

Total No. of Pages :02

Total No. of Questions : 09

B.Tech.(BT) (2011 Onwards) (Sem.-5)

BIOINFORMATICS

Subject Code :BTBT-505

Paper ID : [A2077]

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 :

- Orthologous and paralogous sequence
- E- Value
- MMDB
- ESTs
- Gap Penalty
- T coffee
- COGS
- Loop modelling
- Difference between rooted and unrooted tree
- BLOCK in BLOSUM matrix

SECTION-B

2. Write about the PDB database. Why is it one of the popular protein database?
3. Write any one method of gene prediction of prokaryotes.
4. Explain Needleman-Wunsch algorithm.
5. Describe the bioinformatics method of identifying functional site in DNA.
6. Explain the criteria for selection of template in homology modelling.

SECTION-C

7. Describe any progressive method of multiple sequence alignment. How progressive method is different from iterative alignment method?
8. What is neural network method? Explain its usage in protein secondary structure prediction.
9. Write the application of phylogenetic tree constructions. Describe any one phylogenetic method which is based on genetic distance.