

[Time: 2½ Hours]

[ Marks:60]

Please check whether you have got the right question paper.

- N.B:**
1. All questions are **compulsory**.
  2. All questions carry equal marks.
  3. Draw neat labeled diagrams wherever necessary.

- Q.1 Answer the following:-
- a) Give an account of primary and secondary databases used for storing biological data. 12
- OR**
- a) What are specialized databases? Explain any two. 06
  - b) Discuss the parameters used for designing of PCR primers. 06
- Q.2 (a) Answer **any one** of the following: 08
- i. Give an account of the databases and programs used for motif finding.
  - ii. Discuss the databases and tools for protein structure analysis
- (b) Explain **any one** of the following: 04
- i. Predictive methods for gene finding.
  - ii. Types of sequence alignments.
- Q.3 Answer **any two** of the following: 12
- a) What are cDNA arrays? Give their advantages and disadvantages.
  - b) Schematically explain serial analysis of gene expression.
  - c) Elaborate on the normalization and classification of microarray data.
  - d) Discuss the methods used for photolithographic synthesis of oligonucleotide arrays.
- Q.4 (a) Answer **any one** of the following: 08
- i. Explain the separation and analysis of proteins by 2D PAGE.
  - ii. Give an account of data retrieval tools.
- (b) Answer **any one** of the following: 04
- i. What are sequence logos? How are they generated?
  - ii. Explain *de novo* protein sequencing.
- Q.5 Write short notes on **any three** of the following: 12
- a) Assessment and output of BLAST
  - b) UCSC genome browser
  - c) Nucleotide databases
  - d) Exon intron finder
  - e) Phylogeny
  - f) Protein- Protein Interaction in mammalian system