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BRAINWARE UNIVERSITY

Term End Examination 2025-2026
Programme – B.Sc.(BT)-Hons-2023
Course Name – Genomics and Proteomics
Course Code - BBT60123
(Semester VI)

Full Marks : 60 **Time : 2:30 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 15=15

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

(i) Recall term use for is the collection of all Exons.

a) Transcriptome b) Genome
c) Proteome d) Exome

(ii) Identify which of the following technique NGS relies on.

a) PFG electrophoresis b) SDS PAGE
c) Capilary electrophoresis d) Native PAGE

(iii) Identify which of the following techniques is used to immobilize/amplify a ssDNA primer binding region (known as an adapter) which has been conjugated to the target sequence (i.e. the sequence that is to be sequenced) on a bead.

a) Emulsion PCR b) Nested PCR
c) Hot-start PCR d) All of these

(iv) Select which of the following is false regarding gene ontology.

a) There is standardization of the names and activities b) There is no standardization of associated pathways
c) It provides consistency in describing overall protein functions d) It facilitates grouping of proteins of related functions

(v) Choose the correct answer against the anion exchange chromatography.

a) It has a negative resin column b) It has a positive resin column
c) It has a neutral column d) All answers are incorrect

(vi) Predict the correct order of MALDI-TOF MS.... a. Protein ionization b. Trypsin digestion c. Protein identification by database search d. Protein isolation from tissue

a) d>b>a>c b) a>b>c>d
c) c>a>d>b d) b>d>c>a

(vii) Identify the chemical used by Maxam-Gilbert to sequence a DNA molecule

a) ddNTP b) dNTP
c) Base modifiers d) Base analogues

(viii) Identify the techniques used to immobilize/amplify a ssDNA primer binding region (known as an adapter) that has been conjugated to the target sequence (i.e. the sequence that is to be sequenced) on a bead.

a) Emulsion PCR
b) Nested PCR
c) Hot-start PCR
d) All of these

(ix) Distinguish the false statement on gene ontology.

a) There is standardization of the names and activities
b) There is no standardization of associated pathways
c) It provides consistency in describing overall protein functions
d) It facilitates grouping of proteins of related functions

(x) Identify the average molecular weight of an amino acid residue in a protein.

a) 110
b) 120
c) 130
d) 140

(xi) Identify the ions that pass through the slit and reach the collecting plate.

a) Negative ions of all masses
b) Positive ions of all masses
c) Negative ions of specific mass
d) Positive ions of specific mass

(xii) Identify the wrong statement about mass spectrometry.

a) Impurities of masses different from the one being analysed interferes with the result
b) It has great sensitivity
c) It is suitable for data storage
d) It is suitable for library retrival

(xiii) Identify the laser that can be used for laser radiation in MALDI.

a) Infrared lasers
b) Greenlight lasers
c) Red light lasers
d) Ultraviolet lasers

(xiv) Identify the false statements.

a) Oxidation of cysteine residue with performic acid is done to break disulfide bond in proteins
b) Reduction of cysteine residue with dithiothreitol is done to break disulfide bond in proteins
c) Reduction of cysteine residue with performic acid is done to break disulfide bond in proteins
d) Reduced cysteine is further acetylated by iodoacetate

(xv) Identify the Edman reagent.

a) Phenylisothiocyanate
b) CF3COOH
c) FDNB
d) Phenylthiocarbonyl

Group-B

(Short Answer Type Questions) 3 x 5=15

2. List down the steps of genome browsing using ENSEMBLE browser. (3)
3. Evaluate the importance of Ramachandran Plot. (3)
4. Construct the detailed explanation on Next generation sequencing. (3)
5. Predict the role of genetic factors in pharmacokinetics. (3)
6. Justify the connection of proteomics with biology and chemistry. (3)

OR

Explain the reason for protein solubilization in 2D PAGE. (3)

Group-C

(Long Answer Type Questions) 5 x 6=30

7. Find an importance of genome database in bioinformatics data management. (5)
8. Compare in between Pairwise alignment and Multiple sequence alignment. (5)
9. Describe elaborately the process of protein and peptide microarray based technology. (5)
10. Discuss the use of microbial genome in the agriculture and industry. (5)
11. Develop the experiment design of MALDI-TOF based MS analysis to identify a protein. (5)

12. Justify why DNA is known as blueprint of life. Discuss about role of markers. (5)

OR

Evaluate how pharmacogenetics affect the design, development, and availibility of new drugs. (5)

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