Roll No. | | | | | | | | | | | | **Total No. of Pages : 02**

Total No. of Questions : 20

M.Sc. (Biotechnology) (2018 Batch) (Sem.-3)

GENOMICS AND PROTEOMICS

Subject Code : MBT-303

M.Code : 76730

Time : 3 Hrs. **Max. Marks : 70**

INSTRUCTIONS TO CANDIDATES :

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

SECTION-A

Explain the following in brief :

1. Genomics
2. Biological databases
3. TILLING
4. EST
5. SNP
6. 2D-IEF
7. Comparative genomics
8. Mass spectrometry
9. Protein-protein interactions.
10. Peptide sequencing.

SECTION-B

11. Provide a brief description of the strategies and methods used for genome sequencing.

12. Explain properties of eukaryotic genomes.

13. Give principle and applications of SAGE.

14. What are SNPs? How are these detected in the DNA?

15. Write short notes on the terms, proteome, proteomics and protein databases. Also give applications of the proteomics in biological research.

16. Provide a detailed account of the techniques and application of protein digestion.

17. How are the protein expression profiles investigated? Explain reasons of analyzing such data.

SECTION-C

18. Give an overview of the techniques used in mining genomes and proteomes. Also provide an account of their applications in biological research.

19. Explain principle procedures and applications of mass spectrometry.

20. What do you understand by functional genomics? Give detailed methodology used for assessing expression profiles of the organisms.

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.