Printed Pages : 1 **EBT-404**

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

PAPER ID :	**Roll No.**										

B.TECH.

Theory Examination (Semester-IV) 2015-16

BIOINFORMATICS-I

Time : 3 Hours ***Max. Marks : 100***

SECTION-A

1. Attempt all parts. Write answer of each part in short. **(10x2=20)**

a) What do you understand by primary databases?
b) Write down about ESI.
c) Give the name of two secondary databases.
d) What do you mean by SNP's
e) Write down motifs.
f) What is BLAST?
g) Write down about data retrieval tool.
h) What do you understand by profile?
i) Give the name of gene prediction tool.
j) What method is used for the analysis of protein sequencing?

SECTION-B

2. Attempt any five questions from this section. **(5x 10=50)**

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

SECTION-C

Attempt any two questions from this section. **(2x 15=30)**

3. What do you mean by drug designing and its role in bioinformatics?
4. Write down the Needle-man and Wunsch Algorithm for sequence alignment.
5. Write the short notes on
    a) TFB sites
    b) ENTREZ
    c) ORF prediction