Total number of printed pages – 7 **B. Tech**

PEBT 8406

Eighth Semester Examination – 2008

PROTEOMICS

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) What are the energetic consequences of deleting by mutagenesis of non-polar side chains that occupy substantial volumes in the core of a folded protein ?

   (b) What is the contribution of conformational entropy of a polypeptide chain of 100 amino acids residues to its free energy ?

   (c) Name the rational approaches of protein engineering for affinity purification of designed protein.

   (d) What do you mean by protein differentiation ? What is its significance ?

   (e) How biomarker protein play significant role in drug development and drug delivery ?

   (f) Show the flow diagram of the processes involved in 2-DE gel image analysis.

   (g) What is Prion protein ? What is the effect of changes in amino acid residues on prion protein ?

(h) What minimum concentration bio molecules you need for Electro-spray, MALDI-MS and FAB ?

(i) What are the different algorithms used for secondary structure prediction in protein ?

(j) Name the techniques used for proteomic pattern analysis. What role it play in the strategy of clinical proteomics ?

2. What do you mean by hierarchic protein folding ? Briefly explain the models for thermodynamics and kinetics of polypeptide chain folding. 3+7

3. What is two dimensional poly-acrylamide gel electrophoresis (2-DE) ? Briefly explain the

method and application of 2-DE in proteomic studies. Comment on the software used for 2-D GE data analysis. 2+5+3

4. (a) What is phage antibodies ? What role it plays in proteome analysis ? 5

(b) Why phosphorylation site analysis ? Explain the phosphorylation site analysis strategies using Mass Spectrometer. 5

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

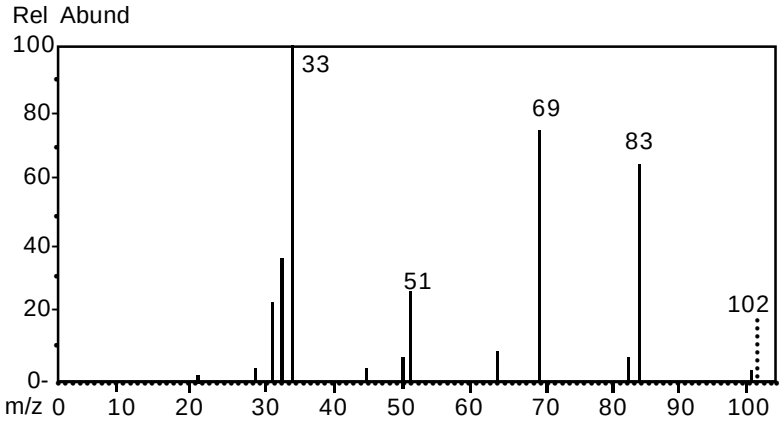
(a) Role of Ligand in Protein Folding

(b) HSP-70 Chaperone system

(c) De novo sequencing of peptides using MS data.

6. (a) Briefly explain the methods used for measurement of m-RNA expression. Add a note on the role of m-RNA in protein engineering. 7

(b) The mass spectra of a constitutional isomer is shown below. It became gas at room temperature. The molecular ion is the small peak at m/z = 102 amu. Name the isomer, which will provide this spectrum. 3



7. (a) What are the basic requirement for protein synthesis ? Briefly explain the methods of in vitro transcription and in vitro translation. 6

(b) A gene is transcribed and translated in a 100 µl reaction. Into that reaction 2 µl of 20 mCi/ml [^{35}S] methionine (2000 Ci/mol.) are added. After incubation at 37 °C for 60 min. a 4 µl aliquot is TCA precipitated to determine incorporation of Radioactive label. In the liquid scintillation counter, the filter gives off 1.53×10^6 cpm. A 2 µl aliquot of the reaction is counted directly in the scintillation counter to determine total counts in the reaction. This sample gives 2.4×10^7 ppm. Estimate

the percent of [^{35}S] methionine has been incorporated into the polypeptide during the process on in vitro translation. 4

8. What do you mean by reverse genetics ? Briefly explain the various approaches of reverse genetics including gene knock out utilized for gene to function assignments both in *vivo* and *in vitro*. 2+4+4

_____