

M.Sc. BIOTECHNOLOGY
FIRST SEMESTER [SPECIAL REPEAT]
BIOINFORMATICS
MBT-104

SET
A

[USE OMR SHEET FOR OBJECTIVE PART]

Duration: 1hr. 30 mins.

Full Marks: 35

Time: 15 mins.

(Objective)

Marks: 10

Choose the correct answer from the following:

1×10=10

1. ATG codes for:
 - a. Methionine
 - b. Proline
 - c. Typtophan
 - d. Tyrosine
2. Exons are:
 - a. Non coding regions
 - b. Coding regions
 - c. Intergenic regions
 - d. None of these
3. Full form of ORF is:
 - a. Open reading fragment
 - b. Open reading file
 - c. Open reading frame
 - d. None of these
4. Northern blotting stands for the separation of:
 - a. DNA
 - b. Protein
 - c. Both DNA and RNA
 - d. RNA
5. Study of whole genome expression profile of an organism can be done by using:
 - a. DNA microarray
 - b. SAGE
 - c. RT-PCR
 - d. NGS-Technology
6. Full form of BLAST is:
 - a. Basic Local Alignment Search Tool
 - b. Basic Large Algorithm Search Tool
 - c. Basic Local Algorithm Search Tool
 - d. None of the above
7. SRA is a:
 - a. Search Engine
 - b. Database
 - c. Software
 - d. None of the above
8. EST stands for:
 - a. Expressed short Tags
 - b. Expressed sequenced Tags
 - c. Enlarged sequenced Tags
 - d. None of the above
9. BLOSUM 82 means:
 - a. Sequences are distantly related
 - b. Sequences are closely related
 - c. Homologous sequences
 - d. None of the above

10. Following is an example of Global Alignment web based program:
- a. SIM
 - b. LALIGN
 - c. GAP
 - d. SSEARCH

-- -- --

(Descriptive)

Time : 1 hr. 15 mins.

Marks : 25

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

- | | |
|--|--------|
| 1. What is Sanger's method of DNA sequencing? How it is different from automated DNA sequencing? | 5 |
| 2. Write down the applications of genomics on agriculture, human health and industry. | 10 |
| 3. Write short notes on:
a) Microarray
b) Differential Display | 5+5=10 |
| 4. What is Ramachandran Plot? Differentiate between Pairwise sequence alignment and Multiple Sequence Alignment. | 4+6=10 |
| 5. Elaborate:
a) Dot matrix method
b) Difference between sequence identity and sequence similarity | 5+5=10 |

== *** ==