

N.A



BRAINWARE UNIVERSITY

Term End Examination 2023
Programme – B.Sc.(BT)-Hons-2020
Course Name – Genomics and Proteomics
Course Code - BBTC602
(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) The most important tools of genomics are
- | | |
|-------------------------------|-------------------------|
| a) Microarray and informatics | b) Microarray and BLAST |
| c) BLAST and FASTA | d) FASTA and PCR |
- (ii) 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 |
- (iii) In prokaryotes, where do introns found?
- | | |
|---------|-------------------|
| a) tRNA | b) rRNA |
| c) mRNA | d) Only a. and b. |
- (iv) Genomics is the sub-discipline of genetics devoted to the
- | | |
|------------------------|-----------------|
| a) Mapping | b) Sequencing |
| c) Functional analysis | d) All of these |
- (v) 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 |
- (vi) If proteins are separated according to their electrophoretic mobility then the type of electrophoresis is identified as:
- | | |
|---------------------|------------------------------|
| a) SDS PAGE | b) Affinity Electrophoresis |
| c) Electro focusing | d) Free flow electrophoresis |
- (vii) What cannot be a reason for using electrophoresis?
- | | |
|--|--|
| a) Comparing two sets of DNA | b) Organizing DNA by shape of backbone |
| c) Organizing DNA fragments from largest to smallest | d) Organizing DNA in order we can see |
- (viii) Select the correct option for Native PAGE:
- | | |
|---------------------------|---|
| a) Proteins are denatured | b) Proteins are reduced |
| c) Proteins are broken | d) Proteins are kept in their native form |

- (ix) In pyrosequencing
- a) One pyro phosphate is released after correct base pairing
 - b) Two pyro phosphate is released after correct base pairing
 - c) Three pyro phosphate is released after correct base pairing
 - d) Four pyro phosphate is released after correct base pairing
- (x) If you have a sequence, but you are not sure what the gene name or ID in Ensembl is, you can align it to the genome with
- a) BLAST
 - b) BLAT
 - c) Both of these
 - d) None of these
- (xi) Genomics can be used in agriculture to:
- a) Generate new hybrid strains
 - b) Improve disease resistance
 - c) Improve yield
 - d) All of these
- (xii) Which of the following is the first completed and published gene sequence?
- a) PhiX174
 - b) T4 phage
 - c) M13 phage
 - d) Lambda phage
- (xiii) If you want to submit a new gene sequence, which one of the following is the best platform?
- a) NCBI
 - b) SWISSPROT
 - c) EMBL
 - d) DDBJ
- (xiv) Name the enzyme that is widely used for MS analysis
- a) Pepsin
 - b) Trypsin
 - c) Peptidase
 - d) All of these
- (xv) The computational methodology that tries to find the best matching between two molecules, a receptor and ligand are called _____
- a) Molecular fitting
 - b) Molecular matching
 - c) Molecular docking
 - d) Molecule affinity checking

Group-B

(Short Answer Type Questions)

3 x 5=15

2. Define genome. What do you mean by WGS? What is NGS? Why it is called NGS? 1+0.5+0.5+1
 3. Define Genomics. What are the steps to study a genome? 1+2
 4. What are the main factors differentiates species? (3)
 5. Identify the importance of 2D PAGE. (3)
 6. Discuss about the steps of pyrosequencing with pictorial representation. (3)
- OR**
- Elaborate the process of bridge PCR in brief. (3)

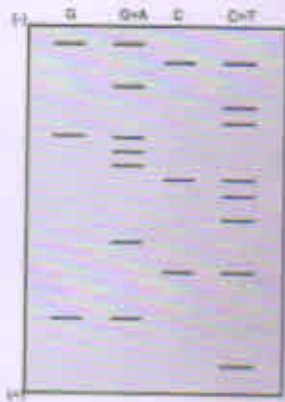
Group-C

(Long Answer Type Questions)

5 x 6=30

7. Compare in between Pairwise alignment and Multiple sequence alignment. (5)
8. Determine the scope of Pairwise alignment. (5)
9. Explain the Clone contig approach of genome annotation. (5)
10. What do you understand by sensitivity and specificity in BLAST? (5)
11. Write down the importance of microarray for gene expression. (5)

12. In a Maxam-Gilbert sequencing process, the following data obtained. Using the data, (5)
 construct the Nucleotide sequence. [5]



OR

- From the given figure formulate out the sequence of the nucleotide. Consider the left side (5)
 as 5' end. The Y axis represents the intensity of illumination of added nucleotides. Briefly
 justify your answer.

