Mid sem 2025
Biophysics(BIOP)

Total Marks:30

Time: 1 Hour

Section A

1. Which of the following best describes the FASTA format?
   A. A file format for storing protein structures
   B. A text-based format for representing nucleotide or peptide sequences
   C. A binary format used in protein alignment
   D. A compressed format for protein motifs

2. Which statement about water-mediated hydrogen bonds in protein folding is TRUE?
   A. They always destabilize folding
   B. They can stabilize transient intermediates
   C. They are weaker than direct hydrogen bonds and irrelevant
   D. They occur only in unfolded states

3. Proteins from thermophilic organisms are usually "harder" because:
   A. They have fewer hydrophobic residues
   B. They are shorter in sequence length
   C. They contain more stabilizing interactions
   D. They lack secondary structure

4. Which of the following correctly represents the hierarchical order in the CATH classification system?
   A. Fold → Architecture → Class → Topology → H-level
   B. Class → Topology → Architecture → Fold → H-level
   C. Class → Architecture → Topology → Fold families → H-level
   D. Architecture → Class → Fold → H-level → Topology

5. Which structural type would most likely occupy a $\varphi \approx -60°$, $\psi \approx -45°$ region in a Ramachandran plot?
   A. Right-handed α-helix
   B. β-sheet
   C. Left-handed α-helix
   D. Random coil

6. Which statement is TRUE regarding the interplay of bonded and non-bonded interactions in protein folding?
   i. Bonded interactions determine long-range tertiary contacts
   ii. Non-bonded interactions only affect unfolded proteins
   iii. Bonded interactions define local geometry

iv. Non-bonded interactions guide folding and stabilization

(A) i&ii (B) i&iii (C) ii&iii (D) iii&iv

7. During transcription, RNA is synthesized in which direction?
   A. 3' → 5' along the RNA strand
   B. 5' → 3' along the RNA strand
   C. 3' → 5' along the DNA template
   D. Both B and C

8. Which of the following is not representing the stop codon?
   A. TAA
   B. TGC
   C. TAG
   D. TGA

9. Match the following algorithms with their applications in bioinformatics:

A. Smith Waterman algorithm	1. Multi-Chaperone system
B. Protein misfolding	2. Pairwise sequence alignment
C. Chou Fasman method	3. Protein secondary structure prediction
D. Protein folding	4. Baculovirus system

   A. A–1, B–2, C–3, D–4
   B. A–2, B–4, C–3, D–1
   C. A–3, B–4, C–1, D–2
   D. A–4, B–3, C–2, D–1

10. Keratin is a structural protein with a hierarchical organization. Which of the following correctly represents the order of assembly from the simplest to the most complex structure?

   A. Protofilament → α-helix → coiled coil → filament
   B. α-helix → coiled coil of two α-helices → protofilament → filament
   C. Coiled coil of two α-helices → filament → protofilament → α-helix
   D. α-helix → protofilament → filament → coiled coil

Section B

1. In a protein, valine is found buried inside the core, while serine is on the surface. Explain the chemical property (VAL & SER) responsible for this placement, and why/how this contributes to stability. **(3 mark)**

2. A ligand binds to a protein and interacts with eight residues that are closely positioned in its quaternary structure.
   a. Does this imply that these residues are also close in the protein's primary sequence? Justify your answer with structural reasoning. **(2 mark)**
   b. What is the primary command to select and highlight only the residues located within a 5 radius of the bound ligand (in Chimera)? **(1 mark)**

3. The evolution of proteins often results in functional diversity. Imagine two genes, initially identical, diverging over time to perform different, yet related, tasks in various organisms

   (a) Define paralogs and orthologs, giving one biological example of each. **(2 mark)**

   (b) If two proteins are homologous, but one performs glucose transport in humans and the other performs amino acid transport in humans, what relationship do they have? **(1 mark**

   (c) If two proteins perform glucose transport in humans and mice, what relationship do they have? **(1 mark)**

Section - C (5 marker)

1. During molecular modeling of a newly designed enzyme, you notice that the folded protein structure shows several steric clashes in the hydrophobic core. Answer the following:

   (a) what happens to energy as interatomic distance (w.r.t LJ Potential) $r \to 0r$ \to $0r \to 0$? **(1 mark)**

   (b) Why are hydrophobic protein cores mainly stabilized by van der Waals interactions? **(1 mark)**

   (c) What do you understand by 'Clashes'? How do van der Waals radii help prevent steric clashes? **(2 marks)**

   (d) Explain how the balance of Lennard–Jones attractive and repulsive forces determines protein packing density. **(1 mark)**

2. A structural biology team is studying a small protein involved in cell signaling. Interestingly, a 10-residue stretch forms an α-helix when the protein is crystallized alone, but the same region forms a β-strand when bound to a partner protein. This conformational switch is thought to influence binding affinity and stability.

   a. What is this type of sequence in proteins called? Explain with an illustrative example **(3 mark)**

   b. Why is it surprising in the context of secondary structure prediction?**(2 mark)**