(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.

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

4 + 4 + 4 = 12

Group - E

8. (a) Briefly explain the phenomenon of surface plasmon resonance. Use a labeled schematic diagram to represent the sensorgram plot of a SPR signal.

(b) Explain the terms "structure factor" and "temperature factor" in the context of protein x-ray diffraction.

(c) How has solid-state NMR been used in structural proteomics? Cite two specific examples.

(d) How can CDS in the far UV be used to determine β-sheets in proteins?

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

9. (a) How can 31 P NMR be used as a non invasive proteomics technique to measure ATP flux?

(b) How has "the immunome" technique been used to identify immune-dominant proteins expressed in the life cycle of the *Plasmodium falciparum* malarial parasite?

(c) What are the three major types of glycosylation in mammalian cells? Where do they occur?

(d) Briefly describe the *enrichment procedure* for detecting protein post translational modifications.

4 + 3 + (2 + 1) + 2 = 12

M.TECH/BT/2ND SEM/BIOT 5241/2018

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 × 1 = 10**

(i) Which of the following statements is not true about sequencing peptides with mass spectroscopy?
(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 characteriscts such as hydrophobicity and solubility
(d) In order to determine the sequence, a pure sample of protein is obtained through 2D-PAGE or HPLC.

(ii) Which of the following is an incorrect statement?
(a) Collecting a SAGE library is very labor intensive and expensive
(b) Collecting a SAGE library is quite economical
(c) SAGE is not suitable for rapid screening of cells
(d) Gene identification from SAGE data is more cumbersome

(iii) Which of these has the smallest genome?
(a) Haemophilus influenzae (b) Mycoplasma genitalium
(c) Mycobacterium tuberculosis (d) Streptococcus pneumoniae.

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

(v) One centiMorgan is defined as ___ percentage of the total recombination events.
(a) 1 (b)10 (c) 0.1 (d) 0.01.

(vi) Which of the following has been extensively studied using protein interaction arrays?
(a) Proteins in yeast that binds 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.

(vii) Which of the following choices represent end-group enzymatic protein modifications?
(a) Adenyl group added to glutamine synthase
(b) Mmyristoylation of Ras
(c) O-glycosylation of Ser in the Golgi
(d) Hydroxylation of proline in collagen.

(viii) Which of the following functional classes of proteins can be identified by function-specific affinity agents?
(a) Serine hydrolase (b) Cysteine protease
(c) Kinases (d) All of the above.

(ix) Change in SPR angle is expressed in which of the following units?
(a) RU (b) ng/mm^{-2} (c) cm^{-1} (d) dl^{3}.

(x) Which one of the following techniques can be used as a label-free method to monitor protein interactions?
(a) Photon correlation spectroscopy
(b) Static light scattering
(c) Isothermal titration calorimetry
(d) All of the above.

Group - B

2. (a) In functional genomics, define the following terminologies and their relationship: Ortholog, paralog, homolog.

(b) Lateral gene transfer occurs in which organism? Mention the mechanisms by which it happens.

(c) Elucidate the relationship between the 'within genome approach' and 'among genome approach' in preview of lateral gene transfer.

(2 × 3) + (1 + 1) + 4 = 12

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

(b) Explain the terms: STS, clone contig, ETS and SNP.

(c) Describe with a flow diagram the technique of chromosome walking.

4 + 4 + 4 = 12

Group - C

4. (a) Give a description of the clone-by-clone shotgun sequencing technique.

(b) What do you mean by high-throughput sequencing? Mention how this technique is advantageous over traditional sequencing approaches.

5 + (4 + 3) = 12

5. (a) Write a brief note on the Hydrogen hypothesis.

(b) What is YAC? Mention the steps in the construction of a cDNA library.

(c) What is snip-SNP?

4 + (3 + 3) + 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 labeled diagram and application about any two of the following:
(i) Affinity pull down assay
(ii) Phage display
(iii) Yeast two hybrid.

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: