M.Sc. MICROBIOLOGY
FIRST SEMESTER
BIOINFORMATICS
MMB-104
[USE OMR SHEET FOR OBJECTIVE PART]

SET
A

Duration: 1hr. 30 mins.

Full Marks: 35

(**Objective**)

Time: 15 mins.

Marks: 10

Choose the correct answer from the following:

$1 \times 10 = 10$

1. The amount of DNA present in haploid genome of species is called:
   a. C-value
   b. C-value paradox
   c. Gene desert
   d. None of these

2. The genome size of *Homo sapiens* is:
   a. 2300 Mb
   b. 3000 Mb
   c. 3300 Mb
   d. 2000 Mb

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

4. A laboratory technique that allows a researcher to compare and identify changes in gene expression at mRNA level between two or more eukaryotic cell samples is:
   a. Subtractive hybridization
   b. Differential display
   c. Both a and b
   d. None of these

5. Full form of SRA is:
   a. Sequence Read Archive
   b. Short Related Archive
   c. Short Read Archive
   d. None of these

6. In protein analysis 3D structure can be generated using:
   a. XRD analysis
   b. Mass spectrometer
   c. Both a and b
   d. Neither a nor b

7. Following are examples of all alpha domain:
   a. Helix turn helix motif
   b. Coiled coil structure
   c. Leucine zipper
   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 Maxam-Gilbert sequencing method.   5

2. What is Northern Blotting? Elaborate differential display technique.   10

3. What do you understand by proteome? Write down the general   10
   scheme to proteomic analysis.

4. What is phylogenetic analysis? Explain the different patterns of tree   2+8=10
   building method.

5. What are secondary structure predictions of proteins? Elaborate.   10

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