45580

BRAINWARE UNIVERSITY

Term End Examination 2025-2026
Programme – M.Sc.(BT)-2025
Course Name – Genomics and Proteomics
Course Code - MBT27504A (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) Select the method best suited for studying the global methylation pattern of a genome.

a) RNA-Seq
b) ChIP-Seq
c) Bisulfite Sequencing
d) Exome Sequencing

(ii) List the correct order of steps in a standard RNA-Seq workflow.

a) Sequencing -> Library Prep -> RNA extraction -> Mapping
b) RNA extraction -> Fragmentation -> cDNA synthesis -> Adapter Ligation -> Sequencing
c) Library Prep -> RNA extraction -> Sequencing -> Analysis
d) Fragmentation -> Sequencing -> RNA extraction -> cDNA synthesis

(iii) Apply the concept of Reversible Terminators to explain how Illumina prevents homopolymer errors.

a) They allow only one nucleotide to be incorporated per cycle, blocking further extension until the image is taken and the block is removed.
b) They terminate the sequencing reaction permanently after one base.
c) They allow continuous addition of nucleotides without stopping.
d) They release a specific pH signal that prevents error.

(iv) Analyze why Ion Torrent technology struggles with long homopolymer stretches (e.g., AAAAA).

a) The fluorophores quench each other.
b) The voltage signal is not linear for large numbers of identical protons released simultaneously.
c) The enzyme Apyrase cannot degrade the excess nucleotides fast enough.
d) The bridge amplification fails for homopolymers.

(v) Identify the chemical reaction that produces light in Pyrosequencing.

a) Luciferin + ATP + O-2 -> Oxyluciferin + AMP + Light
b) Luciferin + H+ > Light

c) PPi + APS -> ATP
d) dNTP + DNA -> DNA-n+1 + PPi

(vi) Interpret the Mass Fingerprint obtained in a MALDI-TOF experiment.

a) The pattern of peptide masses derived from a specific protein digestion, unique to that protein.
b) The physical fingerprint left on the slide.
c) The spectrum of contaminating salts.
d) The amino acid sequence of the protein.

(vii) Calculate the approximate mass of a singly charged ion [M+H]+if the neutral mass M is 1000 Da and a proton is 1 Da.

a) 500.5 Da
b) 1001 Da
c) 999 Da
d) 2000 Da

(viii) Illustrate the mechanism of the Reporter Ion release in iTRAQ.

a) It is released during the MS1 scan by laser desorption.
b) It is cleaved from the tag during Collision-Induced Dissociation (CID) in MS2.
c) It is released by enzymatic digestion.
d) It is released by pH change in the column.

(ix) Apply the concept of Spike-in standards (e.g., AQUA peptides) in proteomics.

a) To increase the total protein concentration.
b) To provide an absolute reference standard for precise quantification of a specific target protein.
c) To digest the protein faster.
d) To visualize the gel better.

(x) Justify the use of a Fusion Tag (e.g., GST or MBP) for the expression of a toxic protein in E. coli.

a) It makes the protein radioactive.
b) It increases the solubility and may mask the toxicity of the passenger protein.
c) It degrades the protein immediately.
d) It exports the protein to the medium.

Group-B

(Short Answer Type Questions) 3 x 5=15

2. Explain the concept of the epigenome. (3)
3. Apply gene variant analysis in the context of inherited disease diagnosis. (3)
4. Describe the function of mass analyzers in MS instruments. (3)
5. Compare SILAC and ICAT techniques used in proteomics. (3)
6. Compare rational and random mutagenesis approaches in protein engineering. (3)

OR

Evaluate the role of engineered proteins in biosensor development. (3)

Group-C

(Long Answer Type Questions) 5 x 3=15

7. Describe the role of chromatin immunoprecipitation sequencing (ChIP-Seq) in epigenomic studies. (5)
8. Synthesize the criteria for selecting an appropriate affinity tag (e.g., His-tag vs. GST-tag) for the purification of a labile protein. (5)
9. Examine the advantages and limitations of Label-Free Quantification (LFQ) compared to isotopic labeling methods. (5)

OR

Analyze why the ICAT method simplifies the complexity of the proteome but potentially biases the results. (5)

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