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Total No. of Pages : 02

Total No. of Questions : 18

B.Tech. (BT) (2012 to 2017) (Sem.-6)

COMPUTATIONAL BIOLOGY

Subject Code : BTBT-604

M.Code : 71075

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**Write briefly :**

1. Radiation hybrid mapping
2. Eulerian cycle
3. AMBER
4. MMDB
5. Gene Hunting
6. Optical maps
7. Restriction mapping tool
8. Application of Lander-waterman in bioinformatics
9. Fuzzy Logic
10. ADME

SECTION-B

11. Write the different features of KEGG database.
12. Explain the hidden Markov Model.
13. Write the important of docking in drug design. Differentiate between rigid and flexible docking.
14. Write the important steps required in finding target template to model the three dimensional structural of protein based on homology modeling approach.
15. Write a perl programme which can be used to convert any sequence fromat to GenBank sequence format.

SECTION-C

16. Explain the concepts of evolutionary computing. With example, write the application of evolutionary computing in bioinformatics.
17. Describe different bioinformatics methods of gene prediction? How prokaryotic gene prediction tool is different from eukaryotic gene prediction tool?
18. Explain DNA double and partial digest. What are the problems encountered during these digestion of DNA? Write solutions to solve the double and partial digest problem.

NOTE : Disclosure of identity by writing mobile number or making passing request on any page of Answer sheet will lead to UMC case against the Student.