(i) Printed Pages : 3 Roll No. .....

(ii) Questions : 9 Sub. Code : 2 9 9 4

Exam. Code : 4 3 7

M.Sc. 3rd Semester

1125

BIOTECHNOLOGY

Paper–MBIO-305 : Advances in Genomics and Proteomics

Time Allowed : Three Hours] [Maximum Marks : 80

Note : Attempt **five** questions in all. Question No. 1 is compulsory. Select **one** question each from Unit I to Unit IV.

1. Write short answers on :

(a) Oligonucleotide Fingerprinting

(b) e-PCR

(c) E-Value

(d) Levenshtein distance

(e) Log Odd Ratio

(f) Electrospray Ionization (ESI)

(g) Rooted vs. Un-Rooted Trees

(h) ChIP-seq. 8×2=16

UNIT–I

2. (a) Discuss methods of eukaryotic gene prediction.

(b) How bioinformatics is useful for discovering information related to protein structure, function and evolution ? 2×8=16

3. (a) How Phase Display technique is used to identify and extract polypeptides with desired properties from a large collection of variants ?

(b) Explain role of proteomics technologies in crop improvement. 2×8=16

UNIT–II

4. (a) What are Expression Libraries ? Explain the process of generation of cDNA expression libraries.

(b) What are DNA Chips ? How is it different from protein chips ? Give applications of DNA chips. 2×8=16

5. (a) Write about protein array technology. How the detection of protein-protein interactions is done on Protein microarrays ?

(b) Give applications of protein chips in proteomics. 2×8=16

UNIT–III

6. (a) Explain Illumina sequence-by-synthesis approach of DNA sequencing.

(b) Define BLAST. Describe its various forms used to analyze DNA and Protein sequences.

(c) Differentiate between local and global alignment. 8+4+4=16

7. (a) Explain DNA sequencing with Nanopores and its advantages over other next generation sequencing techniques.

(b) Why there is a need for 3D structure prediction of macromolecules ? Explain Homology Modeling method of protein structure prediction. 2×8=16

UNIT–IV

8. (a) Explain the Mass spectrometry based protein identification method.

   (b) How DNA microarray can be used to identify disease gene expression profile ? 2×8=16

9. (a) Explain in detail ChIP method for Genome-wide identification of transcription factor binding sites.

   (b) Proteomics studies involve high-resolving Gel based or Liquid-Phase separation techniques. Explain Liquid-Phase proteomics technique for protein separation. 2×8=16