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

Total No. of Questions : 18

B.Tech. (BT) (2012 to 2017)   (Sem.–5)

BIOINFORMATICS

Subject Code : BTBT-505

M.Code : 70506

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

Answer briefly :

1. NCBI

2. Sequin

3. PRINTS

4. PHI-BLAST

5. SWISS-PROT

6. Jukes-Cantor model

7. MMDB

8. Neighbor-Joining method

9. SCOP

10. Ramachandran plot

SECTION-B

11. Briefly describe any three secondary protein databases.

12. Briefly describe about PDB.

13. What are PAM and BLOSUM matrices? Describe their importance.

14. What are molecular markers? Write a note on Rasmol.

15. What is T-COFFEE? Describe about its approach in multiple sequence alignment.

SECTION-C

16. Describe the prediction of protein structure by using threading method.

17. Describe various methods used in phylogenetic tree constructions and their importance.

18. Align the following sequences by using Smith and Waterman algorithm.

    seq 1: ATTCGATCC, seq 2: ACGAT (Use +1 for match and -2 for mismatch and -3 for gap penalty).

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.