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Roll No.	Total No. of Pages : 02
Total No. of Questions : 09	
M.Sc.(BT) (2011 & Onwards) PROTEOMICS AND GEN Subject Code:MSBT- Paper ID:[F0261]	IÒMICS
Time:3 Hrs.	Max. Marks:60
INSTRUCTION TO CANDIDATES :	

- SECTION-A is COMPULSORY consisting of TEN questions carrying TWO marks 1. each.
- SECTION-B contains FIVE questions carrying FIVE marks each and students 2. have to attempt any FOUR questions.
- 3. SECTION-C contains THREE questions carrying TEN marks each and students have to attempt any TWO questions.

## **SECTION-A**

- 1. Write short notes on following :
  - ercom a. Pairwise and multiple sequence alignment.
  - b. PAM and BLOSUM.
  - c. Name two nucleotide and two protein databases.
  - d. De-novo sequencing.
  - e. Co-immunoprecipitaion.
  - f. Dynamic programming.
  - g. Polymorphism.
  - h. Clone conting.
  - i. Intron-Exon and their significance.
  - j. Expand terms: VNTR, AFLP, DGGE, INSDC.



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## **SECTION-B**

- 2. How scoring matrices are used in sequence analysis?
- 3. Describe the role of biological databases in research.
- 4. What is genome sequencing? Describe the Shot gun method.
- 5. How phylogeny of an organism can be represented using phylogenic tree? Explain with the help of an example.
- 6. How Mass Spectrometry data can be used for protein identification?

## **SECTION-C**

- 7. Define Bioinformatics. Discuss its objectives, scope and applications.
- 8. What do you mean by sequence analysis? Describe various sequence analysis methods.

## 9. Write notes on following :

- a. Role of SDS-PAGE and Native-PAGE for determination of protein size.
- b. Molecular markers and their significance in research.