BRAINWARE UNIVERSITY

Term End Examination 2025-2026
Programme – M.Sc.(BI)-2025
Course Name – Proteogenomics
Course Code - MBI27504 (T)
(Semester II)

Full Marks : 40 **Time : 2:0 Hours**

[The figure in the margin indicates full marks. Candidates are required to give their answers in their own words as far as practicable.]

Group-A
(Multiple Choice Type Question) 1 x 10=10

1. *Choose the correct alternative from the following :*

(i) Proteogenomics improves genome annotation by
- a) Removing introns
- b) Identifying expressed proteins linked to genes
- c) Increasing mutation rates
- d) Suppressing transcription

(ii) SNP detection contributes to personalized medicine by
- a) Mapping genetic susceptibility
- b) Removing alleles
- c) Increasing mutation rates
- d) Modifying ribosomes

(iii) Pharmacogenomics improves therapy outcomes by
- a) Increasing drug toxicity
- b) Tailoring drugs based on genetic makeup
- c) Suppressing immune response
- d) Blocking transcription

(iv) Peptide mass fingerprinting supports protein identification by
- a) Counting amino acids
- b) Matching peptide masses to databases
- c) Measuring UV absorption
- d) Fluorescent tagging

(v) A detector in mass spectrometry mainly performs
- a) Ion acceleration
- b) Conversion of ions into measurable signals
- c) Peptide digestion
- d) Protein labeling

(vi) Multidimensional proteomics increases protein identification rates mainly through
- a) Single-step purification
- b) Enhanced separation of complex peptide mixtures
- c) Elimination of databases
- d) Reduction of ion detection sensitivity

(vii) SILAC enables relative protein quantification through
- a) Metabolic incorporation of labeled amino acids
- b) Post-electrophoretic staining
- c) Chemical crosslinking
- d) Radioactive nucleotide labeling

(viii) iTRAQ labeling is commonly performed at the stage of
- a) Intact protein purification
- b) Peptide derivatization

c) Gel staining
d) Ion acceleration

(ix) A proteome rich in cysteine-poor proteins challenges ICAT mainly because of

a) Incomplete digestion
b) Limited labeling efficiency
c) Excessive reporter ions
d) Reduced chromatography

(x) Design of a high-affinity diagnostic protein probe would most logically involve

a) Elimination of binding assays
b) Affinity maturation and validation assays
c) Random truncation only
d) Denaturation studies only

Group-B

(Short Answer Type Questions) 3 x 5=15

2. Explain the concept of proteogenomics with its relevance to functional genomics. (3)
3. Describe the principle and major applications of cBioPortal in cancer genomics. (3)
4. Classify two major limitations associated with microarray technology. (3)
5. Explain how Ion Torrent sequencing detects nucleotide incorporation using pH change. (3)
6. Judge the impact of random mutagenesis on generating industrially valuable enzyme variants. (3)

OR

Critique the advantages of recombinant protein expression over natural protein extraction. (3)

Group-C

(Long Answer Type Questions) 5 x 3=15

7. Illustrate how DNA methylation and histone modifications together regulate gene expression and gene silencing in a cellular system. (5)
8. Analyze the Illumina sequencing workflow and its role in modern genomics. (5)
9. Assess the significance of protein engineering in developing next-generation biosensors. (5)

OR

Critically assess ethical and biosafety considerations in large-scale protein engineering applications. (5)

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