

Registration No. :

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Total number of printed pages – 2

B. Tech
PCBT 4304

Sixth Semester Examination – 2013

BIOINFORMATICS

BRANCH : BIOTECH

QUESTION CODE : A 149

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 BLOSUM ?
 - (b) What is CSD ?
 - (c) What is the significance of R value in a PDB file ?
 - (d) Differentiate between Swissprot and trEMBL.
 - (e) What is gi number ?
 - (f) What do you mean by Ensemble ?
 - (g) Explain protein threading.
 - (h) Explain any virus database.
 - (i) Name any two protein tertiary structure predicting softwares.
 - (j) What is phylogenetic tree ?

P.T.O.

2. What is dynamic programming ? Explain Needleman - Wunch algorithm. How Smith - Waterman algorithm varies from Needleman - Wunch algorithm ? 2+4+4
3. (a) Explain different Proten domain classification databases. 6
(b) Diffrentiate between PAM and BLOSUM. 4
4. Explain different steps of FASTA algorithm ? How is it different from BLAST ?
7+3
5. (a) Explain different approaches in drug design process. Explain the rules and parameters to describe basic nature of a drug candidate. 2+3.
(b) Explain sequence profile. What is PSSM ? 3+2
6. (a) What is force field ? Explain MD simulation with suitable flowchart explaining the process. 7
(b) Explain Ab - initio method for gene prediction. 3
7. Write notes on : 5×2
(a) QSAR
(b) Homology modelling.
8. Write short notes on : 2.5×4
(a) Pharmacophore
(b) Entrez
(c) Docking
(d) Metacyc.