

Roll No.

Total No. of Questions : 13]

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D-8

[2037]

**M.Sc. (BI) (Semester - 4th)
PROTEOMICS (M.Sc. (BI) - 404)**

Time : 03 Hours

Maximum Marks : 75

Instruction to Candidates:

- 1) Section-A is **compulsory**.
- 2) Attempt any **Nine** questions from Section-B.

Section - A

Q1)

(15 × 2 = 30)

- a) Global alignment
- b) PAM matrix
- c) Homology
- d) Dendrogram
- e) T-coffee
- f) Motif
- g) Tertiary structure
- h) Treading
- i) CATH
- j) Ramachandran Plot
- k) Rasmol
- l) Gap penalty
- m) Dot plot
- n) Geometric hashing
- o) PSI-BLAST

P.T.O.

Section - B

(9 × 5 = 45)

- Q2)** Discuss in short the importance of protein multiple sequence alignment.
- Q3)** Write a short note on CLUSTALW.
- Q4)** Write in brief various steps involved in Homology modelling.
- Q5)** Discuss in detail BLAST output.
- Q6)** Write a note on Deep view.
- Q7)** Write a note on Ab-initio protein structural prediction.
- Q8)** List the differences between BLAST and Fasta.
- Q9)** Write a short note on Substitution matrices.
- Q10)** Discuss in detail dynamic programming.
- Q11)** Discuss in short any three programmes related with automatic structural classification of proteins.
- Q12)** Discuss in detail flexible matching.
- Q13)** Write a short note on protein folding.

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