

Roll No.

Total No. of Pages : 02

Total No. of Questions : 09

M.Sc.(BT) (2016 to 2017) (Sem.-3)

PROTEOMICS AND GENOMICS

Subject Code : MSBT-201

M.Code : 15018

Time : 3 Hrs.

Max. Marks : 60

INSTRUCTION TO CANDIDATES :

1. **SECTION-A is COMPULSORY consisting of TEN questions carrying TWO marks each.**
2. **SECTION-B contains FIVE questions carrying FIVE marks each and students have to attempt any FOUR questions.**
3. **SECTION-C contains THREE questions carrying TEN marks each and students have to attempt any TWO questions.**

SECTION-A

- 1. Write short notes on following :**
- a) What is the difference between proteomics and genomics?
 - b) What are contigs?
 - c) Which software is used for predicting phylogenetic relationship?
 - d) Which scoring matrix is use for pair wise alignment of protein sequence?
 - e) What is the difference between rooted and unrooted phylogenetic tree?
 - f) Which technique is used for de novo sequencing of protein?
 - g) What is the difference between SDS and native PAGE?
 - h) What is splice variant?
 - i) By which genomic technique we study polymorphism in a population?
 - j) What is the difference between global and local alignment?

SECTION-B

2. What is nucleotide databases? Why are they important in bioinformatic studies?
3. Explain in brief the genome complexity and its role in genomics.
4. What are SNP databases? Give example and its significance.
5. Briefly explain co-immunoprecipitation.
6. Discuss about repetitive sequences present in eukaryotic genome.

SECTION-C

7. Explain different methods for preparing genome maps in prokaryotes.
8. Give the schematic representation of MALDI-TOF and their application in proteomics.
9. What is dot matrix? Where is it used? Explain by giving example.

NOTE : Disclosure of Identity by writing Mobile No. or Making of passing request on any page of Answer Sheet will lead to UMC against the Student.