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

Total No. of Questions : 08

M.Tech. (Bio Tech) (Sem.–3)

ADVANCED BIOINFORMATICS

Subject Code : MTBT-303/18

M.Code : 76763

Date of Examination : 16-12-2022

Time : 3 Hrs. **Max. Marks : 60**

INSTRUCTIONS TO CANDIDATES :

1.Attempt any FIVE questions out of EIGHT questions.

2.Each question carries TWELVE marks.

1. **Write a short note on the following :**
   a) Genome assembly and annotation
   b) Homology search tool
   c) Protein structure Databases
   d) Scoring matrices.
2. Discuss roles and applications of bioinformatics in present biological research.
3. a) Expand SMBL? Write a short note on SMBL.
   b) Discuss E-cell and V-cell simulations and their applications.
4. a) What are primary and secondary databases? What is consensus sequence?
   b) What is proteomics? Write a short note on SAGE.
5. What do you understand by e-value, query coverage, sensitivity and specificity in BLAST?
6. If you get a particular protein named 'Gelatin'. Name the databases and describe them that can be used for retrieve of its
   a) Nucleic acid sequence
   b) Protein sequence
   c) Protein chains
   d) Amino acid frequency or properties?

7. a) Explain the concept of scoring matrices for aligning amino acid sequences.

b) Briefly explain how PAM is derived.

8. a) Name two tools used in i) Phylogenetic analysis, ii) Sequence alignment, iii) Genomic data analysis.

b) Explain the principle of mass spectrometry and 2D get electrophoresis.

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.