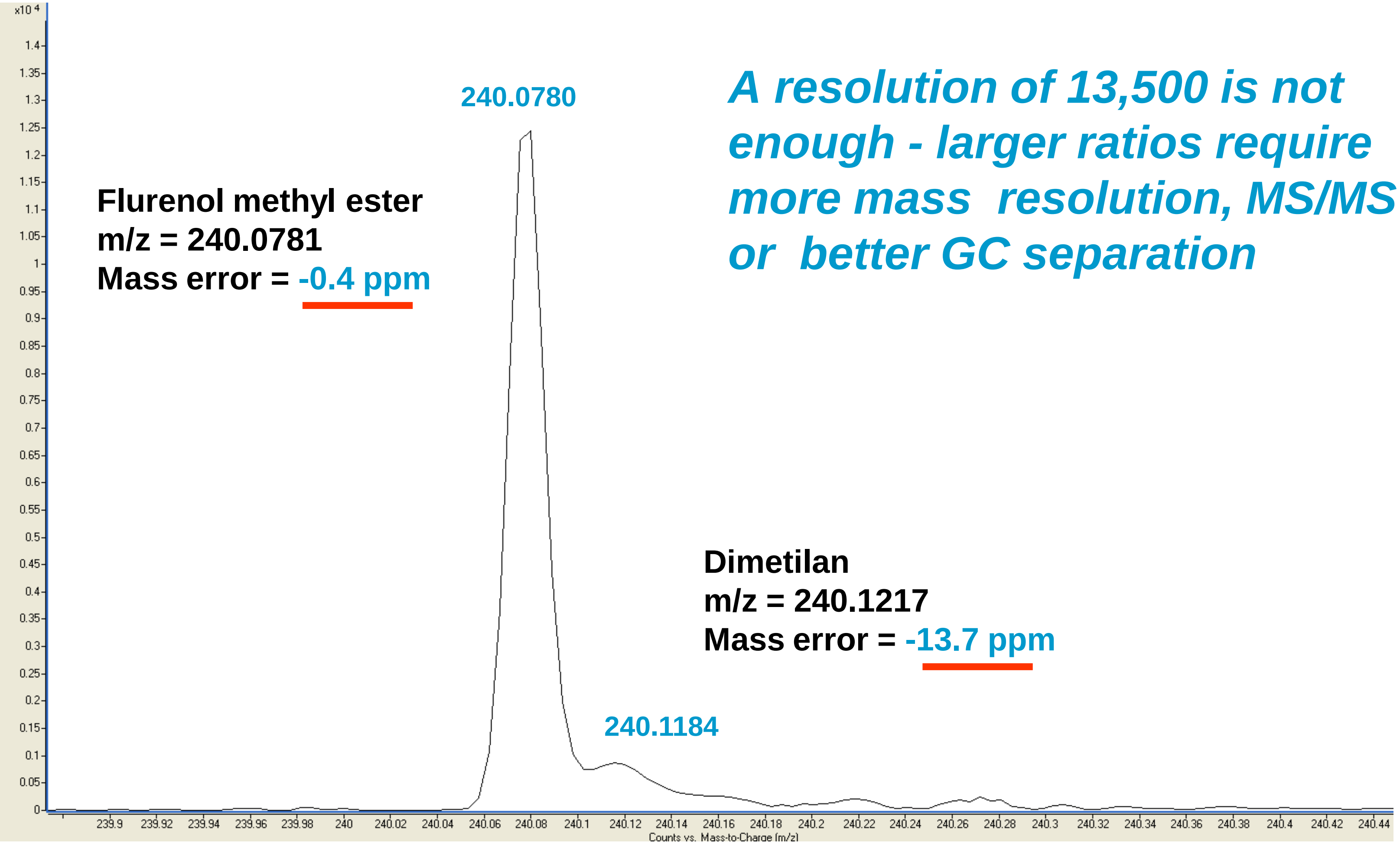
Dimetilan
m/z = 240.1217
Mass error = 0.4 ppm

Δm = 0.043 Da.

~13,500 resolution FWHM

How much resolution is enough?

Intensity Ratio = 10:1



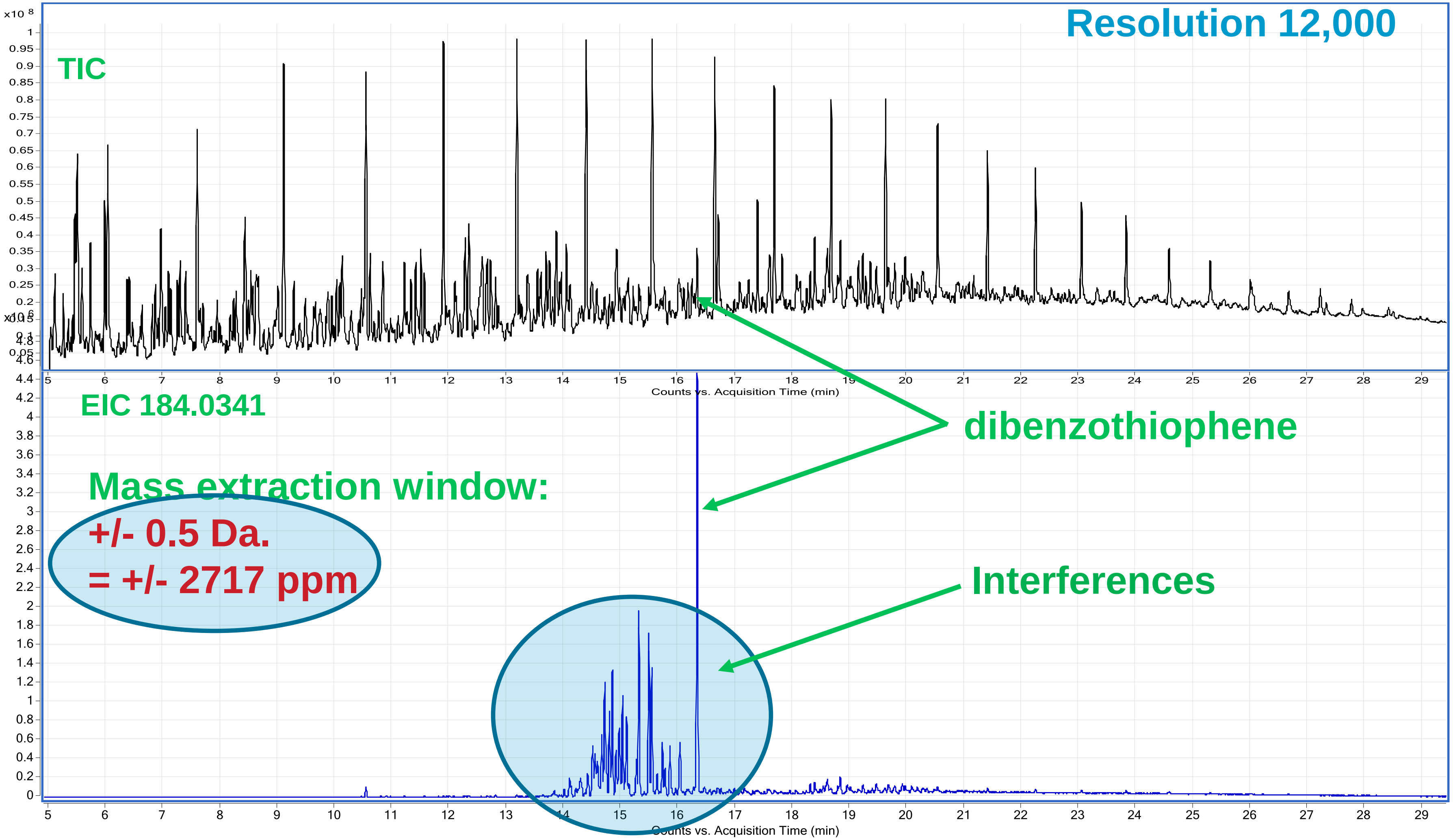
Flurenol methyl ester
m/z = 240.0781
Mass error = -0.4 ppm

Dimetilan
m/z = 240.1217
Mass error = -13.7 ppm

A resolution of 13,500 is not enough - larger ratios require more mass resolution, MS/MS or better GC separation

Crude oil target analysis – target analysis

Problem: identify and quantify dibenzothiophene



Resolution 12,000

dibenzothiophene

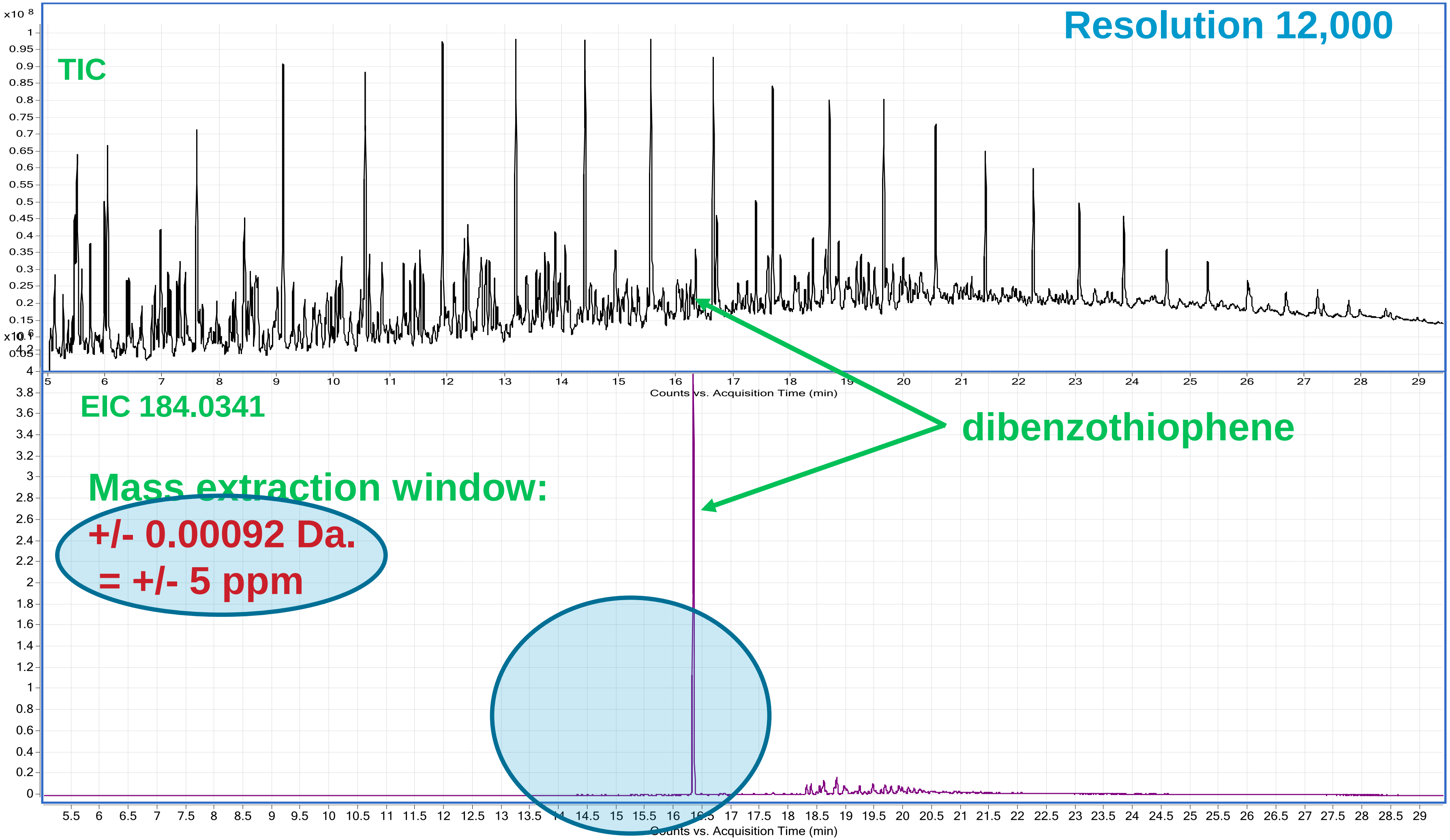
Mass extraction window:

+/- 0.5 Da.
= +/- 2717 ppm

Interferences

Crude oil target analysis – target analysis

Problem: identify and quantify dibenzothiophene

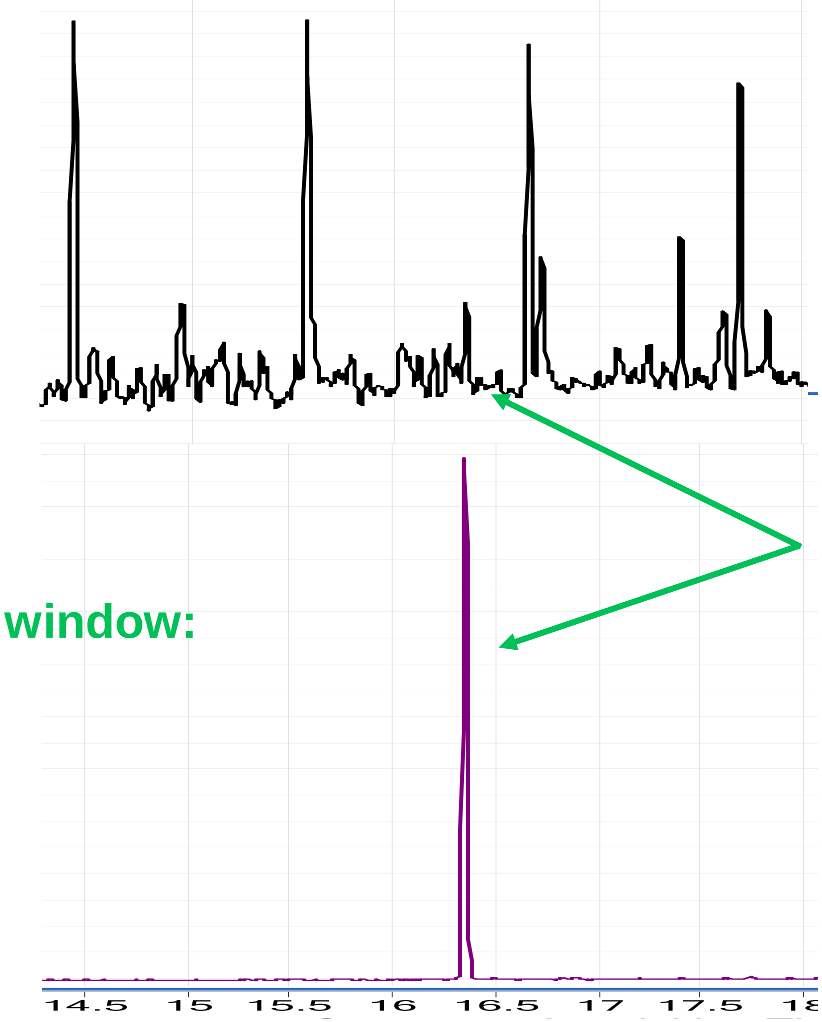


Crude oil target analysis

Problem: identify and quantify dibenzothiophene

Resolution 12,000

TIC



EIC 184.0341

Mass extraction window:
+/- 5 ppm

dibenzothiophene

Summary

- Mass accuracy (MA) is a valuable tool for target quantification and confirmation
- High resolution (HR) ensures mass accuracy over sample range – good test for adequate mass resolution
- How much resolution is required depends on sample, matrix, and their relative abundance
- TOF mass accuracy & high resolution is an important tool for solving complex analytical problems

Thank you for your attention