

## **Edexcel Chemistry A-level**

# Topic 7: Modern Analytical Techniques I Detailed Notes

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### **Topic 7A: Mass Spectrometry**

Mass spectrometry is an **analytical technique** used to identify different isotopes and find the overall relative atomic mass of an element.

#### Time of Flight (TOF) Mass Spectrometry

This form of mass spectrometry records the time it takes for ions of each isotope to reach a detector. Using this, **spectra** can be produced showing **each isotope present**.

- Ionisation A sample of an element is vapourised and injected into the mass spectrometer where a high voltage is passed over the chamber. This causes electrons to be removed from the atoms (they are ionised) leaving +1 charged ions in the chamber.
- 2. Acceleration These positively charged ions are then accelerated towards a negatively charged detection plate.
- 3. **Ion Drift** The ions are then deflected by a **magnetic field** into a **curved path**. The radius of the path is dependent on the charge and mass of the ion.



- Detection When the positive ions hit the negatively charged detection plate, they gain an electron, producing a flow of charge. The greater the current produced, the greater the abundance of that particular ion.
- 5. **Analysis** These current values are then used in combination with the **flight times** to produce a **spectra print-out** with the relative abundance of each isotope displayed.





During the ionisation process, a **2+ charged ion** may be produced. These ions are affected more by the magnetic field producing a curved path of **smaller radius**. As a result, its mass to charge ratio (m/z) is halved and this can be seen on spectra as a trace at **half the expected** m/z value.

Example:



Using this print-out spectra, the *Ar* (relative atomic mass) can be calculated by multiplying each m/z value by its abundance and adding each of these together, before dividing by the total abundance of all species present.

Ar = m/z x abundance Total abundance

Example: Using the above mass spectrum,

Ar = (10x75) + (12x25) = 10.5(75 + 25)

Using this calculated value of Ar, the element can be identified by referring to the Periodic Table.

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#### **Predicting Mass Spectra**

If you know the **abundances** of an isotope you can generate the mass spectra for its molecules, including **relative peak heights**.

Example:

The relative abundance of  ${}^{35}$ Cl atoms is 75% and  ${}^{37}$ Cl atoms is 25%. In other words, for every 100 atoms of chlorine, 25 would be  ${}^{35}$ Cl and 75 would be  ${}^{37}$ Cl.

Spectra produced by the mass spectrometry of chlorine display a characteristic pattern in a 3:1 ratio for  $Cl^+$  ions and a 3:6:9 ratio for  $Cl_2^+$  ions. This is because one isotope is more common than the other and the chlorine molecule can form in different combinations:

 ${}^{70}\text{Cl}_2^{+} = 35 + 35$  ${}^{72}\text{Cl}_2^{+} = 35 + 37 \text{ OR} = 37 + 35$  ${}^{74}\text{Cl}_2^{+} = 37 + 37$ 







### **Topic 7B: Infrared (IR) Spectrometry**

Infrared spectroscopy is an analytical technique that uses **infrared (IR) radiation** to determine the **functional groups** present in organic compounds. The IR radiation is passed through a sample where the different types of bonds **absorb** the radiation in different amounts. These varying amounts of absorbance are **measured and recorded**, allowing certain bonds, and thus functional groups, to be identified.

A **spectrum** is produced from the measurements, which has **characteristic curves** for the different functional groups:

#### -O-H Alcohol Group



The characteristic -O-H alcohol group peak is in the range 3230 - 3550 cm<sup>-1</sup>





The characteristic C=C peak is in the range 1620 - 1680 cm<sup>-1</sup>

#### C=O Carbonyl Group



The characteristic C=O peak is in the range 1680 - 1750 cm<sup>-1</sup>

#### **Fingerprint Region**

Each IR spectrum has a **fingerprint region** on the right-hand side, from 500-1500 cm<sup>-1</sup>. This is unique for each species, containing **tiny differences** between each species. This means it acts as a molecules' 'fingerprint', allowing it to be **identified**.

