

Registration No. :

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Total number of printed pages – 2

B. Tech
PCBT 4304

Sixth Semester Regular Examination – 2015

BIOINFORMATICS

BRANCH : BIOTECH

QUESTION CODE : J 131

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 gi number ?
- (b) Explain dotplot.
- (c) What is dendogram ?
- (d) What is the significance of R value in a PDB file ?
- (e) Explain protein threading.
- (f) What is CSD ?
- (g) Explain Lipenski's rule of five.
- (h) Explain any virus database.
- (i) What is the significance of gap extension penalty ?
- (j) Name any two protein tertiary structure predicting software.

2. (a) Explain different tools attached with primary sequence databases.

5

(b) Describe substitution matrix.

5

P.T.O.

3. Explain FASTA algorithm. How is it different from BLAST ? 10
4. What is dynamic programming ? How Smith-Waterman algorithm varies from Needleman-Wunch algorithm ? 10
5. (a) Explain in silico gene prediction methods. 5
(b) Explain QSAR. 5
6. (a) Explain MD simulation with suitable flow chart explaining the process. 5
(b) Explain force field. 5
7. (a) Differentiate between local and global sequence alignment. 5
(b) Differentiate between Swissprot and trEMBL. 5
8. Write short notes on : 2.5 × 4
(a) Pharmacophore
(b) PSI-BLAST
(c) Log-odd values
(d) CATH.

