

**GENOMICS AND PROTEOMICS
(BIOT 5232)**

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 is UNTRUE about the drawbacks of SAGE?
(a) One or two sequencing errors in the tag sequence can lead to ambiguous or erroneous tag identification
(b) Correctly sequenced SAGE tag sometimes may correspond to several genes or no gene at all
(c) Correctly sequenced SAGE tag always corresponds to several genes
(d) The drawback with this approach is the sensitivity to sequencing errors.
- (ii) To study peptides, proteins and DNA upto 500 kD by mass spectrometry which ionization method will be the best?
(a) Electron impact ionization (b) ESI
(c) MALDI (d) FAB.
- (iii) The private company involved in human genome sequencing in parallel with HGP was
(a) Roche (b) Celera (c) Gilead (d) Genentech.
- (iv) Protein visualization sensitivity by Coomassie Brilliant Blue R-250 Staining per spot is
(a) 1 ng to 1 µg (b) 100 ng to 10 µg
(c) 1 ng and up (d) 1 mg.
- (v) Which vectors were widely used in HGP?
(a) Plasmid and cosmid (b) Lambda phage and M13 vectors
(c) Phagemid and shuttle vectors (d) BAC and YAC.
- (vi) Which of the following techniques has been used to determine Kd in protein-protein interaction assays?
(a) Y-2H assay (b) GST-Pull down assay
(c) Phage display (d) SPR.

- (vii) The human genome contains approximately
(a) 6 million base pairs (b) 5 million base pairs
(c) 3 million base pairs (d) 4 million base pairs.
- (viii) Which of the following statements is not true about sequencing peptides with mass spectrometry?
(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 characteristics such as hydrophobicity and solubility
(d) In order to determine the sequence, a pure sample of protein is obtained through 2D-PAGE or HPLC.
- (ix) Cytologic maps can be considered to be of ____ resolution and hence somewhat ____ physical maps. Fill up the gaps with suitable combination from set below
(a) very high, inaccurate (b) very low, accurate
(c) very high, accurate (d) very low, inaccurate
- (x) Denaturation of a highly helical protein having disulfide bridges and two phenylalanine's can be monitored as function of temperature by which one of the following techniques?
(a) Monitoring the ratio of absorbance at 214 nm and 250 nm at various temperatures
(b) Monitoring the absorbance at 214nm at various temperatures
(c) Estimating the -SH content heat denaturation
(d) Recording circular dichroism spectra at various temperatures.

Group- B

2. (a) What is STS? Discuss its importance in mapping of human genome.
[[CO1](Remember/LOCQ)]
- (b) 'The hybrid sequencing technique is an amalgamation of the hierarchical and whole genome sequencing approaches' – Justify the statement with reasons.
[[CO1](Justify/HOCQ)]
- (c) Analyze the impact of HGP in medical science and pharmaceuticals.
[[CO1](Analyze/IOCQ)]
4 + 4 + 4 = 12
3. (a) Differentiate between partially overlapping genes and genes within genes.
[[CO2](Differentiate/IOCQ)]
- (b) What is the importance of the repetitive sequences present in the human genome?
[[CO2](Understand/LOCQ)]
- (c) Analyze the role of Y chromosome and mitochondrial DNA in tracing human migration.
[[CO2](Analyze/IOCQ)]
4 + 4 + 4 = 12

Group - C

4. (a) In the transcriptome analysis for quantitative analysis of gene expression short fragments of DNA often used as unique markers of the gene transcripts – justify the approach of transcriptome analysis with detailed suitable experimental procedure. [(CO2)(Justify/HOCQ)]
- (b) Mention two softwares which are used for the above purpose and cite its application clearly. [(CO2)(understand/LOCQ)]
- (4 + 3) + (2.5 × 2) = 12**
5. (a) Define the following terminologies and their relationship in functional genomics: Ortholog, paralog, homolog. [(CO2)(Remember/LOCQ)]
- (b) Lateral gene transfer occurs in which organism? Mention the mechanisms by which it occurs. [(CO2)(Analyze/IOCQ)]
- (c) Evaluate the relationship between the ‘within genome approach’ and ‘among genome approach’ in preview of lateral gene transfer. [(CO2)(Evaluate/HOCQ)]
- (2 + 2 + 2) + (1 + 1) + 4 = 12**

Group - D

6. (a) Explain the basic principles of determination of mass of protein by ESI-Q MS with labelled diagram. [(CO3)(Understand/LOCQ)]
- (b) Write three advantages of MALDI-TOF over ESI-TOF. [(CO3)(Remember/IOCQ)]
- (c) A protein was isolated from human tissue and subjected to a variety of investigations. Relative molecular mass determinations gave values of approximately 12 000 by size exclusion chromatography and 13 000 by gel electrophoresis. After purification, a sample was subjected to electrospray ionization mass spectrometry and the following data obtained.
- | | | | | | |
|---------------|-------|-------|-------|-------|--------|
| m/z | 773.9 | 825.5 | 884.3 | 952.3 | 1031.3 |
| Abundance (%) | 59 | 88 | 100 | 66 | 37 |
- Assuming that the only ions in the mixture arise by protonation, deduce an average molecular mass for the protein by this method. [(CO6)(Analysis/HOCQ)]
- 5 + 3 + 4 = 12**
7. (a) Describe the life cycle of protein with a diagram. [(CO1)(Remember/LOCQ)]
- (b) 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. [(CO3)(Explain/IOCQ)]
- (c) Write the names of three techniques to study the protein-protein interactions. Explain with a labelled diagram the principles and steps of any one technique to study protein-protein interaction that you have mentioned. [(CO3)(Explain/IOCQ)]
- 2 + (1 + 4) + (1+4) = 12**

Group - E

8. (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. [(CO6)(Explain/IOCQ)]
- (b) Draw a labelled figure of a SPR sensorgram. Explain, with specifics, the industrial application of SPR to proteomics in the area of two component binding reactions. [(CO6)(Understand/IOCQ)]
- (1 + 2 + 3) + (3 + 3) = 12**
9. (a) Explain stepwise how a biological sample is prepared for cryo-electron microscopy. Itemize the steps in the image processing part of cryo-EM including magnification procedures. What *recently developed* technological trends in cryo-EM made it suitable as an experimental method for the design of vaccines against newly emerging pathogens? [(CO6)(Understand/LOCQ)]
- (b) Draw a labelled diagram of the sensorgram that can be obtained from a surface plasmon resonance (SPR) experiment with the applicable equations for the optical response. What specific types of applications has SPR enjoyed in proteomic research and drug development? In terms of what the technique does, what are the similarities that SPR has with isothermal titration microcalorimetry (ITC)? [(CO6)(Understand/Analyze/IOCQ)]
- 6 + 6 = 12**

Cognition Level	LOCQ	IOCQ	HOCQ
Percentage distribution	33.33	46.88	19.79

Course Outcome (CO):

After the completion of the course students will be able to

- CO1.** Describe recent advances in genomics, transcriptomics, metabolomics and proteomics.
- CO2.** Explain basic and high throughput techniques in Genomics and their applications.
- CO3.** Explain basic and high throughput techniques in Proteomics and their applications.
- CO4.** List and discuss the use of genomics and proteomics in human health.
- CO5.** Propose appropriate methods for analysis of given sample type with respect to purpose of analysis.
- CO6.** Suggest and outline solution to theoretical and experimental problems in Genomics and Proteomics fields.

*LOCQ: Lower Order Cognitive Question; IOCQ: Intermediate Order Cognitive Question; HOCQ: Higher Order Cognitive Question