GENOMICS AND PROTEOMICS
(BIOT 5232)

Time Allotted : 3 hrs **Full Marks : 70**

Figures out of the right margin indicate full marks.

Candidates are required to answer Group A and any 5 (five) from Group B to E, taking at least one from each group.

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

Group – A
(Multiple Choice Type Questions)

1. Choose the correct alternative for the following: **10 × 1 = 10**

(i) Small cDNA sequences that represent a unique sequence of an active gene is called
(a) SNPs (b) snRNAs (c) ESTs (d) Contigs.

(ii) The 2D-Gel Electrophoresis provide information's about the proteins are
(a) MW, pI and quantity (b) MW and pI
(c) pI and quantity (d) none of these.

(iii) Which of the given statements is incorrect about the comparison of proteomes to EST databases of an organism?
(a) ESTs are single DNA sequence reads that contain a small fraction of incorrect base assessments, insertions, and deletions
(b) Many sequences arise from near the 5' end of the mRNA, although every effort is usually made to read as far 3' as possible into the upstream portion of the cDNA
(c) EST libraries are useful for preliminary identification of genes by database similarity searches
(d) An EST database of an organism can be analyzed for the presence of gene families, orthologs, and paralogs.

(iv) Which of the given statements is incorrect about Horizontal Gene Transfer?
(a) The genomes of most organisms are derived by vertical transmission, the inheritance of chromosomes from parents to offspring from one generation to the next
(b) It is the acquisition of genetic material from a different organism
(c) The transferred material becomes a temporary addition to the recipient genome
(d) An extreme example is the proposed endosymbiont origin of mitochondria in eukaryotic cells and chloroplasts in plants

(v) Which of the following statements is not true about sequencing peptides with mass spectrometry?
(a) The entire protein can be sequenced all at once using mass spectroscopy
(b) Two rounds of mass spectroscopy are used to determine sequence
(c) Some purified protein must be digested with proteases to eliminate undesirable characteristics such as hydrophobicity and solubility
(d) In order to determine the sequence, a pure sample of protein is obtained through 2D-PAGE or HPLC.

(vi) X-ray diffraction from a protein requires
(a) a well-ordered protein crystal
(b) integration of an electron density map
(c) surface entropy increase
(d) all of the above.

(vii) For what is co-immunoprecipitation used?
(a) To determine if a protein-of-interest binds to a specific DNA sequence
(b) To examine protein-protein interaction in the nucleus instead of in the cytoplasm
(c) To examine protein-protein interactions in the cytoplasm instead of the nucleus
(d) To allow protein to be expressed in mammalian cell culture.

(viii) For hybrid inter and intra molecular methods for comparison of protein structures which of the following options is true?
(a) Dynamic programming is employed to maximize residue overlap
(b) Internal stabilities are NOT used
(c) Iterative de-optimization is necessary
(d) Identification of non-equivalent residues is done.

(ix) Which of the following is NOT a proteomic technique for serum biomarker determination?
(a) Label free LC-MS/MS
(b) Antibody microarray
(c) Protein chips
(d) Molecular beacon based probes.

(x) Which of the following is NOT a role for programmed enzymatic protein modification?
(a) Protein structure/function
(b) Protein targeting/processing
(c) Flow of genetic information
(d) Site directed mutagenesis.

Group – B

2. (a) What do you mean by Haplotype?

   (b) Comment on the course of human migration using DNA markers?

   (c) Write a short note on importance of SNPs as tools of genome research.

3 + 5 + 4 = 12

3. (a) Briefly describe the principle of Taq-Man assay.

   (b) Illustrate the mechanism of single-base extension assay for SNP genotyping.

   (c) Write a brief note on QTL mapping.

4 + 4 + 4 = 12

Group – C

4. (a) Discuss the applications of genomics in forensics research.

   (b) How do you prepare a cDNA library with the help of DNA markers?

   (c) Explain with a flow diagram the technique of 454 sequencing.

4 + 4 + 4 = 12

5. (a) Mention the goal of minimal genome in comparative genomics.

   (b) Justify the following situation in comparative genomics level where lateral gene transfer events occurred relatively recently. Discuss with suitable example and explanations the following aspect in comparative genomics when the order of a number of linked genes is conserved between genomes.

4 + (3 + 5) = 12

Group – D

6. (a) Define protein and proteome.

   (b) Describe the life cycle of protein with a diagram.

   (c) What are the basic differences between proteomics and protein chemistry?

   (d) Write the basic principles, steps with labeled diagram to study protein-protein interaction about *any two* of the following:
   (i) GFC (ii) Phage display (iii) Tap-tag.

2 + 2 + 2 + (3 × 2) = 12

7. (a) Write the names of different steps of 2-D PAGE and describe the basic principles of the two major steps of 2D-PAGE with labeled diagram.

   (b) An unknown peptide was analyzed by mass spectrometric and chromatographic methods as follows:
   (i) MALDI-TOF mass spectrometry of the peptide gave two signal at m/z = 3569 and 1785;
   (ii) The data obtained from analysis of the peptide using coupled HPLC-MS operating through an ESI source were m/z =510.7, 595.7, 714.6, 893.0 and 1190.3.
   Determine the molecular mass of the peptide.

   (c) Describe the steps of biomarker discovery for cancer using proteomics with a labelled diagram.

4 + 4 + 4 = 12

Group – E

8. (a) Explain why phospho-proteomics represents a prime example of protein modification. Draw the structures of three amino acids that are known to be phosphorylated in a biological context. Draw a flowchart of techniques for the analysis of phosphoproteins.

   (b) Draw a labeled figure of an SPR sensorgram. Explain, with specifics, the industrial application of SPR to proteomics in the area of two component binding reactions.

(1 + 2 + 3) + (3 + 3) = 12

9. (a) Using the example of retinoic acid administration for acute leukemia , explain how study of protein profiles has proved beneficial for the study of drug responses. Name two proteomic technologies that are typically employed for this effort.

   (b) RMSD is the parameter that is typically used to measure similarity between protein structures. What is the mathematical expression for it? Explain a more accurate method that is used for this purpose.

   (c) Explain stepwise how sample preparation is done for a cryo-EM experiment. Outline the principle involved in each of these steps.

   (d) Outline three situations that elucidate why cryo-EM is preferred as a technique for structure determination of viruses. Name two viruses where such successful cryo-EM structure determination has provided for effective vaccine design research.

3 + 3 + 3 + 3 = 12