JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -1 EXAMINATION- 2026

PhD-I & II Semester (BTBI)

COURSE CODE (CREDITS): 25P1WBT101 (3) MAX. MARKS: 15

COURSE NAME: Advances in Bioinformatics

COURSE INSTRUCTORS: Dr. Raj Kumar MAX. TIME: 1 Hour

Note: *(a) All questions are compulsory.*

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

(c) Use of calculator is not allowed

Q.No	Question	Marks
Q1	A research group is studying the molecular mechanisms of antibiotic resistance in bacteria. Develop a PubMed literature search strategy to retrieve relevant research articles published in the last 10 years.	2
Q2	Justify the role of the PubChem database. What are the various categories of chemical compound information stored in the PubChem database?	2
Q3	Two proteins share only 20% sequence identity but contain several conserved residues and similar functional domains. How would you determine whether they are homologous?	2
Q4	Explain what does gaps represent in a sequence alignment? What are types of gap penalty used in sequence alignment methods?	2
Q5	Explain the role of window in dot-plots.	2
Q6	Align the following sequences using Needleman-Wunsch global sequence alignment approach: Scoring scheme: Match = 1, Mismatch = -1, Gap = -2 Seq1 = GCTGT, Seq2 = GCGT	5

12.9