

Q.P. Code :11458

[Time: 2 $\frac{1}{2}$ Hours]

[Marks:60]

Please check whether you have got the right question paper.

- N.B:
1. All questions carry equal marks.
 2. All questions compulsory.
 3. Draw neat and well labeled figure wherever necessary

- Q 1** Describe BLAST algorithm. Write down its features and applications. **12**
OR
Explain the promoter and regulatory elements prediction methods in prokaryotes **12**
- Q 2** Write a note on character based phylogenetic tree building methods **06**
Explain the algorithm of multiple sequence alignment. **06**
OR
Describe the working of a standard Hidden Markov Model. **06**
Explain the algorithm of multiple sequence alignment. **06**
- Q 3** Describe probe design in DNA microarray. **06**
Write a note on the methods used for clustering in Microarray analysis. **06**
OR
Explain proteome expression techniques for characterization / identifying the proteome. **12**
- Q 4** How do you represent a chemical compound using linear notations? **06**
Write a note on substructure searching algorithm **OR**
Explain the features of relational databases for molecules. **06**
Describe various genome mapping techniques. **06**
- Q 5** Short notes on any **three** **12**
- i. Data retrieval system in NCBI
 - ii. Motifs and domain
 - iii. Interpretation of Pattern and profiles in proteins
 - iv. Chou-Fasman structure prediction
 - v. Functional genomics
 - vi. Patent database