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

Total No. of Questions : 18

B.Tech. (BT) (2012 to 2017) (Sem.–7)

GENOMICS AND PROTEOMICS

Subject Code : BTBT-703

M.Code : 71845

Time : 3 Hrs. **Max. Marks : 60**

INSTRUCTIONS 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

Write briefly :

1. Explain HAPPY mapping.
2. Differentiate between bacterial and viral genomes.
3. List out the applications of Human Genome project.
4. Define Proteome?
5. What are protein arrays and its uses?
6. What are the applications of structural proteomics?
7. What are Orthologs? How are they different from paralogs?
8. Explain how is proteomics useful in understanding functions of different proteins?
9. Explain RAPD along with its advantages and limitations.
10. What is exon shuffling?

SECTION-B

11. Explain the principle of the shot gun approach method for the genome sequencing.

12. Describe the serial analysis of gene expression (SAGE) for transcriptome analysis. How is it different from microarray based approach?

13. What is the application of transcriptional profiling using transcriptomic analysis?

14. What is 2D gel electrophoresis? Write a note on its application in proteomics.

15. Define EST and write how it is different from STS? Why is it desirable to select EST from 3'UTR region of genes?

SECTION-C

16. Explain how can X-ray crystallography determine the three dimensional structure of protein?

17. What is the importance of metagenomic analysis of microbial communities?

18. Write short notes on the following :

    a) Multiple Sequence alignment

    b) Proteomic databases

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.