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Total Number of Pages : 01

B.Tech  
PBT6I102

6<sup>th</sup> Semester Regular / Back Examination 2018-19

BIOINFORMATICS

BRANCH : BIOTECH

Max Marks : 100

Time : 3 Hours

Q.CODE : F198

Answer Question No.1 (Part-1) which is compulsory, any EIGHT from Part-II and any TWO from Part-III.

The figures in the right hand margin indicate marks.

Part- I

Q1 Only Short Answer Type Questions (Answer All-10) (2 x 10)

- What is NCBI?
- What is Pfam?
- Why Protein data bank is used?
- Differentiate EMBL and TrEMBL?
- Write the full form of KEGG pathway?
- What is an ORF?
- Differentiate between local and global alignment?
- What are splice sites?
- What is threading?
- What is the use of Ramchandran Plot in Homology modeling?

Part- II

Q2 Only Focused-Short Answer Type Questions- (Answer Any Eight out of Twelve) (6 x 8)

- How data is retrieved from metacyc?
- What are the steps adapted in multiple sequence alignment?
- What you understand by molecular mechanics?
- Write the sequences of dynamic programming?
- In molecular modeling Force field is a special case of energy functions or inter atomic potentials. Justify the version?
- What is Gap penalty?
- How substitution matrix is constructed by 'Log Odds Matrices'?
- What is rational drug designing?
- Differentiate between Rigid ligand-Rigid receptor and flexible ligand –Rigid receptor dockings?
- What is Monte Carlo sampling?
- How Dot matrix method is used in sequence alignment?
- What is signature molecular descriptor?

Part-III

Q3 Only Long Answer Type Questions (Answer Any Two out of Four) (16)

Hidden Markov Model (HMM) is a statistical Markov model in which the system being modeled is assumed to be a Markov process with unobservable (i.e. hidden) states. Prove it?

Q4 How a linear-time algorithm is used for finding a maximum-length ORF in a splice graph? (16)

Q5 Explain in detail about Lipinski's Rule of five? (16)

Q6 What is the mechanism of molecular dynamic simulation? (16)