JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT TEST -1 EXAMINATION- 2023

B.Tech-V Semester (BIBT)

COURSE CODE(CREDITS): 18B1WBI531 (3)

MAX, MARKS: 15

COURSE NAME: Structural Bioinformatics

COURSE INSTRUCTORS: Dr. Raj Kumar

MAX. TIME: 1 Hour

Note: (a) All questions are compulsory.

(b) Marks are indicated against each question in square brackets.

(c) The candidate is allowed to make Suitable numeric assumptions wherever required for solving problems

- Q1. Give a brief description of the availability and dissemination of macromolecular structural data within the global scientific community, emphasizing its open and unrestricted accessibility.

 (CO-1) [2]
- Q2. The primary information of macromolecular structural data is stored in the PDB archive. Describe the file format to store macromolecular structural data in the PDB database. (CO-1) [2]
- Q3. Structural databases aim to provide a detailed and comprehensive description of the structural and evolutionary relationships between all proteins whose structure is known. Discuss two such databases and important differences in classifications by them. (CO-2) [2]
- Q4. In a dataset comprising 200 alpha helix conformations, if the program accurately predicts 160 helices, what would be the resulting Q3 score? (CO-2) [2]
- Q5. Homology modeling is an error prone method for tertiary structure prediction. Discuss potential sources and reasons for these errors. (CO-2) [2]
- Q6. There are several model building steps in homology modelling. Discuss backbone generation and loop modeling steps. (CO-3) [2]
- Q7. Calculate the statistical propensities of Alanine in helix conformation of the given sequence.
 (CO-2) [3]

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