U.G. 4th Semester Examination - 2022

Molecular Biology & Biotechnology

[HONOURS]

Course Code : MBBT-H-403-T-CCR-10

Full Marks : 40   Time : $2\frac{1}{2}$ Hours

The figures in the right-hand margin indicate marks.

Candidates are required to give their answers in their own words as far as practicable

1. Answer any **five** of the following: 2×5=10

    a) Write the URL of Genbank and PDB.

    b) When are Homologous sequences called Orthologous?

    c) Name one space Protein sequence database and one Protein Structure database. NCBI stands for _____.

    d) Define gap in alignment with an example.

    e) Define optimal alignment.

    f) What is ORF? Name one ORF searching tool.

    g) What is the Expect (E) value?

    h) What is the role of Primer-BLAST?

2. Answer any **two** of the following: 5×2=10

    a) Define Twilight zone. What is the significance of Twilight zone?   3+2

    b) What is Blosum? Write three differences between Pam and Blosum.   2+3

    c) What is Pairwise alignment? Define Local Alignment.   3+2

    d) How does TBLASTN operate? What is the full form of PSI-BLAST?   4+1

3. Answer any **two** of the following: 10×2=20

    a) Write short notes on Genbank and TrEMBL.   5+5

    b) Describe FASTA algorithm or Blast algorithm.   10

    c) What is Dot matrix? Align the following two sequences using Dot Matrix method.
        Seq1: Abcdaefghbijkl   Seq2: abcdaefghbijkl.
        What record does HETATM and SSBOND provide in PDB?   2+4+2+2

    d) What is a Phylogenetic tree? What are the differences between Rooted and Unrooted tree? Define HTUs. Which tree does UPGMA produce?   3+4+2+1

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[Turn Over]