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

Total No. of Questions : 09

B.Tech.(BT) (2011 Onwards) (Sem.–7,8)

GENOMICS AND PROTEOMICS

Subject Code : BTBT-703

Paper ID : [A2947]

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 briefly :

a. Define STS.

b. What is the importance of high-throughput sequencing of DNA for whole genome sequencing?

c. Define Orthologs.

d. Write a short note on spotted nylon macroarrays.

e. What is the role of mass spectrometry in proteomics?

f. What are the advantages of NMR over X ray diffraction in solving protein structure?

g. How are SNPs different from point mutations?

h. What do you understand by multi-dimensional liquid chromatography?

i. What are the limitations of whole genome shotgun approach?

j. How are large data sets produced by protein-protein interaction screening managed?

SECTION-B

2. Discuss the advantages and limitations of transcriptomics in comparison with proteomic analysis.

3. What are pathogenicity islands? How can they be detected?

4. Write a short note on protein arrays and their application in proteomics.

5. What is the significance of human genome project in modern biology?

6. What is homology modeling and what is its role in structural proteomics?

SECTION-C

7. Describe yeast two hybrid method for studying protein-protein interactions.

8. Give a detailed account of 2D gel electrophoresis and write about its application in proteomics.

9. Explain AFLP in detail and compare it with RFLP.