

(Following Paper ID and Roll No. to be filled in your Answer Books)

PAPER ID :

Roll No.

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B.TECH.

Theory Examination (Semester-IV) 2015-16

BIOINFORMATICS-I

Time : 3 Hours

Max. Marks : 100

SECTION-A

I. Attempt all parts. Write answer of each part in short.

(10x2=20)

- What do you understand by primary databases?
- Write down about ESI.
- Give the name of two secondary databases.
- What do you mean by SNP's
- Write down motifs.
- What is BLAST?
- Write down about data retrieval tool.
- What do you understand by profile?
- Give the name of gene prediction tool.
- What method is used for the analysis of protein sequencing?

SECTION-B

2. Attempt any five questions from this section.

(5x 10=50)

- What do you understand by secondary databases? Explain prosite in details.
- Write down the principal and procedure of dideoxy chain termination method.
- Explain the method of Edman degradation for protein sequencing.
- What is the sequence alignment method? Write down the global and local alignments.
- What do you understand by protein structure prediction with the help of Chou fasman method?
- What is the microarray technique and what do you understand by micro array data analysis.
- Explain the data similarity search with the help of PSI BLAST.
- What do you understand by homology modeling?

SECTION-C

Attempt any two questions from this section.

(2x 15=30)

- What do you mean by drug designing and its role in bioinformatics?
- Write down the Needleman and Wunsch Algorithm for sequence alignment.
- Write the short notes on
 - TFB sites
 - ENTREZ
 - ORF prediction