N.A

BRAINWARE UNIVERSITY

Term End Examination 2023
Programme – M.Sc.(BT)-2022
Course Name – Genomics and Proteomics
Course Code - MBTE205
(Semester II)

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) Bioinformatics involves

a) Artificial intelligence
b) Only knowledge of Biochemistry
c) Zoological knowledge
d) All of these

(ii) If you have a sequence, but you are not sure what the gene name or ID in Ensembl is, select where to align it

a) BLAST
b) BLAT
c) Both of these
d) None of these

(iii) Genomics can be used in agriculture to:

a) Generate new hybrid strains
b) Improve disease resistance
c) Improve yield
d) All of these

(iv) The activity of drug-metabolizing enzymes often varies widely among healthy people, making metabolism highly variable. Which of the following factors is a major contributor to this variation?

a) Aging
b) Environmental factors
c) Gender
d) Race

(v) In a typical plot of green fluorescent intensity on the Y axis vs. red fluorescent intensity on the X axis, which of the following statements about microarray data analysis is true?

a) Most spots lie on the X=Y axis.
b) Scientists are most often interested in pursuing the spots on the X=Y axis.
c) Greater than 90% of the spots show greater than 10-fold difference in expression.
d) Spots tend to show a complete random scatter with no obvious alignment on the plot.

(vi) Name the phenomenon which shows the lack of correlation in genome size and genetic complexity.

a) Histogram
b) Karyogram
c) Dendrogram
d) C-value paradox

(vii) The 3-D structure of proteins can be determined by_____.

a) Spectroscopy
b) X-ray crystallography
c) Nuclear magnetic resonance
d) Both (b) and (c)

(viii) Human has a_____ genome.

a) About 100 kb
b) About 500 kb
c) About 1000 kb
d) About 3000 kb

(ix) Introns are

a) Non coding regions of genome
b) Coding regions of genome
c) Repetitive regions of genome
d) All of these

(x) Mass spectrometers are used to identify which of the following?

a) Composition in sample
b) Concentration of elements in sample
c) Relative mass of atoms
d) Properties of sample

(xi) Mass spectrometer selects ions on the basis of which of the following?

a) Mass
b) Charge
c) Molecular weight
d) Mass to charge ratio

(xii) C-value in genome represents_____

a) Genetic disorders
b) Phenotypic variation
c) Amount of DNA present in the genome
d) Qualitative traits

(xiii) Most of the eukaryotic nuclear genome has

a) Repetitive DNA
b) Unique DNA
c) GC island
d) Single copy

(xiv) Connect the relation of time of flight with the molecular mass of the ion in the TOF mass analyzer?

a) Time of flight is inversely proportional to the square root of the molecular mass of the ion
b) Time of flight is inversely proportional to the molecular mass of the ion
c) Time of flight is directly proportional to the molecular mass of the ion
d) Time of flight is directly proportional to the square root of the molecular mass of the ion

(xv) If a charge has a mass of 3 kg and it is traveling at a speed of 10 m/s in-flight tube, then asses it's kinetic energy?

a) 300 J
b) 90 J
c) 100 J
d) 150 J

Group-B

(Short Answer Type Questions) 3 x 5=15

2. Define microsatellite. (3)
3. Illustrate the process of bridge PCR. (3)
4. Discuss about the usefulness of BLAST. (3)
5. Infer about the drug efficacy of any suitable drug. (3)
6. Justify the connection of proteomics with biology and chemistry. (3)

OR

Evaluate the functions of expression proteomics. (3)

Group-C

(Long Answer Type Questions) 5 x 6=30

7. Define the different types of genome mapping. Which type is useful for the identification of protein coding portion? (5)
8. Determine the role of fluorescence in illumina sequencing. (5)
9. Write down the importance of microarray for gene expression. (5)
10. Explain a Root, Node and Clade of a phylogenetic tree. (5)
11. Estimate how doctors use pharmacogenetics to treat their patients. (5)
12. Explain the steps of DNA sequencing in a human genome, how much gene is protein coding? (5)

OR

Describe elaborately the process of protein and peptide microarray based technology. (5)

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