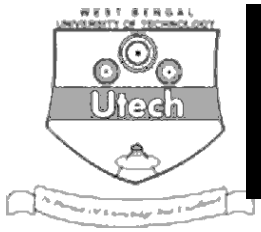
CS/M.Tech (BT)/SEM-2/MBT-202/09
PROTEOMICS AND GENOMICS (SEMESTER - 2)



1. .....
Signature of Invigilator

2. .....
Signature of the Officer-in-Charge

Reg. No.

Roll No. of the Candidate

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CS/M.Tech (BT)/SEM-2/MBT-202/09
ENGINEERING & MANAGEMENT EXAMINATIONS, JULY – 2009
PROTEOMICS AND GENOMICS (SEMESTER - 2)

Time : 3 Hours] [Full Marks : 70

INSTRUCTIONS TO THE CANDIDATES :

1. This Booklet is a Question-cum-Answer Booklet. The Booklet consists of **36 pages**. The questions of this concerned subject commence from Page No. 3.
2. a) In **Group – A**, Questions are of Multiple Choice type. You have to write the correct choice in the box provided **against each question**.
   b) For **Groups – B** & **C** you have to answer the questions in the space provided marked 'Answer Sheet'. Questions of **Group – B** are Short answer type. Questions of **Group – C** are Long answer type. Write on both sides of the paper.
3. **Fill in your Roll No. in the box** provided as in your Admit Card before answering the questions.
4. Read the instructions given inside carefully before answering.
5. You should not forget to write the corresponding question numbers while answering.
6. Do not write your name or put any special mark in the booklet that may disclose your identity, which will render you liable to disqualification. Any candidate found copying will be subject to Disciplinary Action under the relevant rules.
7. **Use of Mobile Phone and Programmable Calculator is totally prohibited in the examination hall.**
8. You should return the booklet to the invigilator at the end of the examination and should not take any page of this booklet with you outside the examination hall, **which will lead to disqualification**.
9. Rough work, if necessary is to be done in this booklet only and cross it through.

No additional sheets are to be used and no loose paper will be provided

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Marks Obtained

	Group – A										Group – B			Group – C				
Question Number																	***Total Marks***	***Examiner's Signature***
Marks Obtained																		

.....
Head-Examiner/Co-Ordinator/Scrutineer

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PROTEOMICS AND GENOMICS
SEMESTER - 2

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GROUP – A

(Multiple Choice Type Questions)

1. Choose the correct alternatives for any *ten* of the following : $10 \times 1 = 10$

i) What is an issue for using 2D-PAGE ?

a) Hydrophobic proteins may not run as expected due to the hydrophobic surfaces.

b) Highly expressed proteins may cover up proteins that are not as abundant but running in the gel nearby.

c) Rare celluar proteins are hard to visualize with coomassie blue protein stain.

d) All of these. ☐

ii) Which of the following is not an example of protease activity ?

a) Some proteases cleave the phosphodiester bond between nucleic acid residues.

b) Some proteases contain serine, cystein threonine, or aspertic acid residues within their active sites.

c) Proteases hydrolyze the peptide bond between amino acid residues.

d) Metalloproteases contain metal ion cofactor within their active site. ☐

iii) In …… order Markov model assumes each base occurs independently.

a) hexamer b) first

c) null d) zero.

iv) GFP tagging & microscopy used in proteomics to

a) investigate proteins-protein interaction

b) identify the proteins

c) investigate the localization of the protein

d) study the structure of the protein.

v) To study peptides, proteins and DNA, up to 500 kD by Mass spectrometry which ionization method will be the best ?

a) Electron Impact Ionization

b) Electro-Spray Ionization (ESI)

c) Matrix Assisted Laser Desorption Ionization (MALDI)

d) Fast Atom Bombardment (FAB).

vi) The full form of IMM is

a) Interpolated Markov Model

b) In situ Markov Model

c) In situ hidden Markow Model

d) Interconnected hidden Markov Model.

vii) Fractional cell coordinates have values between

a) 0 and 1 b) 1 and 2

c) 0·5 and 1,5 d) 1·5 and 2·5.

viii) The human genome project was completed in the year

a) 1999 b) 2001

c) 2002 d) 2003.

ix) The ^{1} H chemical shift for the NH proton in glycine is

a) 8·39 b) 4·29

c) 1·39 d) 2·13.

x) MIAME stands for

a) minimal information about a microarray experiment

b) minimum information about a microarray experiment

c) average information about a microarray experiment

d) set of information about a microarray experiment.

xi) The size of the human genome is

a) 300 Mb b) 3000 Mb

c) 3 Mb d) 300 kb.

xii) The protein aggregate associated with Parkinson's disease in

a) τ-protein b) prion proteins

c) mutant α_1-antitrypsin d) α-synuclein.

xiii) A contig is a

a) continuous stretch of amino acid sequence

b) homologous stretch of genes

c) contiguous stretch of DNA

d) stretch of DNA derived from continuous chromosomal region.

GROUP – B

(Short Answer Type Questions)

Answer any *three* of the following. 3 ∞ 5 = 15

2. What are the different physico-chemical factors that contribute towards the affinity between two soluble proteins ? Give the dissociation constant range for 2 sets of protein-ligand complexes and their biological relevance. 3 + 2

3. Write about the principle (with diagram) and application in proteomics of any *one* of the following tools : 5

a) Edman method of protein sequencing

b) GST pull down assay

c) Yeast two hybrid

d) Phase display.

4. Mention the possible ways to correct the spatial effects in microarray. 5

5. a) What is proteomics ? What are the different types of proteomics ?

b) What is the importance of expressional proteomics ? 2 + 3

6. a) What are rooted and unrooted evolutionary trees ?

   b) Write a brief note on Bootstrapping technique. 2 + 3

7. Describe, in brief, the 6 steps needed for the general method of multiple isomorphous displacement in collecting *X*-ray diffraction data for solving macromolecular structures. Give two examples of heavy atom derivatives for macromolecular crystals. 4 + 1

8. a) What do you mean by digital northern analysis ?

   b) Mention its applications in genomics research. 2 + 3

9. Write short notes on any *two* of the following : $2 \times 2\frac{1}{2}$

   a) Linear regression of log ratio against average intensity.

   b) Non-linear regression of log ratio against average intensity.

   c) Spotted array synthesis in microarray

   d) Image acquisition in microarray.

GROUP – C

(Long Answer Type Questions)

Answer any *three* of the following. $3 \times 15 = 45$

10. a) What are the different steps in 2-D PAGE and what is the basic principle of 2-D PAGE ? (Discuss with diagram).

    b) How set pH gradients are set up in IEF.

    c) What are the advantages and disadvantages of 2-D PAGE ?

    d) What are the different visualization methods of protein spot in PAGE ? Compare different protein gel staining methods. 4 + 3 + 4 + 4

11. a) Diagrmmatically respresent (with proper labeling) the phenomenon of spin-spin relaxation in NMR.

b) Briefly describe and diagrammatically represent a 2D-NOESY pulse sequence.

c) If the preparation time is 3 sec, t_1 varies from 0 to 51 msec at 200 μ sec intervals and the FID is collected for 1 sec, how many repetitions of each t_1 FID can one collect and complete the measurement of a COSY in about 15 hrs ?

4 + 5 + 6

12. a) Describe the basic principle and steps of MALDI-TOF Mass spectrometry.

b) Write about the different matrixes and laser source of MALDI.

c) Write the steps of Peptide Mass Finger Printing (with flowdiagram).

d) An unknown peptide and an enzymatic digest of it were analysed by mass spetrometro-metric and chromatographic methods as follows :

i) MALDI-TOF of the peptide gave two signals at m/z = 3569 and 1875 :

ii) MALDI-TOF of the hydrolysed showed singals at m/z = 766, 891, 953 and 1016 ;

iii) 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. 4 + 3 + 3 + 5

13. a) What is microarray ?

b) Mention briefly the steps involved in measuring gene expression in a lab through microarray.

c) How do you correct the information generated by the colour intensities of Cy3 and Cy5 channels in a microarray experiment ? 2 + 8 + 5

14. a) Describe briefly the AFLP technique.

b) What are the ethical issues that one should consider before gene testing ?

c) Discuss the importance of SNPs in genomics research.

d) Elucidate the role of N-Acetyltransferase in the development of personalized medicine. 5 + 3 + 4 + 3

15. a) Elucidate the prediction method followed by neural network and Hidden Markov model in gene prediction approaches.

b) Mention the drawbacks of homology based programmes in gene prediction approaches.

c) In *ab initio* based gene identification programmes gene signals play a major role. Mention any two signals with suitable software used for identifying them.

[(4 ∞ 2) + 3 + (2 ∞ 2)]

16. a) Define : Ortholog, Paralog, Homolog.

b) What are the salient features of mitochondrial genome ?

c) Explain the role of gene duplication in the evolution of the human genome.

d) Write short notes on any *two* of the following :

i) Horizontal gene transfer

ii) Exon shuffling

iii) Arabidopsis Knock-Out strategies.

e) What do you mean by SINE and LINE ? 3 + 3 + 3 + 3 + 3

17. a) What is the role of RNA polymerase in transcription ? Why are such transcription studies forcused more on prokaryotes than eukaryotes ?

b) In a protein-protein interface, what is the biological role of complementarity of interfaces. Explain quantitatively.

c) What is a two hybrid screening system ? How are protein interactions detected by 2-hybrid screening systems. Illustrate with 2 examples. 4 + 5 + 6

END