

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- 2025

B. Tech-VIII Semester [All except Bio]

COURSE CODE (CREDITS): 21B1WBT833 (3)

MAX. MARKS: 25

COURSE NAME: Computational Biology for Engineers

MAX. TIME: 1 Hour 30 Min

COURSE INSTRUCTORS: Dr. Raj Kumar, Dr. Udayabanu M

Note: (a) All questions are compulsory.

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

Q.No	Question	CO	Marks
Q1	Drug Target is a biomolecule whose interaction with a drug alters a disease process. Explain the goal and approaches involved in the drug target identification.	3,4,5	5
Q2	What are chemical databases, and how do they serve as repositories for chemical compounds and their associated biological and physicochemical data? List some databases you know.	3,4,5	5
Q3	Describe the nucleotide sequences databases. Compare and contrast FASTA and GenBank formats.	1,2,3	5
Q4	Explain the role of structural databases. Describe the PDB file format.	1,2,3	5
Q5	Describe the basis of an intuitive scoring scheme you would devise for aligning two sequences in a simple manner. Use your proposed scheme to determine the correct alignment below. <div style="display: flex; justify-content: space-around; align-items: flex-start;"> <div style="text-align: center;"> <p>Sequence 1 CAATGA</p> <p>CAATGA ATTGAT</p> <p>Alignment 1</p> </div> <div style="text-align: center;"> <p>Sequence 2 ATTGAT</p> <p>CAATGA_ _ATTGAT</p> <p>Alignment 2</p> </div> <div style="text-align: center;"> <p>Sequence 2 ATTGAT</p> <p>CAATGA_ AT_TGAT</p> <p>Alignment 3</p> </div> </div>	3,4	5