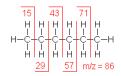
- Separates out the analytes by mass and the fragmentation patterns that occur
  - o Can distinguish between individual isotopes
- Since fragmentation patterns can get quite complex, separation by HPLC can be necessary to get each analyte on its own

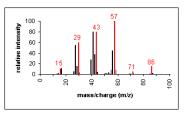
#### Ionisation

- MS relies on ionisation to create a charge that can propel the molecule
- The process typically occurs via bombardment with electrons and forms radicals in the process
- If the parent molecule isn't stable in a charge state, it can fragment as well and will not show up as a peak on the MS

#### Fragment pattern

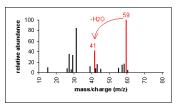
- Fragmentation is typically consistent for a particular molecule
- E.g. Hexane MW=86





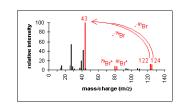
o Fragments into 14 MW fragments (H-C-H)

• E.g. 3-pentanol - MW=88



- o Upon ionisation the C-C bond next to the alcohol is cleaved
- o Sometimes a dehydration can also occur
- o The parent molecule is not stable in an ionised form and thus is not detected
- E.g. 1-bromopentane mw=123





- $\circ \quad \text{Chlorine and bromine can often be detected by multiple isotopes being detected} \\$ 
  - <sup>79</sup>Br and <sup>81</sup>Br have a natural occurrence of 100:98
- Interpretation is based on identification of common molecular fragmentation patterns and their stable ions
  - Identifying what the resulting ion is, can tell you what the parent fragment may have looked like

## Ionisation methods

- Different methods can have different results
- Different methods can be soft or hard
  - $\circ \ \ \text{Soft methods result in less structural damage and thus less structural identification can be carried out}$
  - o Hard methods are usually quite destructive and only useful for smaller mass molecules
- Since MS was originally invented for protein analysis, much larger potential methods have been created to ionise
  proteins.
  - Detection is still limited to a certain range however, so sometimes increasing the energy to decrease the m/z ratio is needed to obtain a satisfactory result.

## Sample introduction and Ionisation

# Electrospray Ionisation (ESI)

- o An aerosol of the eluent is sprayed into the ioniser with a proton source such as acetic acid
- $\circ \ \ \, \text{Thermal evaporation of the aerosol decreases the size of the droplets, but maintains the charged proton count}$
- As the droplets get smaller and smaller, the charges on the molecules and in the solvent increase in a "coulombic explosion" that breaks apart droplets further resulting in a gaseous spray of charged particles
- o Useful for large molecules as they can become multiply charged

# Atmospheric Pressure Chemical Ionisation (APCI)

- A plasma is formed with the eluent and a corona discharge (arcing electricity) is used to pull off electrons
- The corona discharge protonates the analytes by charging gasses to produce cations
- The charged gas charges the solvent molecules which in turn protonates the analytes in question
- o Useful for smaller mass molecules, as there is less chance of multiple charges occurring

# Atmospheric Pressure Photo Ionisation (APPI)

- High power UV is used to ionise the molecules in question
- o When the UV wavelength is greater than the ionisation barrier of the molecule, the electron is liberated
- $\circ \quad \text{Useful where other methods of ionisation don't work, e.g. nonpolar analytes that won't hold a charge} \\$

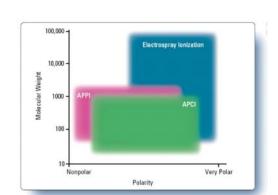
# Solute separation

Quadrupole

Table 20.3

Ionization Method	Typical Analytes	Sample Introduction	Mass Range	Method Highlights
Electron impact (EI)	Relatively small volatile	GC or liquid-solid probe	To 1000 daltons	Hard method. Versatile, provides structure information
Chemical	Relatively	GC or liquid-solid probe	To 1000	Soft method, Molecular
ionization (CI)	small, volatile		daltons	ion peak [M + H]"
Electrospray	Peptides,	Liquid chromatography	To 200,000 daltons	Soft method. Ions often
(ESI)	proteins, nonvolatile	or syringe		multiply charged
Matrix-assisted	Peptides,	Sample mixed in solid matrix	To 500,000 daltons	Soft method, very
laser desorption	proteins,			high mass
(MALDI)	nucleotides			

\*From Web page of Professor Vicki Wysocki, University of Arizona. Reproduced by permission



- o Oscillates a magnetic filed between four electrodes down the path of the MS
- o Only ions with a specific m/z will be resonant and allowed to pass down to the detector

- o Filters ions based on the time it takes them to travel to the detector
- $\circ~$  The ions are magnetically accelerated and will take a different amount of time based on the m/z  $\,$

### Solute detection

- MS detectors continuously scan the whole range of detectable m/z to generate a chromatogram
- Can be presented as:
  - o Total Ion Count (TIC)
    - The m/z are accumulated into a single plot over all time
  - $\circ~$  Show a single m/z over a period of time
- This is because the detector measures data in two dimensions and there are multiple ways to present the data in one dimension

# Standardisation

- Isotopically enriched standards can be used to use MS quantitatively
   The molecules will have the same physical properties and will be eluted at the same time, however will present with a different m/z
  - Comparison of quantity to the known spike can be made

# Analysis

- Comparison/identification is made by both retention time and m/z
   Use of all standardisation methods (single point, calibration curve, standard addition) are possible