2013
M.Sc.
3rd Semester Examination
BIOTECHNOLOGY
PAPER—BIT-304
Full Marks : 40
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.

Answer all questions.

Group—A

1. Answer any five questions from the following : 2×5
   
   (a) What are identifiers? Mention their usage.
   (b) Provide a name of a program or algorithm that
       performs a local multiple sequence alignment.
   (c) What is the ‘E’ value in BLAST?
   (d) What does the 62 mean for the BLOSUM62 scoring
       matrix?
   (e) What is ORF? What is its utility?
   (f) Given the two DNA sequences GCGT and GCT, and
       using +2 for a match, -2 for a mismatch, and a gap
       penalty of -1, give an optimum global alignment and
       its score.
   (g) What is Clastal W? For what purpose it is used?
   (h) Write down the full forms of EBI, PDB, EXPASY and
       NLM.

(Turn Over)
Group—B

Answer any two questions from the following: 5×2

2. Define gap penalty. What is an 'informative' and 'non-informative' site? Describe some common techniques for gene prediction. 1+1+3

3. How you can differentiate 'Orthology' & 'Paralog'? How is tertiary protein structure different from its quaternary structure? Mention 2 important utility of protein 3D structure prediction. 2+2+1

4. Draw a Dot Plot for the following 2 sequences: CACG and GATCACG. Write down the full forms of EXPASY & EMBL. 4+1

5. Expand BLAST. Write short note on PSI-BLAST. Define SNP and epigenetics with one example for each. 1+2+2

Group—C

Answer any two questions: 10×2

6. (i) Describe NJ method. Mention its use with its advantages and disadvantages. 2+2+1+5

(ii) Write a short note on 'human genome project'.

7. Align the following two sequences GTACTACGA & GTACCCGA by the dynamic programming algorithm. 10

8. What is GOR method? Distinguish between proteomics and genomics. What is 'accession code'? Mention the name of 2 mutation Databases. Mention one point mutation resulting a human disease. 2+3+1+2+2

9. (i) Briefly describe about post translational modifications. 4+4+2

(ii) Discuss about the methods of whole genome sequence.

(iii) Define FASTA.