

Registration No. :

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Total number of printed pages – 2

B. Tech
PCBT 4304 (New)

Sixth Semester (Back) Examination – 2013

BIOINFORMATICS

BRANCH : BIOTECH

QUESTION CODE : B225

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 BLAST?
 - (b) What is affine gap penalty?
 - (c) What is Pharmacophore?
 - (d) What is PIR?
 - (e) Differentiate between Swissprot and TrEMBL
 - (f) What is force field?
 - (g) What do you mean by Ensemble?
 - (h) Explain ORF.
 - (i) Explain any virus database.
 - (j) Name any two docking software.
 - (k) What is dendogram ?
2. Describe different primary sequence databases. Name the search tools of each of them. 7+3



P.T.O.

3. (a) Explain are different protein domain classification databases. 6
(b) What are molecular descriptors ? 4
4. (a) Explain different steps of FASTA algorithm. 6
(b) Explain different metabolic pathway databases. 4
5. (a) Describe homology modeling of protein. 6
(b) Explain sequence profile. What is PSSM. 4
6. Differentiate between : 5×2
(a) PAM and BLOSUM
(b) Needleman-Wunch algorithm and Smith-Waterman algorithm.
7. (a) What is MSA ? Explain different applications of MSA. 5
(b) What is PDB ? Explain the PDB file. 5
8. Write short notes on the following : 2.5×4
(a) Dynamic pogramming
(b) QSAR
(c) Docking
(d) HMM.

