Registration No. :

Total number of printed pages – 2

B. Tech

PCBT 4304

Sixth Semester Regular Examination – 2014

BIOINFORMATICS

BRANCH(S) : BIOTECH

QUESTION CODE : F 212

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 Entrez ?

(b)   What is docking ?

(c)   What is PIR ?

(d)   Differentiate between local and global alignment.

(e)   What is force field ?

(f)   What do you mean by threading ?

(g)   What is force field ?

(h)   What is affine gap penalty ?

(i)   Explain any virus database.

(j)   Explain prosite.

2.   Explain the need of substitution matrices. Describe the amino acid substitution matrices most used.   3+7

3.   (a)   Explain the MD simulation algorithm.   6

(b)   What are molecular descriptors ?   4

P.T.O.

4. (a) Explain CATH database. 6

(b) What is PDB ? Explain the PDB file. 4

5. (a) Expalin different gene predicyion methods. 6

(b) Explain sequence profile. What is PSSM ? 4

6. Differentiate between : 5×2

(a) Swissprot and trEMBL

(b) Needleman-Wunch algorithm and Smith-Waterman algorithm.

7. (a) What is MSA ? Explain application of HMM. 5

(b) Explain Uniprot. 5

8. Write short notes : 2.5×4

(a) Pfam

(b) Pharmacophore

(c) metabolic pathway databases

(d) SCOP.

———————