CONCEPT: MASS SPECTROMETRY

●*Mass Spectrometry* (*MS*): ionizes, quantifies, & separates molecules based on their _____-to-_____ ratio (*m/z*).

□ m/z: _____ property used to identify molecules & get structural/chemical information.

□ Since z is almost always equal to ____, m/z is often considered to be the _____.

●Mass spectrometers typically operate in the following order:

1) Purified peptide first converted to a _____ & _____ in a vacuum.

□ Ionization occurs via controlled bombardment with _____ or a noble gas (ex. He).

□ Leads to random _____ of *most* peptide molecules (usually breaks at peptide bonds).

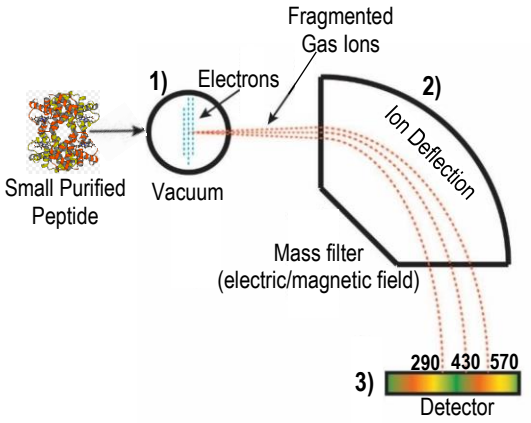
2) Ionized gas peptide fragments are exposed to an _____ or magnetic field.

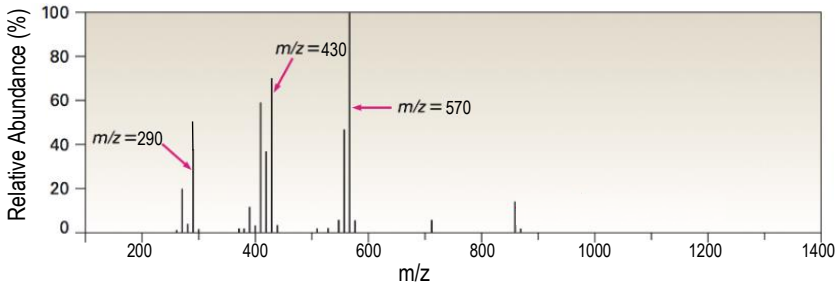
□ Electric field _____ the ionized gas fragments & the _____ they take are a result of their m/z.

□ Fragments with _____ m/z ratios are deflected _____ than those with larger m/z ratios.

3) A detector measures the relative _____ & m/z of each ionized gas peptide fragment.

EXAMPLE: Mass Spectrometry.





PRACTICE: Considering the mass of each residue (shown below) and the fact that not every peptide bond will break in mass spectrometry of a protein, answer the following questions.

A) If cleavage between two Gly residues does not occur, which amino acid would be identified in place of the two glycines?

a) Gly. c) Asp.

b) Asn. d) Ser.

B) What amino acid would be identified if a bond between Ser and Val did not break?

a) Trp. c) Thr.

b) Tyr. d) Val.

Amino Acid	Mass of Residue (g/mole)
Alanine	71.08
Arginine	156.18
Asparagine	114.16
Aspartate	115.08
Cysteine	103.18
Glutamate	129.08
Glutamine	128.14
Glycine	57.08
Histidine	137.18
Isoleucine	113.18
Leucine	113.18
Lysine	128.18
Methionine	131.18
Phenylalanine	147.18
Proline	97.08
Serine	87.08
Threonine	101.08
Tryptophan	186.16
Tyrosine	163.18
Valine	99.08