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

Total No. of Questions : 09

B.Tech.(BT) (2011 Onwards) (Sem.–6)

COMPUTATIONAL BIOLOGY

Subject Code : BTBT-604

Paper ID : [A2286]

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. KEGG

b. Gene hunting

c. Eulerian cycle

d. ADME

e. Consensus folding

f. MMDB

g. Molecular dynamics

h. Fuzzy logic

i. Application of Lander-waterman in bioinformatics

j. Rasmol

SECTION-B

2. Describe system biology with few applications.

3. Write about the computational methods which are used in sequence similarity search.

4. What is DNA double digest problem? Write about any algorithm which can be used to solve the DNA double digest problem.

5. Write a perl programme which can be used to convert EMBL sequence format to GenBank sequence format.

6. Mention few databases of metabolic pathway. Explain atleast two such databases.

SECTION-C

7. What is markov model and hidden markov model? With examples, explain hidden markov model. Write its application in bioinformatics.

8. Describe the different computational methods of computer aided drug design. How docking is useful in drug design?

9. Describe different bioinformatics methods of gene prediction. How prokaryotic gene prediction tool is different from eukaryotic gene prediction tool?