

electrospray ionization mass spectrometry and the following data were obtained:

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

Given that  $n_2 = (m_1 - 1) / (m_2 - m_1)$  and  $M = n_2 (m_2 - 1)$  and assuming that the only ions in the mixture arise by protonation, deduce average molecular mass for the protein by this method.

$$5 + 3 + 4 = 12$$

- 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) Describe the protein-protein interaction study by Yeast two hybrid assay with labelled diagram.
- (c) Describe the steps of biomarker discovery for cancer using proteomics with a labeled diagram.

$$4 + 4 + 4 = 12$$

#### Group - E

- 8.(a) What are the pulse sequences that are typically used to characterize a protein molecule using NMR?
- (b) What specific interactions do these pulse sequences measure?
- (c) What is a typical number of ensemble models of a protein structure produced by NMR analysis?
- (d) Name and briefly explain four methods by which NMR resonance signals can be improved.

$$3 + 3 + 2 + 4 = 12$$

- 9.(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 diagram of a SPR sensorgram. Explain, the industrial application of SPR to proteomics in the area of two component binding reactions.

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

## M.TECH/BT/2<sup>ND</sup> SEM/BIOT 5241/2017 GENOMICS AND 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 × 1 = 10**
- (i) Which type of genomics study describes the transcripts and proteins expressed by a genome?
- (a) Comparative genomics  
(b) Structural genomics  
(c) Functional genomics  
(d) Transcripto-genomics.
- (ii) X-ray diffraction on 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) The first genome sequencing project was carried on
- (a) Haemophilus influenza (b) E. coli  
(c) ØX 174 (d) Drosophila melanogaster.
- (iv) Which of the following information about proteins can be obtained by 2D-Gel Electrophoresis?
- (a) MW, pI and quantity (b) MW and pI  
(c) pI and quantity (d) none of these.
- (v) Individual genetic maps in a given species are
- (a) genetically similar  
(b) genetically identical  
(c) genetically dissimilar  
(d) not useful in species analysis.

- (vi) Which of the following statements is not true about sequencing peptides with mass spectroscopy?
- The entire protein can be sequenced all at once using mass spectroscopy.
  - Two rounds of mass spectroscopy are used to determine sequence.
  - some purified protein must be digested with proteases to eliminate undesirable characteristics such as hydrophobicity and solubility.
  - In order to determine the sequence, a pure sample of protein is obtained through 2D-PAGE or HPLC.
- (vii) Why co-immunoprecipitation is used?
- to determine if a protein-of-interest binds to a specific DNA sequence.
  - to examine protein-protein interaction in the nucleus instead of in the cytoplasm.
  - to examine protein-protein interactions in the cytoplasm instead of the nucleus.
  - to allow protein to be expressed in mammalian cell culture.
- (viii) Structural proteomics is concerned with
- coverage of fold space
  - low throughput determination of protein structures
  - high-throughput determination of protein structures
  - all of the above.
- (ix) Expression of genes can be analyzed by
- Northern analysis
  - Southern analysis
  - Comparative genomics
  - RNA interference.
- (x) A lab-on-a-chip is
- a laboratory on a microchip
  - a DNA microarray
  - a protein chip
  - a small device that can perform electrophoretic separations.

**Group - B**

- 2.(a) Define STS. Analyze the usage of STS in genomics research.
- (b) What do you mean by polymorphic STS?

- (c) What is snip-SNP?
- (d) Define pseudogene.
- (2 + 3) + 3 + 2 + 2 = 12**
- 3.(a) Discuss the applications of genomics in tracing human migration and evolution.
- (b) Illustrate the process of TaqMan assay for identifying SNPs.
- (c) Describe with a flow diagram the technique of AFLP.

**4 + 4 + 4 = 12****Group - C**

- 4.(a) "In the transcriptome analysis by quantitative analysis of gene expression fragment lengths of more than 200 nucleotides are used" – justify the statement with suitable experimental procedure.
- (b) (i) To tackle the huge nonredundant data in transcriptomics, some special processing is needed for this purpose. Mention the processes citing suitable reasons.
- (ii) Describe briefly any such database which is used for this purpose.
- 6 + (3 + 3) = 12**
- 5.(a) "Microarray based method is followed to study the global gene expression profiling". Mention the detailed procedure using oligo nucleotide followed for this microarray based method.
- (b) To design an optimal oligonucleotide probe certain criteria are needed to follow. Mention those criteria citing the reason behind it.

**6 + 6 = 12****Group - D**

- 6.(a) Describe the basic principles of determination of mass of protein by ESI - TOF MS with labeled diagram.
- (b) Write the advantages of MALDI - TOF over ESI - TOF.
- (c) 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