Name : .....

Roll No. : .....

Invigilator's Signature : .....

CS/M.Tech (BT)/SEM-2/MBT-215A/2011

2011

PROTEOMICS AND GENOMICS

Time Allotted : 3 Hours Full Marks : 70

The figures in the margin indicate full marks.

Candidates are required to give their answers in their own words as far as practicable.

GROUP – A

(Multiple Choice Type Questions)

1. Choose the correct alternatives/fill in the blank for any *ten* of the following : 10 × 1 = 10

   i) Chromosomal and cytogenetic maps are generated by

   a) Family data b) RFLPs

   c) Positional cloning d) Chromosome walking.

   ii) The 2*D*-Gel electrophoresis provide information about the proteins are

   a) MW, pI and quantity b) MW and pI

   c) pI and quantity d) none of these.

   iii) Protein visualization sensitivity by Coomassie Briliant Blue *R*-250 staining per spot is

   a) 1 ng to 1 μg b) 100 ng to 10μg

   c) 1 ng and up d) 1 mg.

iv) The Gene prediction results are said to be accurate when

a) Sn and Sp is high

b) Sn and Sp is low

c) Sn is high and Sp is low

d) Sn is low and Sp is high.

v) Trypsin cleave the peptide bond containing

a) Arg or Lys b) Glu or Asp

c) Met, Trp d) None of these.

vi) Neural network is constructed with multiple layers

a) Input, output and hidden layers

b) Input, output, middle and hidden layers

c) Input, hidden, processing and output layers

d) Input, processing, hidden and output layers.

vii) GFP tagging and microscopy is used in proteomics to

a) investigate protein-protein interaction

b) identify the protein

c) find out the localization of the protein

d) study the structure of the protein.

viii) Fill in the blank :

A common post0translational modification is *N*-myristoylation in which myristate is attached to ..... .

ix) 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) ESI

c) MALDI

d) FAB.

x) IN network structure and dynamics and unlabelled, undirected graph gives a

a) static structure of network topology

b) time-dependent structure of network topology

c) periodic sinusoidal network topology

d) all of these.

xi) Which of the following is not a aggregate with dynamic properties ?

a) GroEL-GroES chaperonin

b) Pyruvate kinase

c) F1-ATP-ase

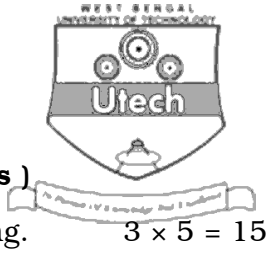
d) β_2-adrenergic receptor.

xii) Funding for the Human Genome Project came from

a) the NIH

b) the DOE

c) the NIH and the DOE.



GROUP – B
(Short Answer Type Questions)

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

2. Write the principle, application and describe with diagram about any *one* of the following tools :

   a) Affinity pull down assay

   b) Phage display

   c) Yeast two hybrid

   d) Protein microarray.

3. a) Define Contig, STS, Minimal tilling path.

   b) What are the advantages of a capillary DNA sequencer ? 3 + 2

4. Write the mechanism of ubiquitin-proteosome mediated protein degradation pathway.

5. a) Draw a flowchart of the approach used in NMR spectroscopy to derive protein structures from torsion angle and distance measurements.

   a) Why is generation of an ensemble of 'low energy' conformations necessary in the above approach ? $3\frac{1}{2}+1\frac{1}{2}$

6. Mention the steps for designing a micro- array experiment with diagram.

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

   b) Write a brief not on Bootstrapping technique. 2 + 3

8. a) Define the factor, R, used in X-ray crystallography in mathematical terms.

   b) What is the need for this parameter in X-ray diffraction measurements ?

   c) What is an acceptable range of values for R ?

   d) For biological macromolecules what is a R-factor value that would make you decide that it is a good fit value ?

9. Mention the differences between any *one* of the following :

   a) *Ab initio* based and homology based gene prediction programs.

   b) Local alignment and Global alignment.

GROUP – C

(Long Answer Type Questions)

Answer any *three* of the following. 3 × 15 = 45

10. a) What is proteome ?

    b) What is protein ? What is the life cycle of protein ? (write with a diagram)

    c) What are the basic differences between proteomics and protein chemistry ?

    d) What are the different types of proteomics and the tools and techniques used to study these ?

    e) What are the needs of expressional proteomics ? 1 + 4 + 3 + 4 + 3

11. a) Describe the steps of computational gene finding ?

    b) Mention briefly the approaches of computational gene annotation citing with suitable example.

    c) Mention briefly the approaches of computational methods towards prediction of miRNA with suitable example.

    d) Mention the characteristic feature on which basis *t*-RNA can be identified. 2 + 6 + 4 + 3

12. a) What are the ethical issues that one should consider before gene testing ?

    b) Discuss the importance of SNPs human genomics research.

    c) Elucidate the role of cytochrome p450 in the development of personalized medicine.

    d) What do you mean by snip-SNP ? 4 + 4 + 4 + 3

13. a) What are the basic principles of SDS-PAGE and IEF ? (with diagram)

    b) What are disadvantages of 2-*D* PAGE ?

    c) Describe the basic principles of ESI-MS.

    d) Write the advantages of MALDI-M over ESI-MS.

    5 + 3 + 4 + 3

14. a) Heuristic methods is a type of sequence alignment. Mention how it is different from the other methods.

    b) Mention the stages of BLAST with suitable example.

    c) Explain with suitable example the relationship between *E*-value and *P*-value in the results of BLAST.

    d) Give a comparative account of BLAST and FASTA. 2 + 7 + 3 + 3

15. Foote and Winter compared the dissociation constant of a natural mouse antilysozyme antibody (*D* 1·3), an engineered 'humanized' antibody in which the antigen-binding site was grafted onto a human framework (human-original) and several mutants of the 'humanized form', including Human-mutated. The antigen was HEWL (hen egg white lysozyme) :

Antibody	Number of sequence differences to *D* 1·3	$K_{on}\left(M^{-1}s^{-1}\right)$	K_D
D 1·3	0	$1{\cdot}4 \times 10^{-6}$	$3{\cdot}7 \times 10^{-9}$
Human-original	48	$0{\cdot}7 \times 10^{-6}$	260×10^{-9}
Human-mutated	44	$1{\cdot}3 \times 10^{-6}$	14×10^{-9}

a) Calculate the 'off-rate' for each antibody.

b) Which has the major effect on the dissociation constant : differences in 'on-rate' or differences in 'off-rate' ?

c) What general conclusion can you draw about the importance of equilibrium and kinetic parameters in molecular biology from the above experiment and data ? 6 + 5 + 4

16. Why is burial of protein surface an important parameter in proteomics ? What makes adoption of the spherical model appropriate calculate ASA ? How is surface buried calculated ? Draw a histogram which is a typical representation of buried surface area in binary protein complexes. What amino acid residues enrich protein-protein interfaces ? Explain your answer. Why is Lysine an unusual residue in this regard ? Why is complementarity of surfaces an important parameter in measuring protein binary interactions that are of importance in areas as diverse as signalling and drug design ? 3 + 2 + 2 + 2 + 2 + 1 + 3

17. a) Write short notes on any *two* of the following :

i) Horizontal gene transfer

ii) Exon shuffling

iii) Arabidopsis Knock-out strategies.

b) What are retrogenes ? Give an example.

c) Define Ortholog, Paralog, SINE, LINE.

(2 × 4) + (2 + 1) + 4