2013

P.G. Diploma in

Quality Control and Assurance in Microbial Technology

PAPER—MT-101

Full Marks : 50

Time : 2 Hours

The figures in the right-hand margin indicate full marks.

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

Illustrate the answers wherever necessary.

Write the answers of each question of each Group in Separate Book.

Answer any *Five* Questions from Each Group.

Group—A

[Marks—25]

Answer any *five* questions.

1. What do you mean by selective media? How will you select nitrogen fixing and spore forming bacteria from the soil? 1+(2+2)

2. Define Tm. Why is ribosomal RNA considered for identification of the organism? What is type strain? 2+2+1

3. Compare the way of the formation of image in TEM and SEM. Why is the resolution superior in electron microscope ? 2+2+1

4. Explain what happens in negative staining that causes the final result. What characteristics are used to classify bacteria ? 2+3

5. Write notes on (any *two*) : 2.5×2

   (a) Prions;

   (b) E D pathway;

   (c) Pasteurization;

   (d) Basis of five kingdom classification system.

6. Where do superoxide ions and hydrogen peroxide originate ? What are their toxic effects and how aerobic bacteria mitigate these toxic effects ? 2+3

7. How will you enumerate the bacteria from the supplied soil sample ? What is metagenomics ? 3+2

8. Draw the structure of a typical gram negative bacterial flagella and write down the molecular mechanism of movement. 2+3

Group—B

[Marks—25]

Answer any *five* questions.

1. How can molecular biology be considered as an information science ? Write the scope of bioinformatics ? 2+3

2. What do you mean by database ? What are the various types of protein databases ? Which are the most important examples of the types ? 1+2+2

3. Define and point out the differences between global and local alignment methods. 5

4. Apply the Needleman-Wunsch Algorithm to determine the best alignment for The following amino acid sequences. Use a BLOSUM 62 matrix for your match scores and a gap penalty of 8.

   Sequence # 1 : TVVTGRVE

   Sequence # 2 : TVATRIE

5. Why do you need multiple sequence alignments ? Can they be done globally ? 5

6. What are the advantages of phylogenetic analysis ? What parameters will you use for building phylogenetic trees ? 2+3

7. Write a short note on BLAST with its extension and applications. 5

8. How can you predict protein sequence from DNA sequence through Bioinformatics tool? Define motifs. 3+2

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