# Biochemistry CUME October 2019

Topic: Protein Structure Analysis

Protein structures can be described and characterized at four different levels: primary structure (1°), secondary structure (2°), tertiary structure (3°) and quaternary structure (4°).

## 1. Primary Structure (25 points)

(a) **(10 points)** Give the chemical structure of a peptide shown on the left, write down the amino acid sequence from the N-terminus to the C-terminus in a single-letter format.

Single-letter sequence:

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | |
| | | | | | | | | | |

(b) **(5 points)** Circe three peptide planes. Explain why a peptide bond cannot rotate freely.

c) **(10 points)** Name one method that be used for determining the amino acid sequence of a peptide or protein. Explain the physical or chemical principle of your selected method.
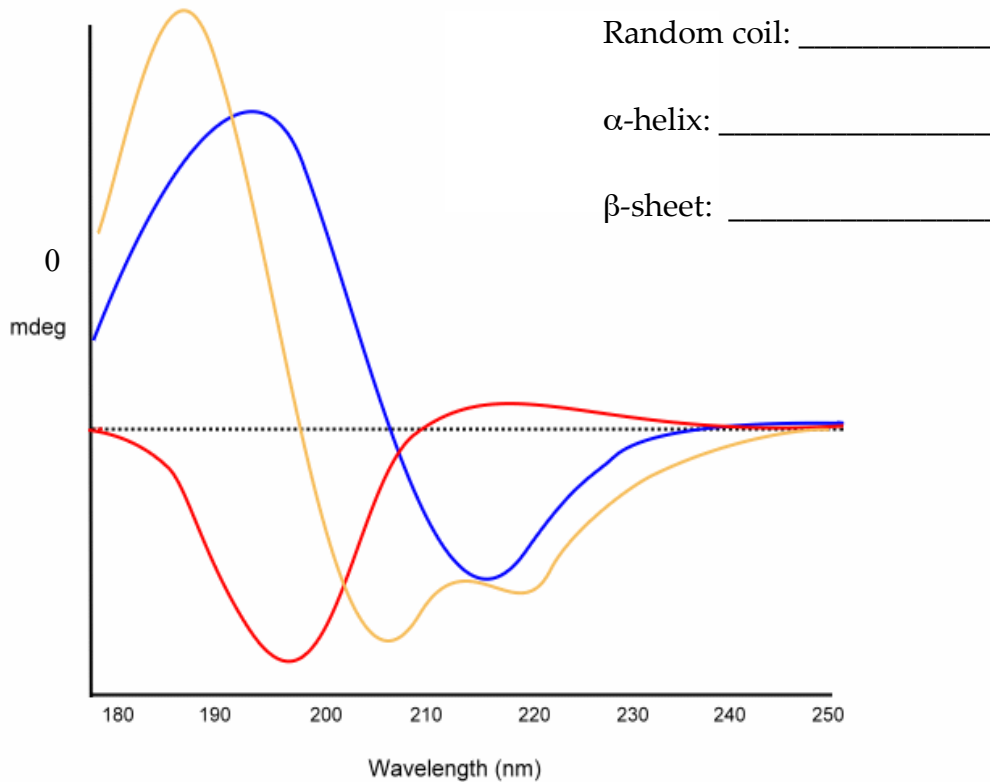
## 2. Secondary Structure (25 points)

α-helix and β-sheet represent two major types of protein secondary structures. They are characterized by the distinct patterns of hydrogen bonds between the main-chain atoms.

(a) **(10 points)** Use dashed lines to mark all possible main-chain hydrogen bonds between the adjacent β-strands shown below.



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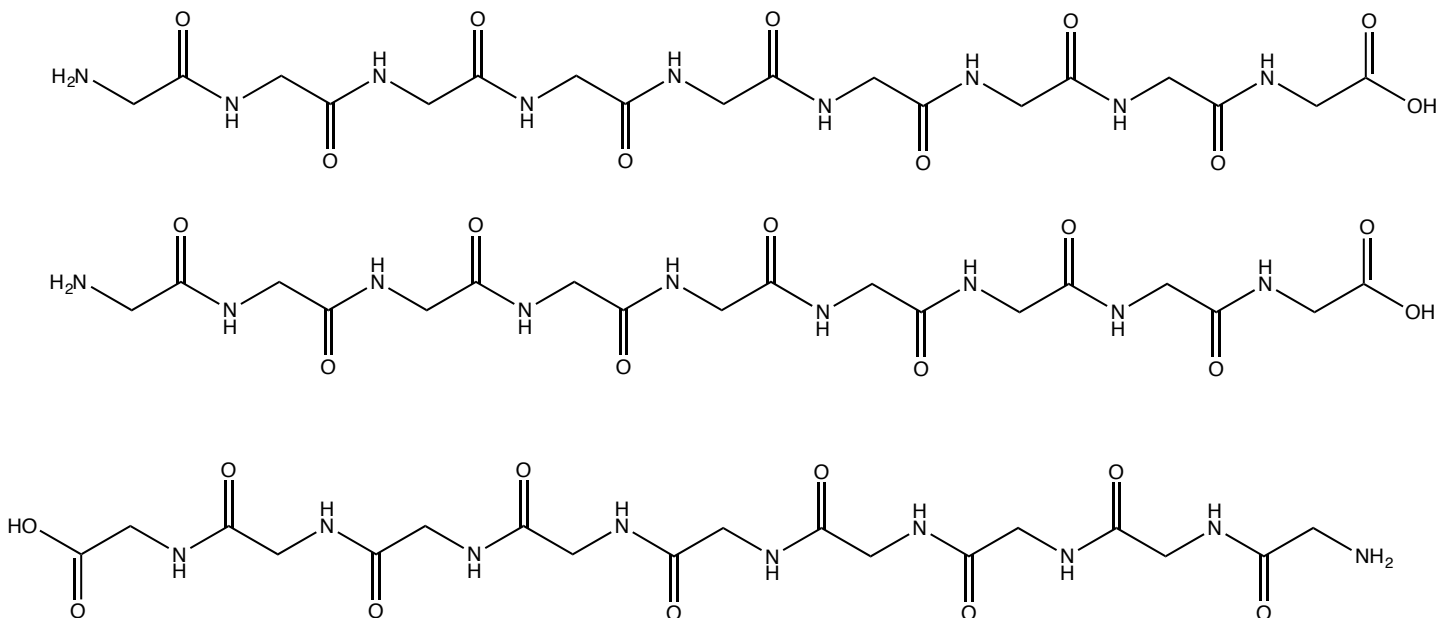
(b) **(5 points)** Describe the major differences in hydrogen bonding pattern between the parallel β-sheet and antiparallel β-sheet.

(c) **(10 points total)** Protein secondary structures have distinct optical activities, which can be detected by circular dichroism (CD) spectroscopy in the far-UV region. The figure below shows the characteristic CD spectra for the three common types of secondary structures, namely α-helix, β-sheet and random coil. Can you establish the correspondence between each colored curve and the named secondary structure (5 points)?

Random coil: _____

α-helix: _____

β-sheet: _____

Explain the origin for such optical activities (5 points).

**3. Tertiary Structure (25 points)**

(a) **(5 points)** Protein folding is a process by which a linear polypeptide chain is folded into a specific, functional three-dimensional structure. What are the major interactions or molecular forces that drive the protein folding process?

(b) **(10 points)** The backbone conformation of a protein structure can be depicted by the main chain dihedral angles, phi ($\phi$) and psi ($\psi$). A scatter plot between phi ($\phi$) and psi ($\psi$) for all amino acids of a protein structure is known as the Ramachandran plot. In the plot shown below, please **circle** and **mark** those region(s) where you expect to find a residue from the α-helix or β-strand, respectively.
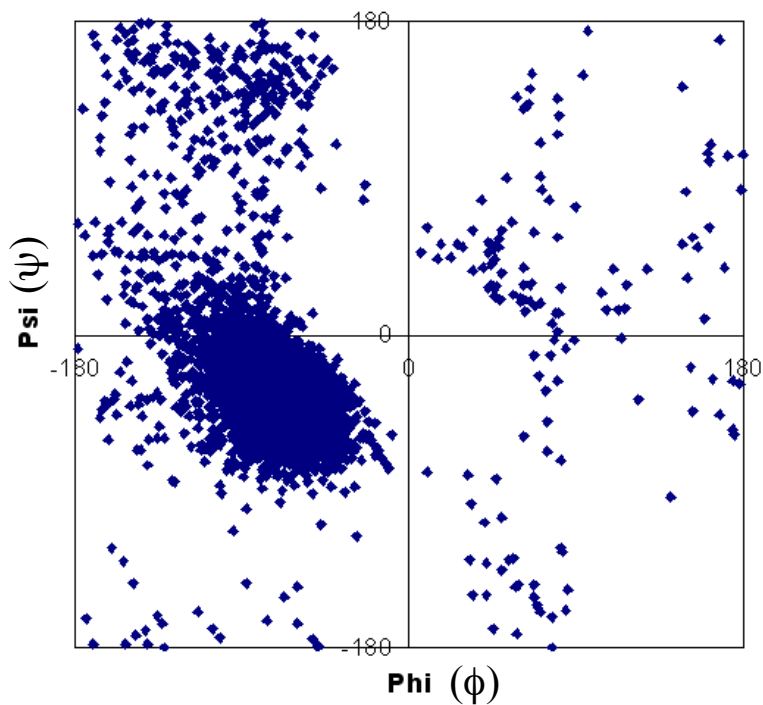


(c) **(10 points)** Name three major biophysical methods that have been widely used for 3D protein determination at the atomic or near-atomic resolution. Use a table to directly compare their strengths and limitations.

**4. Quaternary Structure (25 points)**

(a) **(15 points)** Many proteins form high-order oligomers for desired functions that cannot be accomplished by monomers. Use human hemoglobin (Hb) or any other system as an example to explain the importance of the quaternary structure in protein functions.

(b) **(10 points)** Discuss one or two biochemical (NOT structural) methods that are commonly used to determine the quaternary structure of a multi-subunit biological assembly. Explain why and how.