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) Expression of genes can be analyzed by
(a) Microarray (b) Southern analysis
(c) Comparative genomics (d) RNA interference

(ii) 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

(iii) Physical maps are maps of locations of identifiable landmarks on a genomic DNA _____ inheritance patterns. Fill up the gap with suitable one from the set below
(a) remotely related to (b) related to
(c) regardless of (d) associated with

(iv) A lab-on-a-chip is
(a) a laboratory on a microchip
(b) a DNA microarray
(c) a protein chip
(d) a small device than can carry on electrophoretic separations

(v) SAGE x Profiler – provide information about
(a) over-expressed or silenced genes.
(b) "virtual subtraction" of an expression profile of one library (e.g., normal tissue) from another.
(c) allows matching of experimentally obtained SAGE tags to known genes.
(d) protein expression

(vi) Which of the following techniques has been used to determine K_d in protein-protein interaction assays?
(a) Y-2H assay (b) GST-Pull down assay
(c) Phage display (d) SPR

(vii) You have transiently expressed a new protein (for which no antibody is available) in a cell line to establish structure function relationship. Which one of the following strategies is the most straight forward way to examine the expression profile of this new protein?
(a) By metabolic labelling using ^{35}S lablled amino acids
(b) Making a GFP fusion protein with this new protein
(c) Immunoprecipitating this protein with the help of another protein for which antibody available.
(d) Running SDS-PAGE and identify the protein.

(viii) A protein undergoes post-translational modifications. In an the following experiment to identify the nature of modifications, following experimental results were found:
(1) Proteins moved more slowly in an SDS-PAGE. (2) Isoelectric focusing (IEF) showed that there was no change in the pI. (3) Mass spectrometruic analysis showed that the modification was on serine. The modification that the protein undergoes is likely to be
(a) phosphorylation (b) glycosylation
(c) ubiquitination (d) ADP-ribosylation.

(ix) Small cDNA sequences that represent a unique segment on active gene is called
(a) STSs (b) ESTs
(c) SNPs (d) contigs

(x) In co-immunoprecipitation,the interacting proteins can be purified /analysed by which of the following methods
(a) ESI-MS (b) MALDI-TOF-MS
(c) Western blotting (d) All of the above

Group – B

2. (a) Give a comparative analysis between satellite DNA, minisatellite DNA and microsatellite DNA with examples.
(b) What are the functions of snoRNA genes?
(c) What do you mean by genes within genes?

6 + 3 + 3 = 12

3. (a) What is haplotype? Mention the application of Hap Map project on human healthcare.
(b) What do you mean by pharmacogenomics?
(c) How does junk DNA help to understand genome evolution?

(2 + 4) + 3 + 3 = 12

Group – C

4. (a) Write two main characters of ESTs.

   (b) Describe the process of EST index construction.

   (c) Write short notes on how gene index is constructed of the following databases: (i) TIGR, (ii) Unigne.

(2 + 4) + 2 + (2 + 2) = 12

5. (a) In genomics part functional genomics analysis is a major topic - mention briefly how in sequence based expressed sequence tags sequencing is achieved.

   (b) Mention the advantages and limitation of this approach.

   (c) Write a short note on UniGene.

   (d) Briefly outline the steps to process EST sequences for constructions of the UniGene database.

4 + (2 + 2) + 2 + 2 = 12

Group – D

6. (a) Describe the basic principle of 2D-DIGE with labelled diagram.

   (b) A protein was isolated from human tissue and subjected to a variety of investigations. Relative molecular mass determinations gave values of approximately 12000 by size exclusion chromatography and 13000 by gel electrophoresis. After purification, a sample was subjected to electrospray ionization mass spectrometry and the following data obtained.

m/z	773.9	825.5	884.3	952.3	1031.3
Abundance (%)	59	88	100	66	37

Assuming that the only ions in the mixture arise by protonation, deduce an average molecular mass for the protein by this method.

   (c) Write three standard techniques to study protein-protein interaction (PPI) where HT is possible. Describe the basic principle of PPI study by the techniques where multiple tags are used, with labelled diagram.

   (d) A protein with average mass M, was used in a mass spectrometry study**.** In the mass spectrum the m/z value for two consecutive peaks from origin was m_1 and m_2 and the corresponding charges were n_2 +1 and n_2. Now derive the following expression: (i) $M = n_2 (m_2 - 1)$, (ii) $n_2 = (m_1-1) / (m_2 - m_1)$.

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

7. (a) Write names different types of proteomics? Describe the life cycle of protein. Write principle and applications of PMF.

   (b) Write short notes on following techniques in the context of proteomics, with diagram: (i) Phage display, (ii) GST pulldown assay.

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

Group – E

8. (a) Briefly explain the principle of surface plasmon resonance (SPR) spectroscopy using a labelled diagram to depict measurement of antibody-antigen binding. What are two methodological advantages of SPR? Illustrate each with one example.

   (b) What necessitated the emergence of cryo-electron microscopy (cryo-EM) as a complementary technique to x-ray crystallography? Use TWO examples to highlight how cryo-EM is ideally suited as a technique for the development and design of virus based platforms for biomedical and biotechnological applications. How can the comparatively low-resolution data of cryo-EM be sometimes supplemented by associated NMR and crystallographic data for quality improvement?

(3 × 2) + (3 × 2) = 12

9. (a) What are the three major modes of glycosylation in mammalian cells? Where do they occur? Give three example of disease associated with altered glycan chains on glycoproteins. Name the corresponding structural alteration and glycoprotein involved.

   (b) Post translational modifications (PTMs) can be typically detected by mass spectrometry in protein sequencing experiments. HEWL (hen egg white lysozyme) has a relative molecular mass about 14300. If mass resolution is within 0.01% accuracy using the particular mass spectrometry technique, could it be used to unambiguously distinguish the phosphorylation of a serine residue from the unmodified protein. Use a simple example to explain how chemical derivatization can be used for the isolation of a phosphoprotein.

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

Department & Section	Submission Link
BT	https://classroom.google.com/c/MzMzNTE5NzEyNTEz/a/MjI2NDA1NzI3MjA2/details