

1. In nature, we can find many types of helical structures. These helical structures can be described in several geometric characteristics (e.g. pitch  $p$ , radius  $r$ , the rise per residue  $\Delta z$ , angular distance between successive residues  $\Delta\theta$ ). Fill the blank in the following table (10 points)

Table 1. Geometry of Helix

Secondary structure	Residues per turn (n)	pitch $p$ (Å)	the rise per residue $\Delta z$ (Å)	radius $r$ (Å)
$\alpha$ -helix	3.6	5.4	1.5	2.3
$3_{10}$ -helix	3.0	6.0	2.0	1.9
$\pi$ -helix	4.3	4.7	1.1	2.8

2. There are a variety of -omics sciences that often indicate the totality of information at a given scientific field. List at least 5 different -omics nomenclatures (e.g. genome, proteome) (5 points)

Transcriptome, physiome, metabolome, metagenome, protein interactome...

3. When you surveyed the protein structures and functions, you may classify them into various general classes. List these classes of protein structures and functions (5 points)

Fibrous proteins, Enzymes, Antibodies, Inhibitors, Carrier proteins, Membrane proteins, Receptors, Regulatory proteins, Motor proteins

4. List at least three applications of microarray techniques (3 points)

Expression chip, genome hybridization (ChiP), mutation analysis (SNP)

5. List at least three disadvantages of microarray techniques (3 points)

Limitation to low expressed mRNA, Experimental biases, Protein turnover

6. Define and compare following pairs (or triples) of terms (4 points each)

- Molecular function, Cellular function
- Homology, Analogy
- Orthology, Paralogy, Xenology
- Protein folding, inverse protein folding
- Domain, motif, module
- Homology modeling, threading
- Contact order, folding rate

7. What are three major structural classification systems? What are the major differences among them? (6 points)

**SCOP (visual inspection by human), CATH (semi-machine based), FSSP (machine based)**

8. Many viruses show icosahedral shape and the number of subunits in this structure can be determined by a triangular number (T). If a virus conforms icosahedral structure having T=3, how many subunits are needed to build intact icosahedral coat? (3 points)

**180 subunits**

9. Proteins are stabilized by many energetic factors such as various chemical bonds and their interactions. The stabilization energy of proteins is usually small, about ( 20 )-( 60 ) kJ/mol (2 points)

10. As an environment for proteins, the membrane differs from a conventional aqueous solution not only in containing an organic medium, but in being (**anisotropic**) - that is, having a favored direction (2 points)

11. List all amino acids which do not describe 'Chi'( $\chi$ ) torsion angles (5 points)

**Glycine, Alanine**

12. How do proteins develop new functions? (three mechanisms) (3 points)

**Divergence, recruitment, mixing and matching of domains**

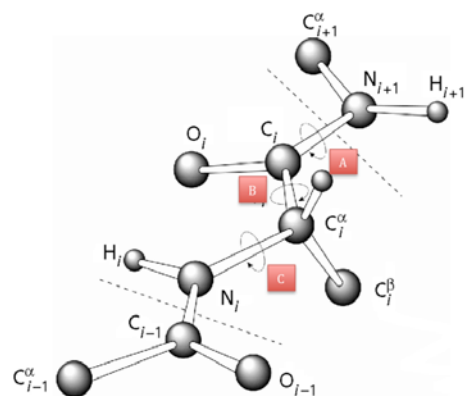
13. You determined the structure of a protein complex having an interfacial area of  $1700 \text{ \AA}^2$ . According to typical properties of protein-protein interface, how many water molecules can be existed in this interface (3 points)

**10 molecules**

14. Indicate psi( $\psi$ ), pi( $\phi$ ), omega( $\omega$ ) torsion angles in the right figure (3 points).

**A-omega, B-psi, C-pi**

15. What is two-state equilibrium? How do we know that the protein folding pathways of small proteins follows two-state equilibrium model? (4 points)

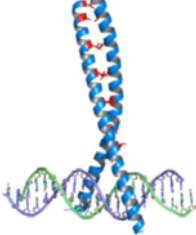
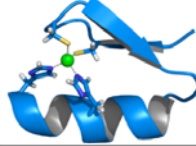



**Only two state can be observed during the reaction such as initial state (Native) and final state (Unfolded state). We cannot observe any stable folding intermediates.**

16. What is 'Ramachandran plot'? When can you use it for what purpose? (6 points)

Plot of torsion angle of peptide backbone in a protein structure (x-axis= $\phi$ , y-axis= $\psi$ ).  
Ramachandran plot can be used for assessment of protein structure validation.

17. Draw lines between DNA binding features and appropriate structures (6 points)

Zinc finger	
Helix-turn-helix	
Leucine zipper	

18. What is  $\Phi$ -value? What is its implication in protein folding study? (6 points)

Empirical expression of importance of a given residue in a protein during the folding pathways. When  $\Phi$ -value is zero, the residue is not involved in interactions with other residues in a transition state. If  $\Phi$ -value is 1, then the residue interact with other residue in the protein contributing the folding pathway from the transition state.

19. What are three major methods to determine protein structures? (3 points)

X-ray crystallography, NMR, and EM