2015
BIOCHEMISTRY
Paper – BCT-303
(Molecular Interaction)
Full Marks – 25

The figures in the margin indicate full marks

Candidates are required to give their answers in their own words as far as practicable

Answer ***any eight*** questions of which ***Question no. 1*** is compulsory

1. Fill in the blanks : 3

Tyrosine and tryptophan are significantly more polar than phenylalanine, because of the tyrosine _____ and the _____ of the tryptophan indole ring. Tryptophan and tyrosine and to a much lesser extent _____ , absorb ultraviolet light.

The secondary amino (imino) group of _____ residues is held in a rigid conformation that reduces the structural flexibility of polypeptide regions containing _____.

The polarity of serine and threonine is contributed by the _____ groups; that of cysteine by its _____ group; and that of asparagine and glutamine by their _____ groups.

Cysteine is readily oxidized to form a covalently linked dimeric amino acid called _____, in which two _____ molecules or residues are joined by a disulfide bond.

2. Fill in the blanks : 3

If a polypeptide chain has a long block of _____ residues, this segment of the chain will not form an α helix at pH 7.0. The negatively charged carboxyl groups of adjacent _____ residues repel each other so strongly that they prevent formation of the α helix. For the same reason, if there are many adjacent _____ and/or _____ residues, which have positively charged R groups at pH 7.0, they will also repel each other and prevent formation of the α helix. The bulk and shape of _____ , Ser, Thr, and Cys residues can also destabilize an α helix if they are close together in the chain.

Or

A _____ residue introduces a destabilizing kink in an α helix. In addition, the _____ atom of a Pro residue in peptide linkage has no substituent hydrogen to participate in hydrogen bonds with other residues. For these reasons, _____ is only rarely found within an α helix. _____ occurs infrequently in α helices for a different reason : it has more conformational flexibility than the other amino acid residues. Polymers of _____ tend to take up coiled structures quite different from an α helix.

3. The stabilization of the tertiary structures of polypeptide chains is ensured by certain restrictions on the organization of the motifs. Describe them in brief. 3

4. What is the prerequisite condition for reformation of eight disulfide bonds while folding denatured ribinuclease ? How did Anfinsen demonstrate that ? 3

5. What form of helix is RNA and what are its characteristics ? Is the RNA chain a helix or random coil ? 3

6. Briefly describe how MC- SYM program proceeds to predict RNA conformation. 3

7. Can the β sheets of proteins and Stem-Loops in RNA be described as secondary structures ? If not, explain why ? 3

8. Describe how the residues at the interface of a protein-protein complex are identified from the PDB file representing the 3D structures of the protein-protein complex. 3

9. Describe the basic principle of 'Yeast two hybrid system' method for detecting protein-protein interactions. 3

10. Provide a schematic diagram of surface plasmon resonance detection unit. 3

11. Name the factors on which the SPR angle depends. Correlate : Shift in SPR angle and Resonance unit. 3

12. Explain the parameters describing chain initialization and chain elongation. Consider a hypothetical chain element containing four elemental residues A each having either + or – states (+ representing helix and – representing coil). What will be the partition function? 3

13. Consider 30C values for σ and s values for glycine L-Alanine, L-Serine and L-Leucine as given by $(10^{-5}, 0.62)$; $(8\times 10^{-4}, 1.06)$; $(7.5\times 10^{-5}, 0.79)$; $(33\times 10^{-4}, 1.14)$. Interpret. 3

14. Sketch out the differences in the mechanisms of binding of a zinc finger protein and a 434 repressor protein with a double stranded DNA. 3

15. Discuss the basic advantages of using microcalorimetry to study DNA-protein interaction. 3

16. You are working with a single stranded RNA virus and found that the terminal RNA sequences are involved in binding with a protein which is important for the viral proliferation. Outline a strategy based on peptidomimetics for developing an antiviral compound in relation to your observation. 3

17. Mention five different methods used for characterising RNA protein interactions. 3

One mark for neatness