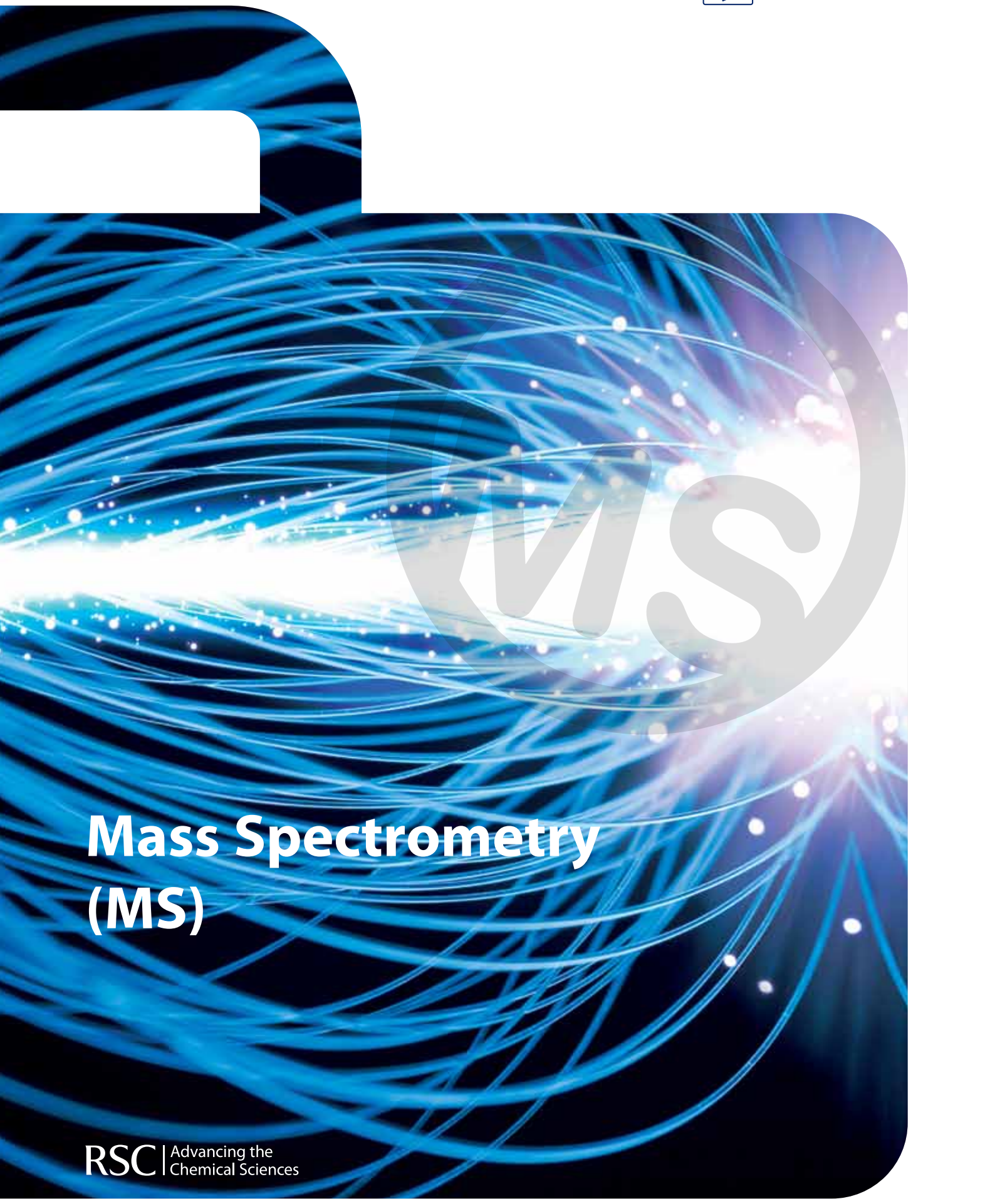
Spectroscopy in a Suitcase



Mass Spectrometry (MS)

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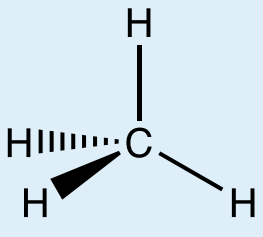
Introduction to Mass Spectrometry (MS)

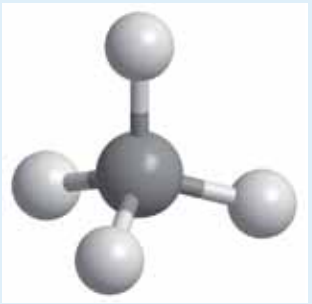
Mass Spectrometry (MS)

This is a very powerful analytical tool that can provide information on both molecular mass and molecular structure.
Molecules come in all shapes and sizes. Here are just a few examples.

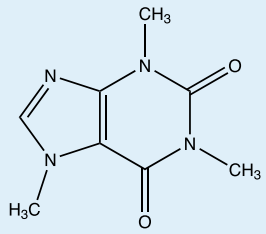
SUBSTANCE **Hydrogen**
FORMULA **H_2**
RELATIVE MOLECULAR MASS **2**

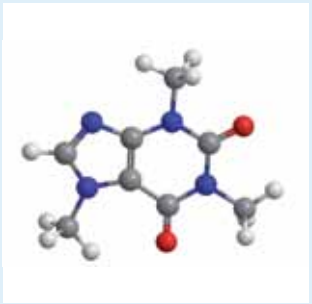
SUBSTANCE **Methane**
FORMULA **CH_4**
RELATIVE MOLECULAR MASS **16**



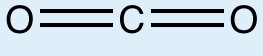


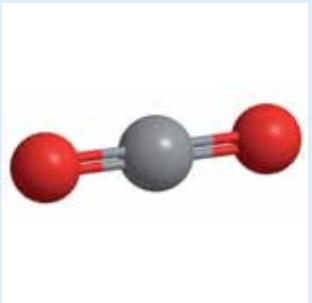
SUBSTANCE **Caffeine**
FORMULA **$C_8H_{10}N_4O_2$**
RELATIVE MOLECULAR MASS **194**



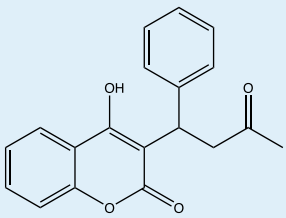


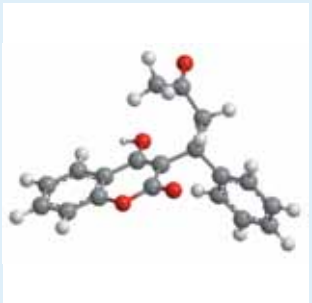
SUBSTANCE **Carbon dioxide**
FORMULA **CO_2**
RELATIVE MOLECULAR MASS **44**





SUBSTANCE **Warfarin**
FORMULA **$C_{19}H_{16}O_4$**
RELATIVE MOLECULAR MASS **308**





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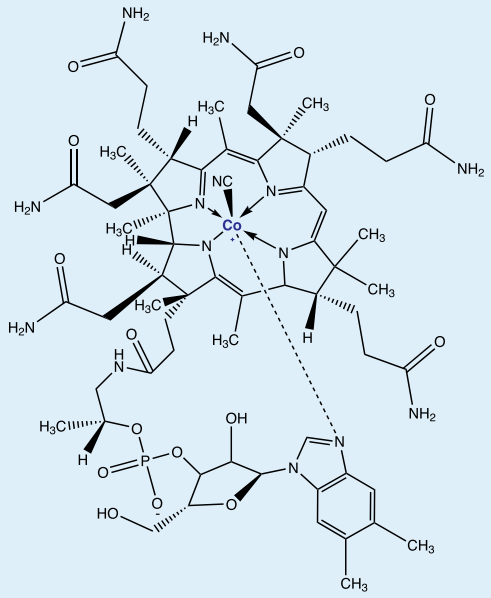
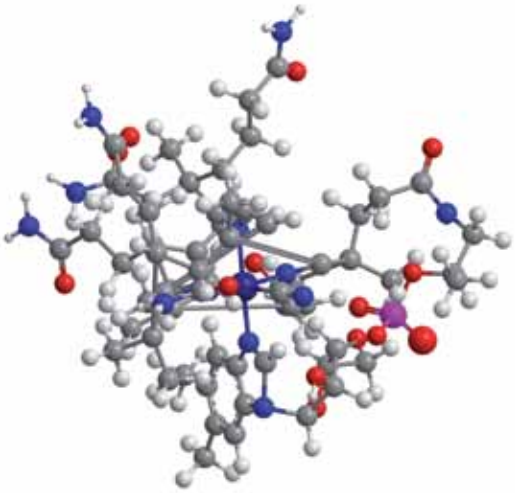
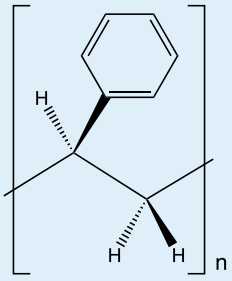
SUBSTANCE **Cyanocobalamin (Vitamin B-12)**
FORMULA **$C_{63}H_{88}CoN_{14}O_{14}P$**
RELATIVE MOLECULAR MASS **1355**

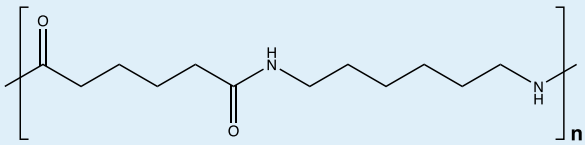




SUBSTANCE **Polystyrene (1 monomer)**
FORMULA **$(C_8H_9)n$**
RELATIVE MOLECULAR MASS **170,000**



SUBSTANCE **Nylon 6,6 (1 monomer)**
FORMULA **$(C_{14}H_{28}N_2O_2)n$**
RELATIVE MOLECULAR MASS **14,000-20,000**



In the same way that fingerprints can be used to identify individuals, mass spectrographs can be used to identify substances and large comparison sites can be accessed for this purpose.

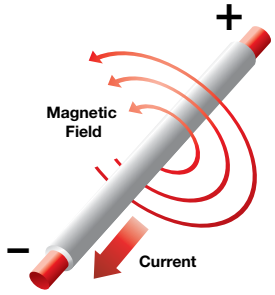
Mass Spectrometry

This technique is about 1000 times more sensitive than IR or NMR analysis. Extremely **small samples** (a few nanograms) can be analysed using this technique.

VALUE	SYMBOL	NAME
10^3 g	kg	kilogram
10^{-3} g	mg	milligram
10^{-6} g	µg	microgram
10^{-9} g	ng	nanogram

Background information

Any wire carrying an electric current – a flow of negative electrons - has a magnetic field surrounding it, known as an electromagnetic field. If a current carrying wire is placed in an external magnetic field it would 'jump' as it is deflected when the two magnetic fields interact.



An electromagnetic field can also be generated by a flow of positively charged ion, such as those generated by a mass spectrometer.

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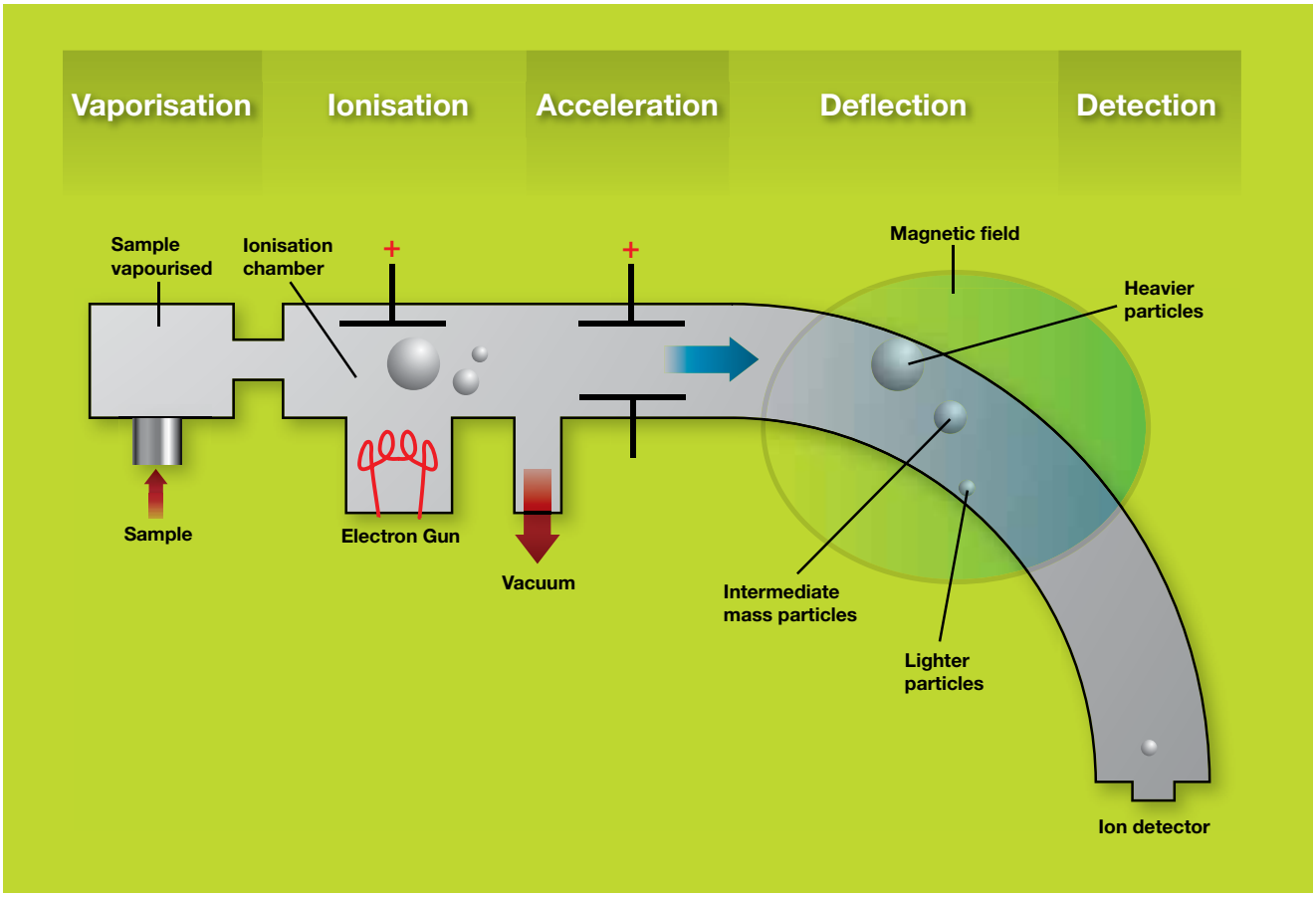
How it works

In a mass spectrometer a stream of positively charged ions is produced along with an associated magnetic field and their deflection in a controlled external magnetic field is studied in detail.

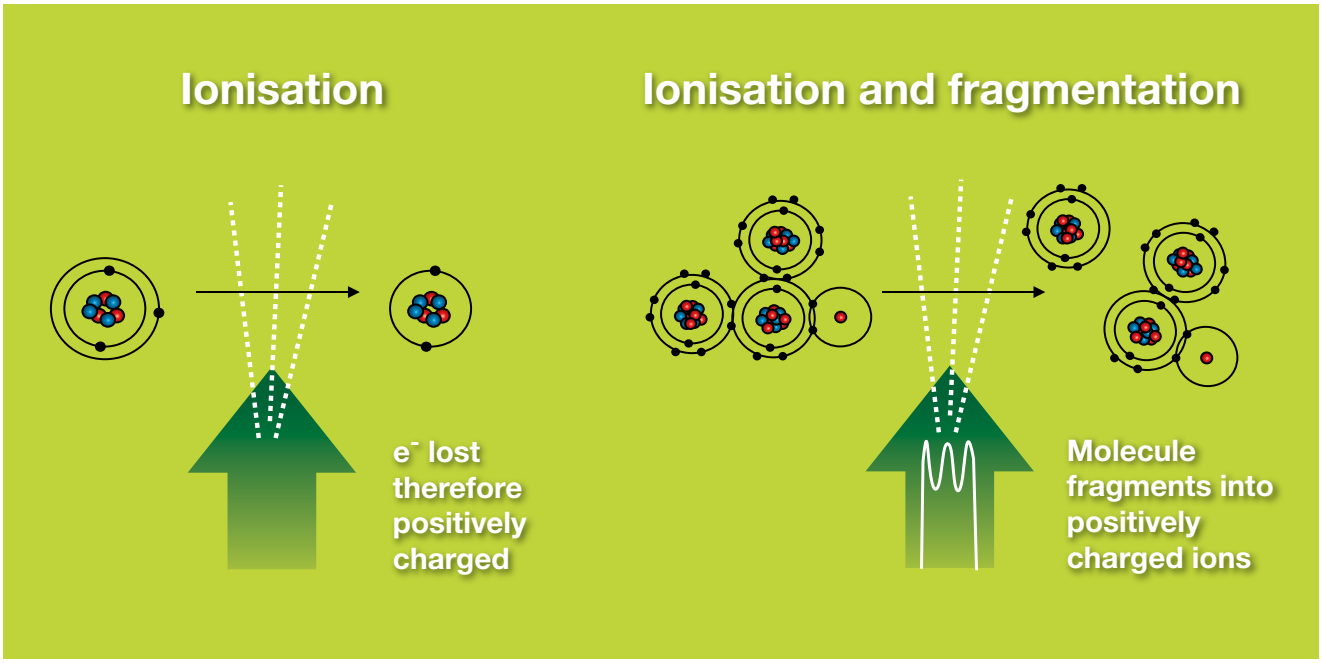
It is important that the atoms or the molecules of the substance being investigated are free to move so if the sample is not a gas it must first be **VAPORISED**.



Next, the sample must be **IONISED**. This is achieved by bombarding the sample with **high energy electrons** from an electron gun. These knock off an electron to produce a **positive** ion.

e.g. consider a helium atom $He(g) + e^- \rightarrow He^+(g) + 2e^-$

Sometimes doubly charged ions may also be produced but this only occurs in smaller amounts because more energy would be required.



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The high energy electron bombardment may also cause molecules to be broken into many different fragments.

e.g. methane molecules CH_4 can be fragmented to produce CH_3^+ CH_2^+ CH^+ and C^+

Fragmentation is dealt with in more detail in a later section.

NOTE: Because the positive ion formed has an unpaired electron it is sometimes shown with a dot indicating that it is a free radical, e.g. $CH_3^{+\bullet}$

The positive ions are then **ACCELERATED** by an electric field and focused into a fine beam by passing through a series of slits with increasing negative potential. It is important that the ions can move freely through the apparatus without colliding with air molecules so the system has all the air removed to create a vacuum.

The beam of fast moving positive ions is **DEFLECTED** by a strong external magnetic field. The magnitude of deflection depends upon two factors:

- The mass (m) of the ion – the lighter it is the more it will be deflected.
- The charge (z) on the ion – ions with 2^+ charges are deflected more than 1^+.

These two factors are combined into the **mass to charge ratio (m/z)**. When m/z is small the deflection is large.

Finally ions which make it right through the machine are **DETECTED** electronically. As the positive ions arrive at the detector they pick up electrons to become neutral. This movement of electrons is detected, amplified and recorded. The external magnetic field involved in deflection can be adjusted so that ions with different m/z ratios can be detected. A printout of intensity vs m/z ratio is produced.

A simple mnemonic may help you remember these stages

VICTOR	Vaporisation
IS	Ionisation
A	Acceleration
DAFT	Deflection
DUCK	Detection

Interpreting the printouts

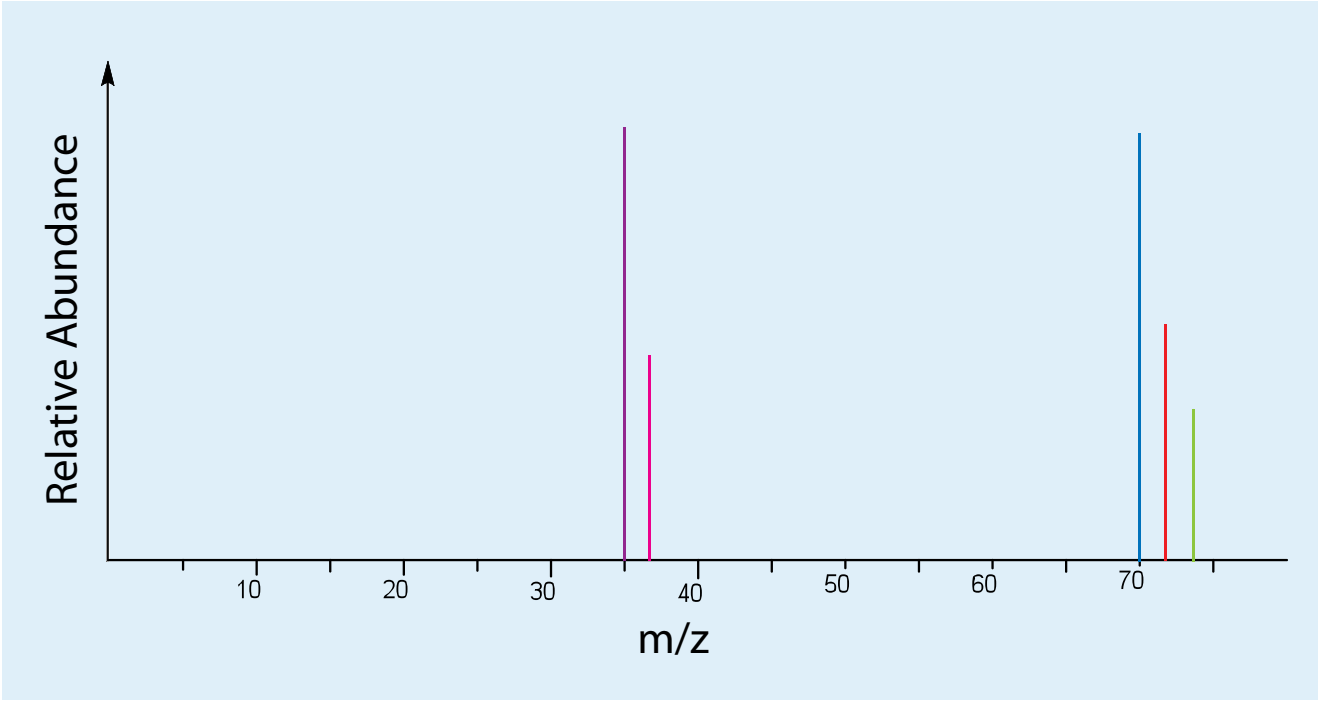
The mass spectrum of chlorine Cl_2

ISOTOPE	OBSERVED MASS
^{35}Cl	35 m/z
^{37}Cl	37 m/z
^{35}Cl-^{35}Cl	70 m/z
^{35}Cl-^{37}Cl	72 m/z
^{37}Cl-^{37}Cl	74 m/z

The multitude of peaks is seen because chlorine has two common isotopes ^{35}Cl and ^{37}Cl.

The peak at **m/z=35 represents the $[^{35}Cl]^+$ ion** and that at **m/z=37 the $[^{37}Cl]^+$ ion**. The ratio of the peak heights is 3:1 indicating the relative abundance of these isotopes; accounting for the Relative Atomic Mass of 35.5 a.m.u.

The cluster of peaks at the higher mass result from the diatomic molecules i.e. Cl_2 where **m/z=70 represents the $[^{35}Cl$-$^{35}Cl]^+$ ion**. That at **m/z=72 the $[^{37}Cl$-$^{35}Cl]^+$ ion** and that at **m/z=74 the $[^{37}Cl$-$^{37}Cl]^+$ ion**.



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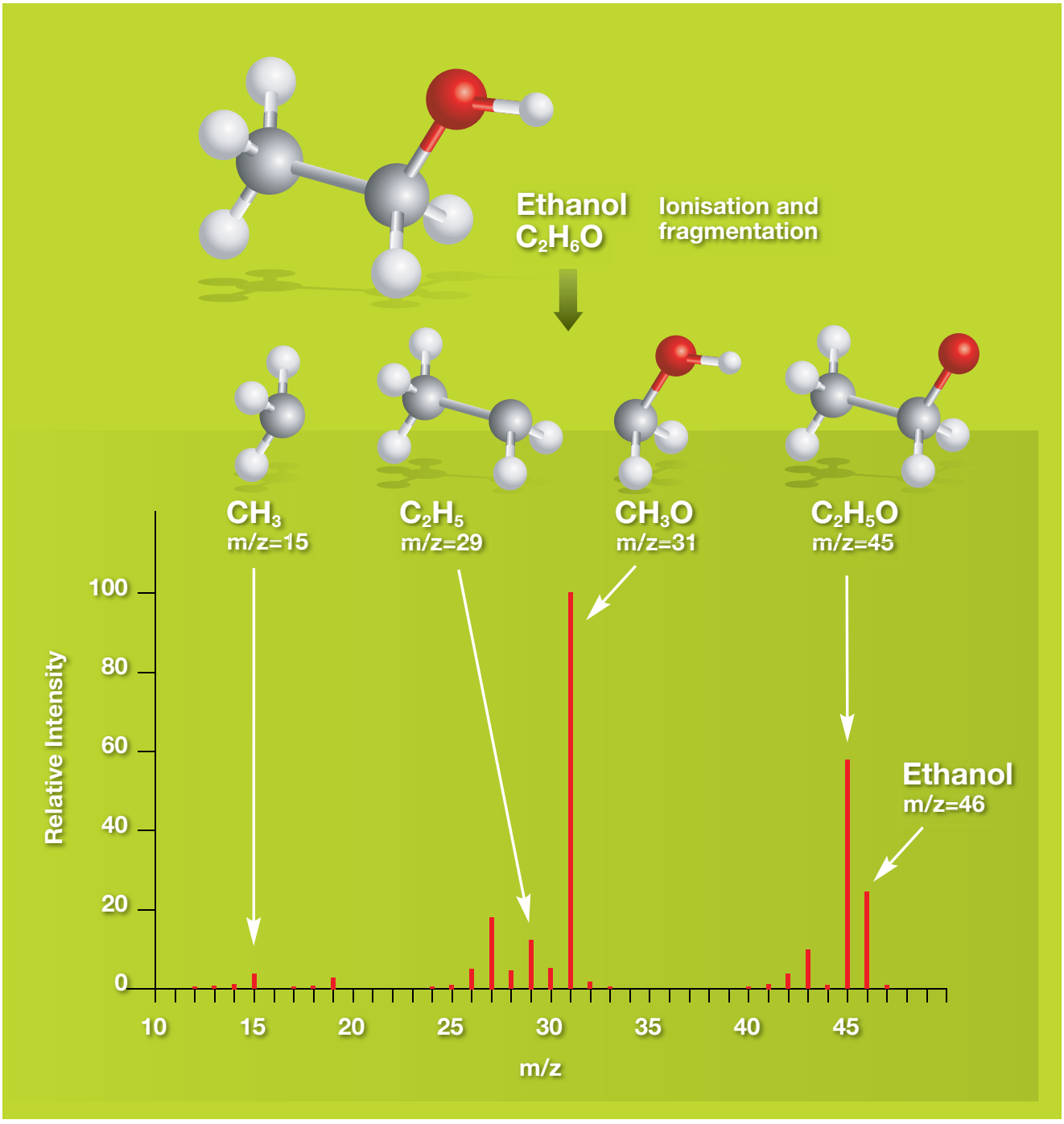
As the molecule gets bigger the possibility of fragmentation increases and the mass spectra become more complex. Final decisions about structure are made after combining evidence from mass spectroscopy with other analytical tools such as IR, UV and NMR.



Many more mass spectra are available at http://www.le.ac.uk/spectraschool/

Modern Applications of MS

LC-MS (Liquid Chromatography-Mass Spectrometry)

This process allows complex mixtures to be separated by liquid chromatography using small capillary columns. The most up to date are less than 100µm across allowing very small quantities of sample to be used. This is very important as mass spectrometry destroys the sample. As the separated substances leave the column they are automatically fed into a mass spectrometer so that identification of each component of the mixture can be made.

This technique has many applications including:

- Proteomics – the study of proteins including digestion products.
- Pharmaceutics – drug development, identification of drugs and drug metabolites – remember the Olympics and the competitors drug testing.
- Environmental – detection and analysis of herbicides and pesticides and their residues in foodstuffs.

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GC-MS (Gas Chromatography-Mass Spectrometry)

This technique is growing in popularity due to the compact nature of the equipment, the speed of use (less than 90 seconds for the best equipment) and it's relatively low cost. Again it combines a chromatography step to separate out the components in a mixture, this time using an inert gas as the mobile phase.

Some of its many applications include:

- Airport security – for drug and explosive detection.
- Fire forensics – using the debris from fires to try to explain the causes.
- Astrochemistry – probes containing GC-MS have been sent to Mars, Venus and Titan to analyse atmosphere and planet surfaces. The Rosetta space mission aims to rendezvous with a comet in 2014 to analyse its constituents.

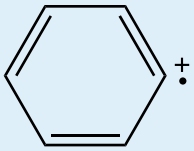
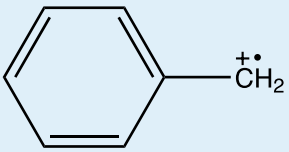
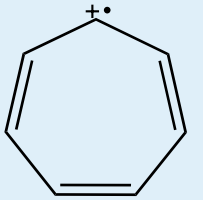
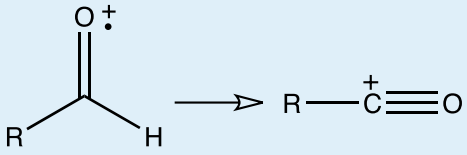
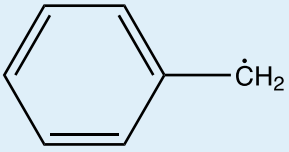
High resolution mass spectrometry

High resolution mass spectrometry can distinguish compounds with the same nominal mass but different actual mass caused by the different elemental composition. For example C_2H_6, CH_2O and NO all have a nominal mass of 30, however their exact masses are 30.04695039, 30.01056487 and 29.99798882, respectively. These subtle differences can be distinguished by this high resolution technique.

It is becoming increasingly important as a technique for analysing the interactions between drugs and body tissues at the scale of DNA.

Common Fragmentations

When a molecule is split during fragmentation the pieces formed tend to be the more stable types and the height of the detected peak provides an indication of how stable the fragment is. Some typical examples are provided in the table.

COMMONLY LOST FRAGMENTS		COMMON STABLE IONS	
m-15	$\cdot CH_3$	m/z = 43	$H_3CC^{+\bullet}{\equiv}O$
m-17	$\cdot OH$	m/z = 77	
m-26	$\cdot C{\equiv}N$	m/z = 91	
m-28	$H_2C{=}CH_2$	m/z = 91	
m-29	$\cdot CH_2CH_3$	m/z = m-1	
m-29	$\cdot CHO$		
m-31	$\cdot OCH_3$		
m-35	$\cdot Cl$		
m-43	$H_3C\dot{C}{=}O$		
m-45	$\cdot OCH_2CH_3$		
m-91			

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