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Total Number of Pages: 01

B.TECH
PCBT4304

6th Semester Regular / Back Examination 2015-16

BIOINFORMATICS

BRANCH: BIOTECH

Time: 3 Hours

Max Marks: 70

Q.CODE: W470

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

Q1 Answer the following questions: **(2 x 10)**

- a) What is local alignment?
- b) Explain Pharmacophore?
- c) What are Log-odd values?
- d) What is the significance of R value in a PDB file?
- e) What is dynamic programming?
- f) Explain any metaboloc database.
- g) Explain Lipenski's rule of five.
- h) What is OMIM?
- i) What is the significance of gap extension penalty?
- j) Name any two protein tertiary structure predicting software.

Q2 a) Describe PIR. **(5)**
b) Describe substitution matrix. **(5)**

Q3 Explain different primary sequence databases along with the tools. **(10)**

Q4 Explain the methods of insilico gene prediction **(10)**

Q5 a) Explain CSD. **(5)**
b) Explain PDB file. **(5)**

Q6 a) Explain MD simulation with suitable flow chart explaining the process. **(5)**
b) Explain docking with its application. **(5)**

Q7 a) Differentiate between CATH and SCOP. **(5)**
b) Differentiate between 2D and 3D QSAR. **(5)**

Q8 Write Short Notes (Any two) **(5 x 2)**

- a) Phylogenetic tree.
- b) PSI-BLAST.
- c) protein threading
- d) force field