Total number of printed pages – 2

B. Tech

PEBT 5401

Seventh Semester Examination – 2011

PROTEIN ENGINEERING

Full Marks – 70

Time : 3 Hours

Answer Question No. **1** which is compulsory and any **five** from the rest.

The figures in the right-hand margin indicate marks.

1. Answer the following questions : 2×10

   (a) The molecular formula for glycine is $C_2H_5O_2N$. What would be the molecular formula for a linear oligomer made by lining ten glycine molecules together by condensation systhesis ?

   (b) An amino acid has three ionizable groups with PKa of 2.0, 10.5 and 3.8., What is the PI of this amino acid ?

   (c) Define Beer and Lambert's law.

   (d) Write down the significance of Rama Chandran Plot.

   (e) What is electromagnetic radiation ?

   (f) Define the Q.

   (g) What is quanta ?

   (h) If there are 20 kinds of amino acids and they can be assembled in any order, then how many different proteins of 100 amino acid long can theoretically be produced ?

   (i) What do you mean by "cotton effect" in circular Dichroism ?

   (j) What is chaperons ? What role it plays in protein architecture ?

2. Briefly explain the principle, instrumentation, and application of X-ray crystallography. 10

3. What is mutagenesis ? Explain the various strategies of site directed mutageneis used for genetic engineering of novel protein. 2+8

4. Write short notes on : 5×2

    (a) Spectrophotometer

    (b) ORD

5. What is residue ? Describe various hierarchical level of protein structure. Briefly explain the various kinds of bonds and interactions at various level of structure. 2+4+4

6. (a) Briefly explain the different methods to develop a novel protein with suitable diagram. 5

    (b) Briefly explain the different applications of protein engineering in health science. 5

7. Scientist used specially designated DNA chip of search of SNPs in 85 protein coding genes in 74 individuals. They scanned about 139 kb of genomic sequence consisting of 87kb of coding, 25kb of intron and 77kb of untranslated but transcribed sequences. They identified a total of 874 possible SNPs of which 287 were within coding sequence, these are designated cSNPs, of the cSNPs, 109 would change the amino acid sequence in one of 68 predicted proteins. At least 41,000 human ESTs have already been identified and a reasonable estimate of the human gene number is about 76,000

    (i)   About how many SNPs exist in human genes ? $2\frac{1}{2}$

    (ii) how many are estimated to be in noncoding regions ? $2\frac{1}{2}$

    (iii) How many are in coding regions but do not affect protein structure ? $2\frac{1}{2}$

    (iv) How many are in coding regions and could effect protein structure ? $2\frac{1}{2}$

8. Write short notes on any *two* of the following : 5×2

    (a) Ramachandran Plot

    (b) Molecular chaperon

    (c) Amino acid sequencing