

Time allowed: 3 Hours

Max. Marks: 60

NOTE: Attempt five questions in all, including Question No. 1 which is compulsory and selecting two questions from each Unit.

x-x-x

1. Answer the following:-

- a) What are the sequence patterns and profiles?
- b) On which concept are protein families based?
- c) What is MEME?
- d) What are the advantages of GOR, Over Chou Fasman method for protein secondary structure prediction?
- e) Briefly discuss alpha fold.
- f) How is structural variation done? (6x2)

UNIT - I

2. (a) Compare and contrast protein motifs and domains giving suitable examples.
(b) Discuss PSI BLAST algorithm. (6,6)
3. (a) Differentiate between PSI-BLAST and PHI-BLAST.
(b) What are the applications of profiles and patterns? (6,6)
4. Write notes on the following:-
(a) Types of pattern representations.
(b) Two tools for searching patterns and profiles. (6,6)

UNIT - II

5. (a) How is protein structure predicted using PSI-PRED?
(b) Discuss structure prediction using threading approach. (6,6)
6. (a) How is protein tertiary structure predicted using homology modeling?
(b) What is the basis for secondary structure prediction in Chou Fasman method? (6,6)
7. (a) Differentiate between threading and fold recognition.
(b) Discuss GOR algorithm for protein structure prediction. (6,6)

x-x-x