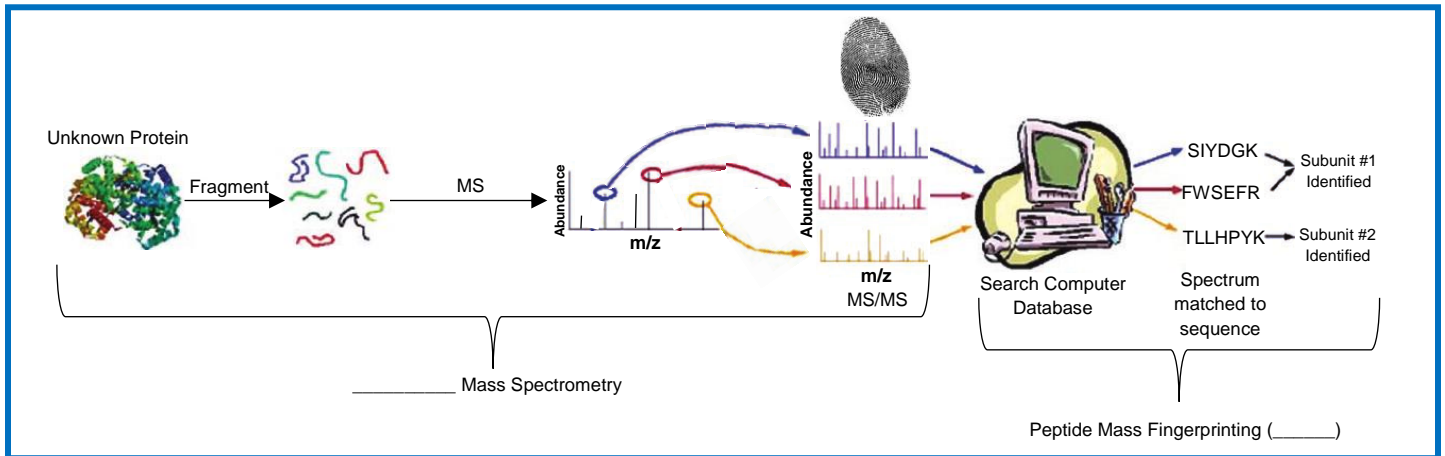


CONCEPT: PEPTIDE MASS FINGERPRINTING

- **Peptide Mass Fingerprinting (PMF)**: uses MS spectrums from databases to identify _____ proteins.
 - Actual spectrum of unknown protein is compared to spectrums of all known proteins until a match is found.
 - Usually only necessary to analyze _____ portions of an unknown protein to identify it.
 - _____: the database must already include the protein to identify it.

EXAMPLE: Peptide mass fingerprinting.



PRACTICE: Peptide mass fingerprinting (PMF) is a method used to determine the sequence of an unknown peptide. In the sequencing of peptides by PMF, tandem mass spectrometry fragments peptides into smaller molecules to obtain the mass spectrum, which acts like a fingerprint & can be compared to theoretical spectrums in a database to derive the amino acid sequence. Mainly which types of bonds are broken to fragment the peptide & generate tandem mass spectra data?

- Carbon-carbon bonds within the amino acid R-groups.
- Disulfide bonds.
- Omega bonds.
- Phi bonds.
- Psi bonds.

PRACTICE: Explain how a 5-residue amino acid sequence *could* uniquely identify a 200-residue protein via PMF.

Hint #1: Compare the number of pentapeptides in a 200-residue protein to the total number of all possible pentapeptide sequences.

Hint #2: A protein sequence of "n" residues has the potential to give rise to "n-4" pentapeptides.

So, a 200-residue protein could give rise to _____ pentapeptides.

Hint #3: Total # of all possible pentapeptides = (# of α -amino acids)^{# of Positions in Peptide} = 20^5 = _____