Register Number:……………………..

B.TECH DEGREE EXAMINATIONS: NOV/DEC 2014

(Regulation 2009)

Sixth Semester

BIOTECHNOLOGY

BTY119: Protein Engineering

Time: Three Hours   **Maximum Marks: 100**

Answer all the Questions:-

PART A (10 x 1 = 10 Marks)

1. Which of the following amino acid has the highest hydropathic score?

    a) Val   b) Arg

    c) Thr   d) Phe

2. The amino acids which destabilize alpha helices are

    a) Asp, Glu   b) Val, Leu

    c) Gly, Pro   d) Lys, Arg

3. Acid hydrolysis of proteins mainly destory the following amino acid

    a) Lys   b) Trp

    c) Tyr   d) Asp

4. You have isolated an unknown protein from nerve cells. It has a molecular weight of 10 KDa as judged by SDS-PAGE. Digestion with CNBr gives equal amounts of five peptides. A chymotryptic digest yields equal amounts of 8 peptides.. One cycle of the Edman degradation gave a Gln-PTH derivative. Which of the following statements could not be concluded from this information's.

    a) This protein would have absorbance at   b) This protein would contain approximately
        280nm   100 aa residues

    c) This protein would have 4 internal Met   d) This protein has 2 disulphide bonds
        residues

5. Molten globule is the one having

    a) Random coil structure   b) disordered 2D & 3D structure

    c) ordered 2D & disordered 3D structure   d) Natively folded structure

6. Syncroton radiation is usually in the range of

    a) 0.2- 2.0 A   b) 2.0-3.2 A

    c) 2.5 – 4.0 A   d) 4. 0- 5.0 A

7. Leucine zipper are conserved motifs in

    a) DNA polymerases   b) Transcription factors

    c) RNA polymerases   d) gyrases

8. Subtilisins are

    a) Thiol proteases   b) Serine proteases

    c) Asp proteases   d) Alkaline proteases

9. Which one of the method is not used for combinatorial library screening of mutant peptides?

    a) mRNA display   b) Ribosomal display

    c) Phage display   d) microarray

10. Which of the following approach is not appropriate to increase the thermal stability of proteins?

    a) Increasing S-S bridges   b) Increasing ionic interactions

    c) Increasing alpha helices   d) Increasing beta sheets

PART B (10 x 2 = 20 Marks)

11. Outline the significant features of a peptide bond in proteins.

12. Sketch a Ramachandran plot indicating the alpha R, beta and alpa L regions.

13. Associate each of the amino acids listed with one of the properties a -e that help to determine the folding and higher level structure of protein.

    Asp, Pro, Leu, Val, Gly, Met, Ile, Lys

    a) steric hindrance of the side chain favors beta sheet.

    b) can fit into tight turns.

    c) helps determine the N-terminal end of α-helix due to its imino N being unavailable to hydrogen bond.

    d) clusters with similar amino acids in the core of the protein.

    e) shows a marked preference for being on the outer surface of protein.

14. Draw the structure of Greek key motif.

15. List out few denaturants of protein.

16. Why do we use X ray to analyze the protein structure?

17. Outline the function of Homeodomain.

18. What are the main structural characteristics of membrane proteins?

19. How the aggregation of insulin can be prevated?

20. Distinguish between rational and irrational design of proteins in protein engineering with their advantages and limitations.

PART C (5 x 14 = 70 Marks)

21. a)   Explain the different types of non covalent interactions and their contribution in stabilizing the protein structure.

(OR)

b)   Give a detailed account on the various types of post translational modifications with suitable examples.

22. a)   Outline the different types of supersecondary structures existing in proteins with suitable examples? Explain any one method commonly used for the prediction of secondary structure.

(OR)

b)   Write in detail the automated Edman degradation method with a suitable example.

23. a)   How is the protein folding pathway elucidated? Explain the role of molecular chaperonins in folding of protein.

(OR)

b)   Describe the structural characteristic features of an α/β domain with an example.

24. a)   What are the essential residues participate in catalysis of serine protease? Outline its catalytic mechanism.

(OR)

b) Outline the structure of different classes of immunoglobulin and how it contribute to specificity of antigen binding.

25. a) Describe in detail any one method used to engineer protein by site directed and random mutagenesis

(OR)

b) Describe how recombinant insulin is engineered to prevent aggregation and inactivation?

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