M.TECH/BT/2ND SEM/BIOT 5241/2015
2015

Genomics & Proteomics
(BIOT 5241)

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 x 1=10**

(i) Protein-nucleic acid complexes include
(a) Ribosomes, (b) Splicing and repair particles
(c) Transcription regulation complexes (d) All of the above.

(ii) The interspersed repeats are
(a) repeats whose individual repeat units are distributed in genome in random fashion
(b) repeats distributed alternately in genome
(c) are distributed evenly throughout the genome
(d) all of these.

(iii) The intermolecular approach to protein structure comparison is normally applied to
(a) relatively dissimilar structures (b) relatively similar structures
(c) structures with a RMSD > 5 Angstroms (d) structures that cannot be aligned.

(iv) The first crop plant genome sequenced was
(a) Rice (b) Wheat (c) Maize (d) Barley.

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

(vi) Co-immunoprecipitation is 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.

(vii) Which of the following has been extensively studied using protein interaction arrays?
(a) protein in yeast that bind to GST
(b) proteins that are able to bind to biotin and streptavidin
(c) proteins that are able to bind to various cofactors present in the sample
(d) proteins in yeast that bind calmodulin or phospholipids.

(viii) The best method to study peptides, proteins and DNA upto 500 kD by mass spectrometry :

(a) Electron impact ionization (b) ESI (c) MALDI (d) FAB.

(ix) In the determination of macromolecular structure by NMR, which of the following statements is true?

(a) the final spectrum yields a single structure
(b) the final spectral data analysis yields 10-20 related structures
(c) the final spectrum is of low resolution
(d) the final structure has a low B-factor.

(x) The goal of _____ is to determine the location of specific genes within the genome.

(a) Cloning (b) annotation (c) proteomics (d) PCR.

Group - B

2.(a) How can you create a minimal cell genome?

(b) Mention the main features of human mitochondrial genome.

(c) Give a comparative analysis between functionally related, functionally similar and functionally identical genes.

4+4+4=12

3.(a) Illustrate the process of the hybrid sequencing approach.

(b) Describe with a flow diagram the technique of 454 sequencing.

(c) What is HapMap project? Mention its applications in genomics research.

4+4+4=12

Group – C

4.(a) Define EST. Mention its drawbacks.

(b) Define gene index construction. Describe the process of EST Index Construction.

(c) Write short notes on how gene index is constructed in any one of the following databases:

i) TIGR ii) UniGene.

(1+1)+(2+4)+4=12

5.(a) "In order to illustrate a high degree of relationship between related gene groups clustering methods are useful"- mention any one clustering method briefly in support of this statement.

(b) Describe the utility of unsupervised analysis in micro array data analysis and briefly discuss the bottom-up and top-bottom approach.

6+(4+2)=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 labelled diagram and application of any one of the following:
(i) Affinity pull down assay (ii) Phage display (iii) Yeast two hybrid

2+2+2+6=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 labelled 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 a molecular mass of the peptide.

(4+2)+6=12

Group – E

8.(a) Define phoshoproteomics. What are the layers of information provided by phosphoproteomics? Using examples, explain how signal transduction dynamics are analyzed through phosphoproteomics**.**

(b) Define glycoproteomics. Name 3 methodological approaches and 3 bioanalytical techniques used in glycoproteomics. Draw a flowchart of glycoproteomics analysis. Name 2 clinical applications of glycoproteomics.

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

9.(a) What are the three algorithmic approaches to compare protein geometric properties? Describe the essential principles of any two of these approaches. Cite one example each of databases/webservers in the number of possible approaches.

(b) In x-ray crystallography of proteins, both multiple isomorphous replacement (MIM) and multiwavelength anomalous diffraction (MAD) techniques have found utility. What are the advantages? Define the crystallographic R factor. What is its importance and how is it related to the resolution of the same crystal structure?

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