MTBT-301

Roll No.

M. Tech. (BIOTECHNOLOGY)

THIRD SEMESTER EXAMINATION, 2011-12

BIOINFORMATICS, GENOMICS & PROTEOMICS

Time : **3 Hours**

Total Marks : **100**

Note : (i) Attempt any **FIVE** questions.
   (ii) Marks are indicated against each question.

1. (a) What do you understand by transcriptome and transcriptomics? Explain the process of separation and identification of proteome in proteame analysis.   **10**

   (b) Briefly discuss the basic principle of DNA micro array and explain its applications.   **10**

2. Write explanatory notes on database similarity searching tool and also discuss various methods of Multiple Sequence Alignment (MSA).   **20**

3. Write short notes on the following :   **5 x 4 = 20**

   (a) Application of Human Genome Project (HGP)
   (b) Secondary protein database
   (c) Nucleotide Database
   (d) EST

4. What is homology Modelling? Explain the basic steps involved in homology modelling.   **20**

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5. Briefly discuss the following :   4 x 5 = 20

   (a) KEGG

   (b) OMIM

   (c) Chromosome walking

   (d) Subtractive hybridization

   (e) Phylogenetic analysis

6. Define Drug and Target. Discuss in detail the various phases of drug designing with special reference to Bioinformatics application.   20

7. Write short notes on any **Four** :   5 x 4 = 20

   (a) Swiss prot

   (b) SNPs

   (c) Motifs

   (d) Gene expression profiling

   (e) Biological databases

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