Quiz1 2025
Biophysics(BIOP)

Total Marks:20

Time: 45 minutes

Section-A (MCQ 1*10 Marks)

1. A Nucleoside differs from a nucleotide in the following way:
   a. Nucleotide has a phosphate group; nucleoside does not
   b. Nucleotide lacks a sugar; nucleoside has a sugar
   c. Nucleotide lacks a nitrogenous base; nucleoside has a base
   d. Nucleotide lacks hydrogen bonding; nucleoside has hydrogen bonding

2. The basic principle of X-Ray Crystallography is based on:
   a. Diffraction of X-rays by protons in a crystal lattice.
   b. Absorption of X-rays by crystal lattice.
   c. Diffraction of X-rays by electrons in a crystal lattice.
   d. Emission of X-rays from atoms

3. The 2017 Nobel Prize in Chemistry was awarded for the development of which technique?
   a. X-ray crystallography
   b. Cryo-electron microscopy (Cryo-EM)
   c. Nuclear magnetic resonance (NMR) spectroscopy
   d. Mass spectrometry

4. The parameter 'σ' in the Lennard-Jones potential best corresponds to which of the following definitions?

   a. The depth of the energy well.
   b. The distance where the potential energy V(r) is zero.
   c. The distance of maximum repulsion.
   d. The sum of the minimum van der Waals radii from the table.

5. Identify the correct bond representation of torsion angle ϕ(phi) and ψ(psi) in the proteins?

   a. ϕ(C-N-CA-C) and ψ(N-CA-C-N)
   b. ϕ(C–N–CA–N) and ψ(C–N–CA–N)
   c. ϕ(N–CA–N–C) and ψ(CA–N–CA–C)
   d. ϕ(CA–C–N–CA) and ψ(N–C–N–CA)

6. How does the hydrogen bonding in an alpha-helix differ from that in a beta-sheet?

a. Alpha-helices uses side-chain donors/acceptors, while beta-sheets use the protein backbone.
b. ~~Alpha-helices form intra-chain H-bonds, while beta-sheets form inter-chain H-bonds~~.
c. Beta-sheet form inter-chain H-bonds, while alpha-helices form intra-chain H-bonds.
d. Apha helices and beta sheets both form inter-chain H-bonds

7. During protein synthesis, the polypeptide chain is elongated in which direction?

a. From the C-terminus to the N-terminus, adding new amino acids to the carboxyl group.
b. From the N-terminus to the C-terminus, adding new amino acids to the carboxyl group.
c. From the C-terminus to the N-terminus, adding new amino acids to the amino group.
d. From the N-terminus to the C-terminus, adding new amino acids to the amino group.

8. Which two discoveries were most critical for Watson and Crick's determination of the double-helix structure of DNA?

a. Pauli exclusion principle and London dispersion forces
b. Anfinsen's dogma and Levinthal's paradox
c. Chargaff's rules and X-ray diffraction patterns
d. Alpha-helix H-bonding and beta-sheet formation

9. A protein is identified as being insoluble, highly regular in structure, and forms strong aggregates. It is most likely classified as a:

a. Globular protein
b. Fibrous protein
c. Membrane protein
d. Enzymatic protein

10. The Lennard-Jones potential describes interactions between atoms. Which of the following correctly identifies its two components and the forces they represent?

a. Attractive term ($-1/r^6$): van der Waals forces; Repulsive term ($+1/r^{12}$): Pauli repulsion
b. Attractive term ($-1/r^6$): Ionic forces; Repulsive term ($+1/r^{12}$): Covalent bonding
c. Attractive term ($-1/r^{12}$): van der Waals forces; Repulsive term ($+1/r^6$): Pauli repulsion
d. Attractive term ($-1/r^6$): Hydrogen bonding; Repulsive term ($+1/r^{12}$): van der Waals forces

Section-B (2*5=10 mark)

1. The Buckingham and Lennard-Jones potentials both model van der Waals interactions. Justify why the more accurate Buckingham potential is often replaced by the Lennard-Jones potential in molecular simulations.

Ans: The Buckingham potential uses an exponential term ($Aexp^{(-Br)}$) to model quantum repulsion. Calculating exponential functions is computationally expensive and slow for a computer, especially when done for millions of atom pairs in a simulation. [1 mark]
Computational Efficiency: The Lennard-Jones potential uses a $1/r^{12}$ term for repulsion. This is extremely efficient to compute because the attractive $1/r^6$ term must already be calculated for the dispersion force. The repulsive term can be found with just one additional multiplication: $(1/r^6) * (1/r^6)$. [1 mark]

2. Justify why α-helices are considered more flexible yet more stable compared to β-sheets.

Answer: α-helix is generally more stable, it has regular intra-chain H-bonds (i → i+4) that satisfy backbone donors/acceptors within the same strand, producing a compact, low-energy conformation. β-sheets depend on inter-strand H-bonds and proper strand alignment; they can be very stable when many strands form an extended network (e.g., amyloid), but individual strands are more susceptible to edge exposure and solvent, so β-sheets are not intrinsically more stable than helices in isolation.

3. Describe the utility of a Ramachandran plot in the process of validating a protein's three-dimensional model. What specific structural features does it help to identify?

Ans: A Ramachandran plot displays the allowed dihedral angles (φ and ψ) of amino acid residues in a protein. It is used to validate protein 3D models by checking whether residues fall within favored regions. It helps identify specific secondary structures like α-helices and β-sheets, and highlights residues in disallowed regions that may indicate errors in the protein model.

4. A short peptide has 3 residues. Its Φ and Ψ angles are sampled in 90-degree increments.

a. Calculate the number of possible conformations. **(1.5 mark)**

Ans. 360°/90° = 4 states per angle. [0.5 mark]
$4^2 = 16$ conformations per residue. [0.5 mark]
For 3 residues: $16^3 = 4096$ possible conformations. [0.5 mark]

b. Name the paradox that this type of calculation illustrates? **(0.5 mark)**

Ans. **Levinthal paradox**: random search of all possible conformations to find the native one

5. Which conformation is generally not observed in peptide bonds and why? Give two reasons. State the exception.

Ans. **Cis** conformation is extremely rare. [0.5 mark]

Reason:

Steric clash: In the cis geometry, the two adjacent Cα substituents (and their side chains) lie on the same side and collide sterically, which raises the energy compared with the trans arrangement. [0.5 mark]

Peptide resonance & planarity: The peptide bond has strong partial double-bond character (resonance), fixing it planar and making the lower-energy, less-crowded trans orientation strongly preferred. [0.5 mark]

Exception: proline where the cyclic side chain reduces steric hindrance, allowing the cis conformation to occur more frequently [0.5 mark]