REV-01
MBT/05/10

2023/12

SET A

M.Sc. BIOTECHNOLOGY
FIRST SEMESTER
BIOINFORMATICS
MBT-104

[USE OMR SHEET FOR OBJECTIVE PART]

Duration: 1hr. 30 mins. Full Marks: 35

(Objective)

Time: 15 mins. Marks: 10

Choose the correct answer from the following: ***1×10=10***

1. The lack of correlation between genome size and genetic complexity is referred to as:
   a. C-value b. C-value paradox
   c. Gene desert d. None of these

2. The genome size of *S. cerevisiae* is:
   a. 10 Mb b. 15 Mb
   c. 12 Mb d. 20 Mb

3. Chemical sequencing is another name of:
   a. Sanger's Sequencing b. Automated sequencing
   c. Pyrosequencing d. Maxam-Gilbert sequencing

4. All other hybrids are omitted except the dimer hybrid in the technique:
   a. Subtractive hybridization b. Differential display
   c. Both a and b d. None of these

5. ESTs are short DNA sequences of:
   a. <200 bps long b. <1000 bps long
   c. <800 bps long d. <1200 bps long

6. The term "Proteome" was first coined by:
   a. Robert Wilkins b. Josef Wilkins
   c. Marc Wilkins d. None of these

7. Following are examples of all beta domain motifs:
   a. Hair-pin beta motif b. Greek key motif
   c. Up and down structural motif d. All of the above

8. The suitable substitution matrix to align closely related sequences is:
   a. PAM 250 or BLOSUM 80 b. PAM 40 or BLOSUM 80
   c. PAM 120 or BLOSUM 40 d. PAM 250 or BLOSUM 40

9. Lower the value of PAM:
   a. Lower the sequence identity b. Higher the sequence identity
   c. Sequences are distantly related d. None of the above

10. Global alignment uses:
    a. Two sequences of same length
    b. Two closely related sequences
    c. Needleman-Wunch algorithm
    d. All of the above

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Descriptive

Time : 1 hr. 15 mins. Marks : 25

[Answer question no.1 & any two (2) from the rest]

1. Explain the Sanger's sequencing method. 5

2. What is RT-PCR? Elaborate DNA microarray technology. 10

3. Write a brief note on protein motif and domain structures. 10

4. What do you understand by sequence alignment? Explain Global and Local sequence alignment. State the differences between pairwise and multiple sequence alignment. 2+3+5=10

5. What is Ramachandran Plot? Explain homology modelling. 5+5=10

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