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Total number of printed pages – 2

B. Tech
PCBT 4304

Sixth Semester Back Examination – 2015

BIOINFORMATICS

BRANCH : BIOTECH

QUESTION CODE : M 127

Full Marks – 70

Time : 3 Hours

*Answer Question No. 1 which is compulsory and any five from the rest.
The figures in the right-hand margin indicate marks.*



1. Answer the following questions :

2 × 10

- (a) What is Log-odd values ?
- (b) Explain Entrez.
- (c) What is dendogram ?
- (d) What is secondary databases ?
- (e) Write the matrix of Smith-Waterman programme.
- (f) What is Pharmacophore ?
- (g) Explain protein threading.
- (h) Explain any OMIM.
- (i) What is affine gap penalty ?
- (j) Name any two docking software.

P.T.O.

2. (a) Explain different protein domain classification databases. 5
(b) Explain PDB file. 5
3. Explain the process of homology modeling of protein and its application. 10
4. Explain sequence databases with tools attached to it. 10
5. (a) What is multiple sequence alignment ? Explain different applications of multiple sequence alignment. 5
(b) Explain in silico gene prediction methods. 5
6. (a) Explain substitution matrix with suitable examples. 5
(b) Explain Uniprot. 5
7. (a) Differentiate between Ab initio and Comparative methods of gene prediction. local and global sequence alignment. 5
(b) Differentiate between FASTA and BLAST algorithm. 5
8. Write short notes any **two** of the following : 5x2
- (a) QSAR
- (b) MD Simulation
- (c) Dynamic programming
- (d) Lipenski's rule of five.
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