JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -1 EXAMINATION- 2026

M.Sc.-II Semester (MM/MB)

COURSE CODE (CREDITS): 20MS1BT213(2) **MAX. MARKS: 15**

COURSE NAME: Bioinformatics

COURSE INSTRUCTOR: Dr. Shikha Mittal **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 calculators is not allowed

Q.No	**Question**	**Marks**
Q1	Two protein sequences are aligned as shown below: **Seq1: MKTLVAG** **Seq2: MKALVGG** **a.** Calculate the sequence identity (%) and sequence similarity (%). **b.** State whether the sequences are closely related based on identity.	(2)
Q2	Using dynamic programming algorithm, find the optimal alignment for the given pair of sequences using the scoring scheme as follows – match (+1), mismatch (-1) and gap penalty (-1). **Seq1: ATGCT** **Seq2: ATCT**	(4)
Q3	**a.** FASTA format **b.** FASTA and FASTQ format **c.** Quality check	(6)
Q4	Explain Biological databases. Briefly explain protein, nucleotide and structural databases.	(3)

131