

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) Which of the following is responsible for specifying the 3D shape of a protein?  
a) The peptide bond  
b) The amino acid sequence  
c) Interaction with other polypeptides  
d) Interaction with molecular chaperons
- (ii) Genome classifies  
a) Total gene pool of an organism  
b) Total mRNA of an organism  
c) Only DNA of a diploid cell  
d) Only proteins
- (iii) 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
- (iv) Introns are  
a) Non coding regions of genome  
b) Coding regions of genome  
c) Repetitive regions of genome  
d) All of these
- (v) Choose the correct enzyme used in proteomics.  
a) Trypsin  
b) Amylase  
c) Lipase  
d) Maltase
- (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 exact option known as Edman's reagent.  
a) FDNB  
b) CNBD  
c) IDNB  
d) CDNBD
- (viii) What is the main enzyme used in Sanger method?  
a) Nuclease  
b) Polymerase  
c) Gyrase  
d) None of these
- (ix) Which of the following is used for DNA fragments\ ' cluster generation on a microchip?

- a) Emulsion PCR  
c) Both of these
- b) Bridge PCR  
d) None of these
- (x) The first molecular biology server expasy was in the year \_\_\_\_\_.
- a) 1992  
c) 1994
- b) 1993  
d) 1995
- (xi) The process of finding the relative location of genes on a chromosome is called \_\_\_\_\_.
- a) Gene tracking  
c) Genome mapping
- b) Genome walking  
d) Chromosome walking
- (xii) What kind of diseases are studied using genome-wide association studies?
- a) Viral diseases  
c) Diseases caused by multiple genes
- b) Single-gene inherited diseases  
d) Diseases caused by environmental factors
- (xiii) How many configurations of an amino acid are possible?
- a) 1  
c) 3
- b) 2  
d) 4
- (xiv) The identification of drugs through the genomic study is called \_\_\_\_\_.
- a) Genomics  
c) Pharmacogenetics
- b) Pharmacogenomics  
d) Cheminformatics
- (xv) The stepwise method for solving problems in computer science is called \_\_\_\_\_.
- a) Flowchart  
c) Procedure
- b) Algorithm  
d) Sequential design

### Group-B

(Short Answer Type Questions)

3 x 5=15

2. State about comparative genomics in brief. (3)
3. List down the steps of genome browsing using ENSEMBLE browser. (3)
4. Distinguish in between a rooted and an unrooted phylogenetic tree. (3)
5. List down the applications of 2D-PAGE. (3)
6. Site your own opinion on the utility of NCBI in genomic research. (3)

OR

"If you have a sequence, but you are not sure what the gene name or ID in database is, you can align it to the genome with BLAST "..... Simplify this statement in your own word with proper example. (3)

### Group-C

(Long Answer Type Questions)

5 x 6=30

7. Which types of issues or problems related to biological data are dealt with the bioinformatics? (5)
8. Explain the role of SDS, APS and TEMED in SDS PAGE. (5)
9. Compare between Trypsin and Trypsin Gold. Which one is better for proteomic analysis? (5)
10. Hypothesize the principle of stacking gel in SDS PAGE. (5)
11. 9. Consider the following problem: You are given the task of determining the profile of glycosylation carried by a newly discovered anti-angiogenic protein purified from rat hypothalamus. You are given a tube containing approximately 100 micrograms of the purified protein in Tris buffer, and you are told that the gene sequence for the protein is in the NCBI database under the name of NFL1\_mouse. You have two mass spectrometers to use, an Orbitrap with an accompanying nanoLC system, and a MALDI-TOF/TOF. You can also use any protein electrophoresis, staining reagents or Western blotting reagents you need. (i) Explain how you would confirm whether the protein is glycosylated or not. (ii) Explain how knowledge of the gene sequence would assist you in deciding which experiments to perform next. 2.5+2.5 (5)

12. Explain the principle of gel filtration chromatography and briefly explain the term 'Void Volume'. (5)

OR

Explain about Isoelectric focusing and 2D PAGE in detail. (5)

\*\*\*\*\*