

**JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT**

**TEST-2 EXAMINATIONS-2022**

**B.Tech-III Semester (BI)**

**COURSE CODE (CREDITS): 18B11BI313 (4)**

**MAX. MARKS: 25**

**COURSE NAME: Biological computation**

**COURSE INSTRUCTORS: Dr. Shikha Mittal**

**MAX. TIME: 1 Hour and 30**

**Minutes**

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*Note: All questions are compulsory. Marks are indicated against each question in square brackets.*

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**Q1.** An unknown protein sequence was searched against the protein database and similarity identity was above 35%. In which zone this protein was identified? And how can we predict the 3D structure of this protein? [CO-4 & CO-5] (4 marks)

**Q2.** In a phylogenetic tree, the number of topologies varies with the number of taxa. If I have 5 taxa, then what will be the number of rooted and unrooted topologies? [CO-4] (2 marks)

**Q3.** For the construction of Ramachandran's plot values of Phi and Psi are plotted. What are the angles and bonds involved in construction of Ramachandranplot? [CO-5] (3 marks)

**Q4.** If you want to align 18 protein or nucleotide sequences, which method will be preferred? And what will be the interpretation of this alignment? [CO-2 & CO-3] (3 marks)

**Q5.** Calculate BLOSUM substitution matrix for the given sequences – [CO-1 & CO-2] (5 marks)

Sequence	Position			
Seq1	B	A	B	A
Seq2	A	A	A	C
Seq3	A	A	C	C
Seq4	A	A	B	A
Seq5	A	A	C	C
Seq6	A	A	B	C

**Q6. Explain the following – [CO-1, CO-3 & CO-4] (8 marks)**

- a) Difference between directional and undirectional trees
- b) Ab initio modeling
- c) Fold recognition
- d) Orthology with example

12 Examinations October 2022