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PG/IIS/MCB/207/25

M. Sc. 2nd Semester Examination, 2025

MICROBIOLOGY

(*Bioinformatics*)

PAPER – MCB-207

Full Marks : 25

Time : 1 hour

Answer **all** questions

The figures in the right hand margin indicate marks

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

GROUP – A

Answer any **two** of the following questions : 2 × 2

1. What is Proteomics ? Mention any two tools used for predicting the 3D structure of proteins. 1 + 1

2. Explain the Dynamic Programming approaches used in Pairwise Sequence Alignment (PSA).

3. Write down the comparison between PAM and BLOSUM.

4. Describe the various types of BLAST.

GROUP—B

Answer any **two** of the following questions : 4 × 2

5. What is a Genetic Algorithm ? Which algorithms are commonly used for sequence alignment ? 2 + 2

6. What is the FASTA format ? How can you recognize a sequence in FASTA format ? 2 + 2

7. What is a DBMS (Database Management System) ? What are the main goals of biological database ? 2 + 2

8. Differentiate between phylograms and cladograms. Briefly explain the concepts of Maximum Parsimony (MP) and Maximum Likelihood (ML). 2 + 2

GROUP – C

Answer any **one** of the following question : 8 × 1

9. Define Low Complexity Regions (LCRs). What is bootstrapping in phylogenetic analysis ? Which methods are used for constructing distance-based phylogenetic tree ? What is the role of an outgroup in phylogenetic tree construction ? Summarize the key steps involved in constructing a phylogenetic tree. 1 + 1 + 2 + 1 + 3

10. What is an alignment score ? Define k-tuples (ktups). How does BLAST differ from

FASTA ? What are the applications of Multiple Sequence Alignment (MSA) ? When should BankIt and Sequin be used for sequence submission to NCBI ? 1 + 1 + 2 + 2 + 2

[Internal Assessment — 05 Marks]