

What is Mass Spectrometry?

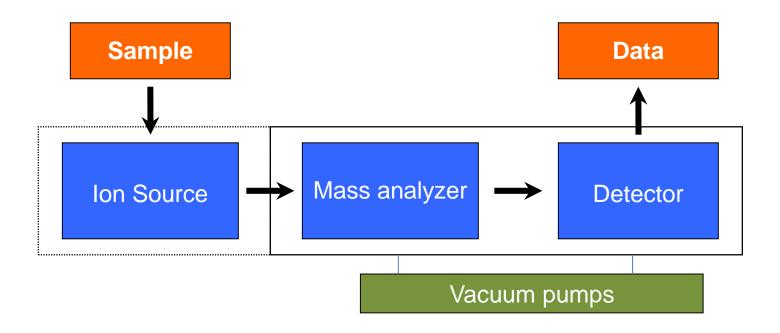
Martin Hubálek

Mass Spectrometry (MS) is an analytical technique that sorts ions based on their mass to charge ratio

Mass spectrometry is the art of measuring atoms and molecules to determine their molecular weight. Such mass or weight information is sometimes sufficient, frequently necessary, and always useful in determining the identity of a species. To practice this art one puts charge on the molecules of interest, i.e., the analyte, then measures how the trajectories of the resulting ions respond in vacuum to various combinations of electric and magnetic fields.

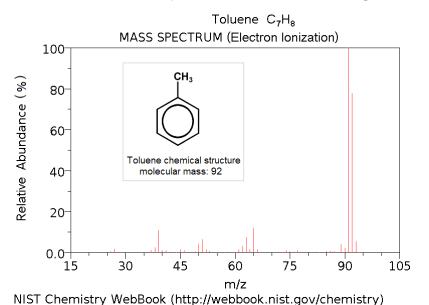
Clearly, the sine qua non of such a method is the conversion of neutral analyte molecules into ions. For small and simple species the ionization is readily carried by gas-phase encounters between the neutral molecules and electrons, photons, or other ions. In recent years, the efforts of many investigators have led to new techniques for producing ions of species too large and complex to be vaporized without substantial, even catastrophic, decomposition.

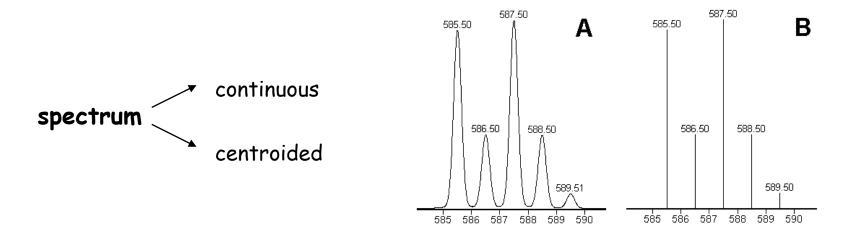
General components of Mass Spectrometer



Mass spectrum

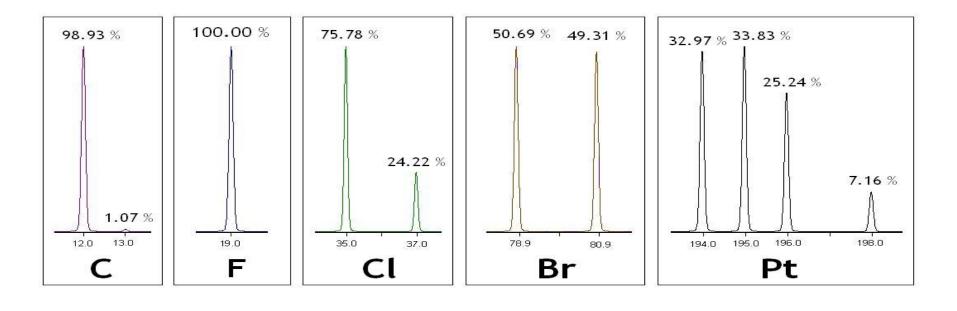
Grafical interpretation of ion intensity on mass to charge ratio (m/z).





Isotopes

Natural mix of isotopes – distribution of individual isotopes is constant in nature



X (monoisotopic): ¹⁹F, ²³Na, ³¹P, ¹²⁷I

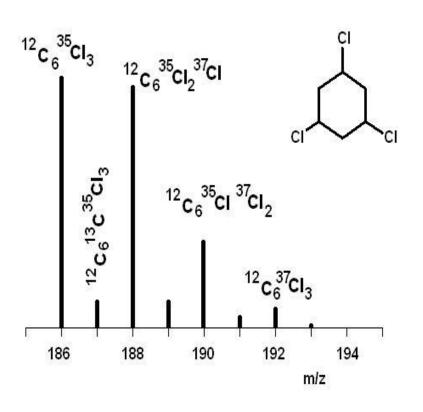
elements X+1: hydrogen (1H

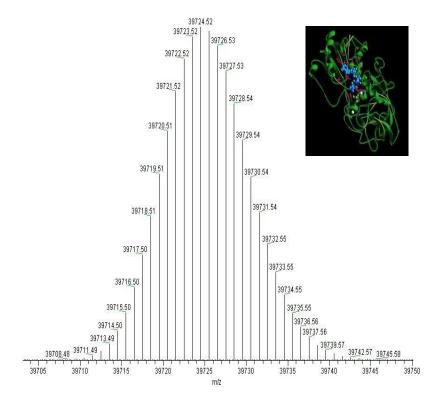
X+1: hydrogen (¹H, ²H), carbon (¹²C, ¹³C), nitrogen (¹⁴N, ¹⁵N)

X+2: chlorine (35Cl, 37Cl), brom (79Br, 81Br) oxygen (16O, 18O)

Isotopic composition of ion

Depends on a combination of isotopes of the atoms within the molecule





trichlorcyklohexan $C_6H_9CI_3$

alcoholdehydrogenase $C_{1764}H_{2859}N_{469}O_{516}S_{26}$

mass units

unified atomic mass unit - non-SI unit

1/12 of the mass of an unbound neutral atom of carbon-12 in its nuclear and electronic ground state

$$u = 1,660 57.10^{-27} \text{ kg}$$

dalton Da - non-SI unit

Da vs u - alternatives for each other

m/z - Mass to charge ration - dimensionless by definition

thomson Th – propossed as unit of mass-to-charge ratio

$$1~{\rm Th} = 1~\frac{\rm u}{e} = 1~\frac{{\rm Da}}{e} = 1.036426 \times 10^{-8}\,{\rm kg}\,{\rm C}^{-1}$$

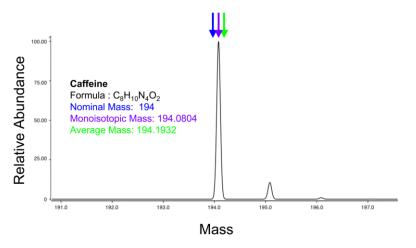
Mass of ion in MS

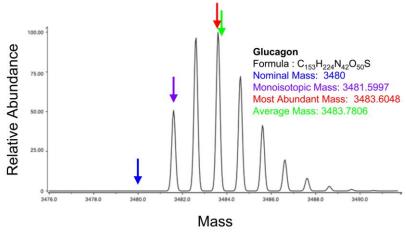
nominal mass: is calculated using the integer mass (ignoring the mass defect) of the most abundant isotope of each element. (ex. CO_2 : $12u + 2 \times 16u = 44u$)

Monoisotopic mass: is the sum of the masses of the atoms in a molecule using the unbound, ground-state, rest mass of the principal (most abundant) isotope for each element instead of the isotopic average mass. (ex. CO_2 : 12.0000u + 2 x 15.9949u = 43.9898u)

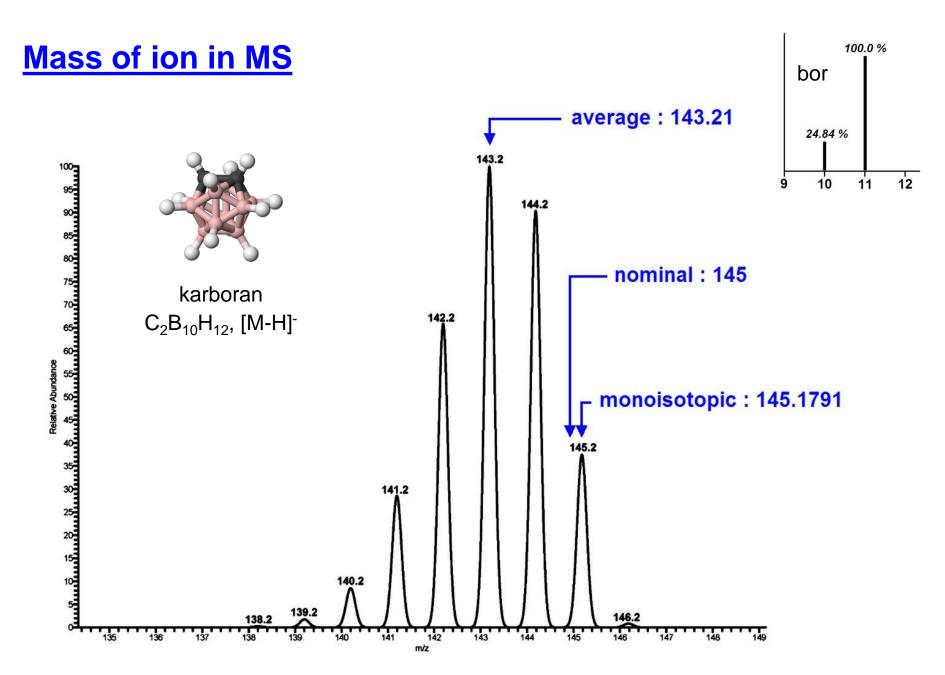
Average mass: obtained by summing the average atomic masses of the constituent elements (ex. CO_2 : $12.01u + 2 \times 16.00u = 44.01u$)

Most abundant mass: mass of the molecule with the most highly represented isotope distribution, based on the natural abundance of the isotopes.





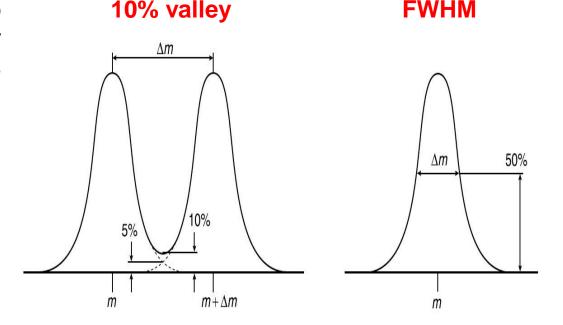
By Kkmurray - Own work, CC BY-SA 3.0, https://commons.wikimedia.org/w/index.php?curid=2680540



Resolution in MS

measures of the ability to distinguish two peaks of slightly different mass-to-charge ratios ΔM , in a mass spectrum

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



Two definitions:

Resolution – 10% valley:

the closest spacing of two peaks of equal intensity with the valley (lowest value of signal) between them less than a specified fraction of the peak height.

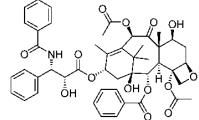
Resolution – FWHM

the width of the peak measured at a specified fraction of the peak height – 50% is called full width at half maximum (FWHM).

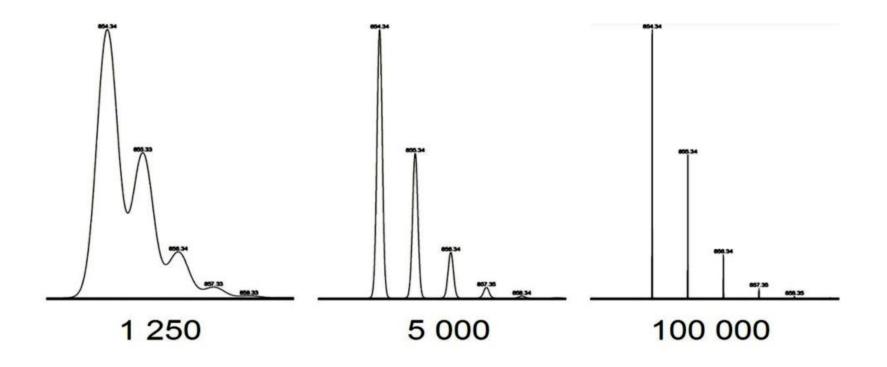
Numerically - FWHM approx. 2times bigger than 10% valley.

Resolution in MS





paclitaxel $C_{47}H_{51}NO_{14}$ (Mw 853.3)



Low resolution

 $\leftarrow \rightarrow$

high resolution

Resolving power of analyzer

Maximum resolving power of different types of analyzers

Time-of-flight (oa TOF):

R = 60 000 FWHM (Maxis 4G, Bruker)

Sector analzer:

R = 80 000 10% údolí (AutoSpec Premier, Waters)

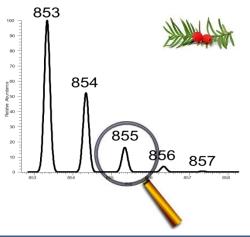
High-Field Orbitrap

R = 240~000~FWHM (m/z~400, Orbitrap Elite, Thermo)

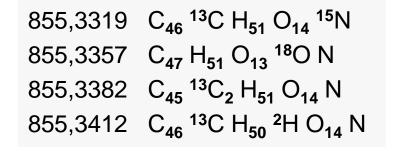
Iontová cyklotronová rezonance (FT-ICR)

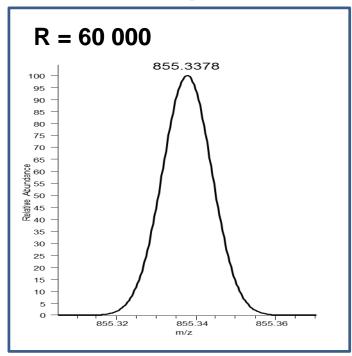
R = 600~000~FWHM (výpočet pro m/z~400~a~1s~sken, Solarix 18T, Bruker)

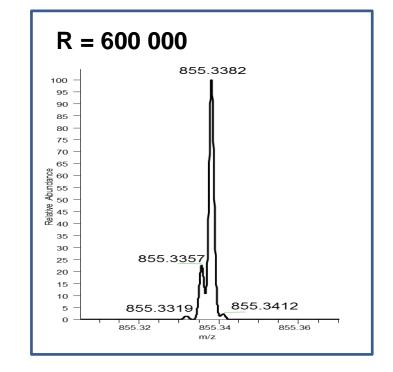
High resolution spectra



Separation of isotopes within nominal mass region







Mass Accuracy

the ratio of the m/z measurement error to the true m/z. Mass accuracy is usually measured in ppm or milli mass units.

$$E_{\it mmu} = 10^3 \left(M_{\it změřená} - M_{\it vypočítaná} \right) \qquad E_{\it ppm} = 10^6 \frac{M_{\it změřená} - M_{\it vypočítaná}}{M_{\it vypočítaná}}$$

Calculation of exact mass of an ion:

Correct values of mass of individual isotopes

G. Audi, A.H. Wapstra, C. Thibault, Nucl. Phys. A 729, 337-676, 2003

Correct charge

Mass of electron (0.5486 mmu) counts!

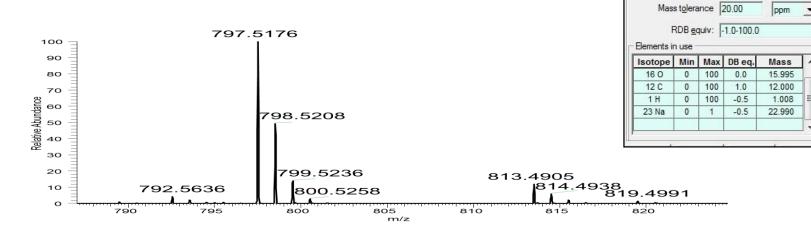
example: naftalen

$$M ([C_{10}H_8]^{-\bullet}) = 128.063149 (+4.3 ppm)$$

$$M (C_{10}H_8) = 128.0626$$

$$M ([C_{10}H_8]^{+\bullet}) = 128.062052 (-4.3 ppm)$$

Elementar composition



tolerance 5 ppm (3 posibilities)

	Elemental	composition	omposition search on mass 797.52					
l	m/z= 792.52-802.52							
ı	m/z	Theo.	Delta	RDB	Composition	ı		
		Mass	(ppm)	equiv.		Ţ		
	797.5176	797.5174	0.20	8.5	C45 H74 O10 Na	l		
ı		797.5198	-2.81	11.5	C47 H73 O10	l		
ı		797.5140	4.55	20.5	C54 H69 O5	l		
ı	,					ı		

tolerance 20 ppm (13 possibilities)

Charge: 1 ÷

Nitrogen-Rule: Do not use

m/z = 792.52 - 802.52								
m/z	Theo. Mass	Delta (mmu)	RDB equiv.	Composition				
797.52	797.52	0.16	8.5	C45 H74 O10 Na				
	797.52	-2.24	11.5	C47 H73 O10				
	797.51	3.63	20.5	C54 H69 O5				
	797.52	-5.71	-0.5	C ₃₈ H ₇₈ O ₁₅ Na				
	797.51	6.03	17.5	C ₅₂ H ₇₀ O ₅ Na				
	797.53	-8.12	2.5	C40 H77 O15				
	797.53	-9.22	21.5	C56 H70 O2 Na				
	797.51	9.50	29.5	C 61 H 65				
	797.53	-11.63	24.5	C58 H69 O2				
	797.51	11.91	26.5	C59 H66 Na				
	797.50	13.01	7.5	C43 H73 O13				
	797.53	-15.10	12.5	C49 H74 O7 Na				
	797.50	15.42	4.5	C ₄₁ H ₇₄ O ₁₃ Na				

Thank you for your attention