



BRAINWARE UNIVERSITY

Term End Examination 2024-2025

Programme – B.Sc.(BT)-Hons-2022

Course Name – Genomics & Proteomics

Course Code - BBTC604

(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) Explain the role of the enzyme apyrase in pyrosequencing.
 - a) It synthesizes the complementary DNA strand.
 - b) It converts ATP to pyrophosphate.
 - c) It removes excess pyrophosphate and unincorporated dNTPs.
 - d) It amplifies the signal.
- (ii) Select the main function of the sulfurylase enzyme in pyrosequencing.
 - a) To catalyze the reaction between ATP and P_{Pi}.
 - b) To degrade unincorporated nucleotides.
 - c) To provide energy for DNA synthesis.
 - d) To cleave the DNA molecule.
- (iii) Select the enzyme that is involved in the detection of base incorporation in pyrosequencing by generating light.
 - a) Luciferase
 - b) DNA polymerase
 - c) Sulfurylase
 - d) Apyrase
- (iv) Select the correct description of the flow cell used in Next-Generation Sequencing (NGS).
 - a) It is the chamber where nucleotides are added to the DNA during amplification.
 - b) It is the region where sequencing takes place through optical detection.
 - c) It filters DNA sequences before amplification.
 - d) It stores the sequencing data for future analysis.
- (v) Write the correct statement regarding the flow cell in the MiSeq system.
 - a) The MiSeq flow cell allows sequencing by synthesis, providing data for a single project per run.
 - b) The MiSeq flow cell uses a membrane to separate the DNA from the detection area.
 - c) It utilizes a two-dimensional grid for sequencing, allowing multiplexing of different samples.
 - d) The MiSeq flow cell is used only for RNA sequencing applications.

- (vi) Judge the amino acid that is considered to have the largest side chain among the 20 standard amino acids.
- a) Arginine
b) Tyrosine
c) Tryptophan
d) Methionine
- (vii) Select the aromatic amino acids from the list below.
- a) Tyrosine and Tryptophan
b) Phenylalanine and Glutamine
c) Alanine and Methionine
d) Cysteine and Leucine
- (viii) Identify the amino acid with a side chain that contains a carboxyl group.
- a) Glutamic acid
b) Glutamine
c) Glycine
d) Serine
- (ix) Genomics is the sub discipline of genetics ,devotes to which one of the following?
- a) Mapping
b) Sequencing
c) Functional analysis
d) All of these
- (x) Maxam-Gilbert used which of the following chemical to sequence a DNA molecule?
- a) ddNTP
b) dNTP
c) Base modifiers
d) Base analogues
- (xi) A ddNTP devoids OH group at _____
- a) 2' Carbon of ribose sugar
b) 3' Carbon of ribose sugar
c) 4' Carbon of ribose sugar
d) 5' Carbon of ribose sugar
- (xii) Chain-termination is a type of _____
- a) Sequencing
b) Vector generation
c) Antibiotic production
d) Gene manipulation
- (xiii) Which one of the following is not belonging from NGS?
- a) Pyrosequencing
b) Ion torrent semiconductor sequencing
c) Illumina techniques of sequencing
d) Dideoxy method of sequencing
- (xiv) Basic genome annotation includes the study of
- a) Genomic location
b) Gene model structure
c) Transcripts
d) All of these
- (xv) Choose the incorrect statement regarding gene annotation.
- a) The gene annotation of the human genome employs a combination of theoretical prediction and experimental verification
b) Gene structures are first predicted by ab initio exon prediction programs
c) The predicted genes are compared with experimentally determined cDNA and EST sequences
d) The pairwise alignment programs are not involved

Group-B

(Short Answer Type Questions)

 $3 \times 5 = 15$

2. Explain how do sequencing errors affect downstream applications like genome assembly and variant detection? (3)
3. Explain the use of sequencing technologies in cancer genomics and their role in identifying driver mutations. (3)
4. Explain the limitations of NGS in detecting structural variations in the genome? How can these be addressed? (3)
5. Explain the error rates in different DNA sequencing methods and discuss how errors are mitigated in NGS. (3)
6. Analyze the difference between X-ray crystallography and mass spectrometry in protein analysis. (3)

OR

Analyze how Van der Waals interactions contribute to protein stability. (3)

Group-C

(Long Answer Type Questions)

5 x 6=30

7. Analyze the impact of amino acid mutations on protein structure. (5)
 8. Evaluate the role of post-translational modifications in protein function. (5)
 9. How do genome annotation pipelines predict protein-coding genes and functional elements in a newly sequenced genome? (5)
 10. Describe how has the development of sequencing technologies influenced the field of metagenomics and microbiome research? (5)
 11. Design a gene editing experiment in *Drosophila melanogaster* using CRISPR-Cas9. (5)
 12. Critique the utility of UCSC Genome Browser in functional genomics studies (5)
- OR**
- Recommend improvements in existing genome databases for better accessibility and usability. (5)

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