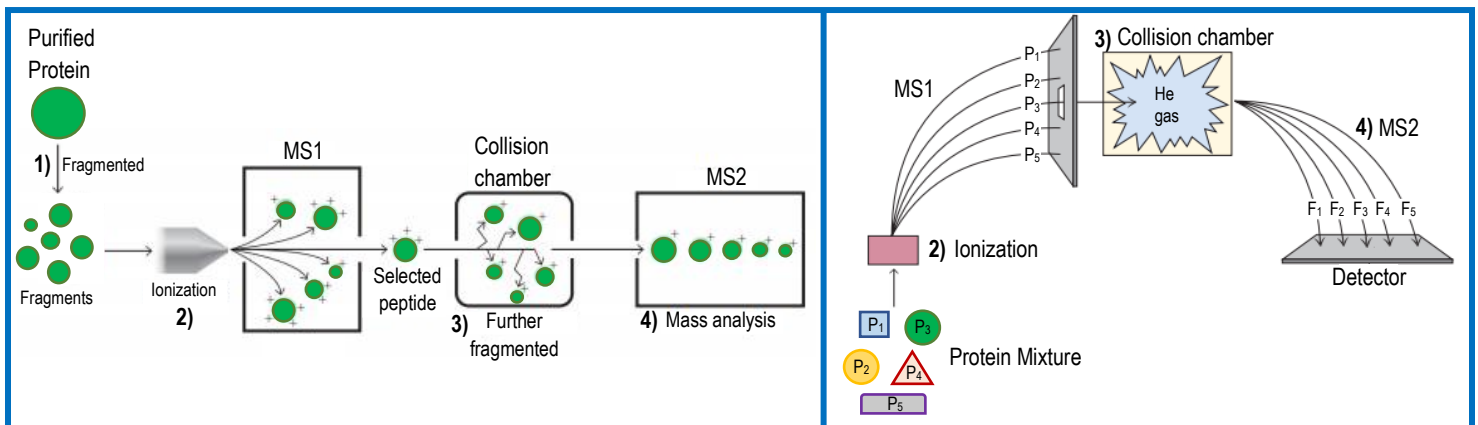


CONCEPT: TANDEM MASS SPECTROMETRY

- **Tandem MS (or MS/MS):** _____ mass spectrometers are hooked up in tandem.
 - It's the _____ standard for sequencing proteins & can analyze purified protein or a single protein in a mixture.
 - Allows for _____ of unwanted ions to obtain a much cleaner/simpler mass spectrum.
- **Tandem MS** consists of the following _____ steps:
 - 1) Purified protein is first _____ with a chemical or a protease.
 - 2) Protein fragments are *ionized* & subjected to _____ so one fragment is filtered/selected to emerge at the end.
 - Selected protein fragment enters a _____ cell vacuum chamber.
 - 3) A _____ gas (ex. He or Ar) further fragments the selected protein (usually breaks at peptide bonds).
 - 4) Generated protein fragments enter a _____ mass spectrometer, which measures all the m/z ratios.

EXAMPLE: Tandem Mass Spectrometry of a Purified Protein & a Single Protein in a Mixture.



PRACTICE: Tandem mass spectrometry combines which of the following devices?

- a) Mass spectrometer with HPLC.
- b) Mass spectrometer with chromatography.
- c) Mass spectrometer with a PMF database.
- d) Mass spectrometer with a mass spectrometer.

PRACTICE: In your tandem mass-spectrometry of a pure protein, you focused a fragment with an m/z of 1,268 through the process & into the second mass-spec and found y-ion peaks of 1,137 and 1,022. The mass in Daltons for the possible relevant amino acids are provided: Y (163), N (114), W (186), D (115), G (57), L (113) and M (131). What is the order of the first two amino acid residues in the 1,268 fragment from N-terminal to C-terminal?

- a) N-M.
- b) N-Y.
- c) M-D.
- d) M-L.
- e) D-N.