JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATIONS- 2026

M.Sc.-II Semester (Biotechnology)

COURSE CODE (CREDITS): 20MS1WBT233 (02) MAX MARKS: 35

COURSE NAME: Protein Engineering

COURSE INSTRUCTOR: Dr. Saurabh Bansal MAX. TIME: 2 Hours

Note: (a) All questions are compulsory.

(b) Use of calculator is allowed.

Q. No.	Question	Marks
Q1	Explain the principle of directed evolution. Why is it often considered superior to rational design in generating novel protein functions?	2
Q2 a)	What do you understand by screening and selection? Explain each with suitable example.	3
Q2 b)	Explain the importance of HTS in directed evolution.	2
Q3 a)	Explain the principle of phage display. How does it establish a link between genotype and phenotype?	3
Q3 b)	Compare yeast surface display with bacterial display systems. What advantages does yeast offer in terms of protein folding and post-translational modifications?	4
Q3 c)	How is the ternary complex (mRNA–ribosome–polypeptide) stabilized in ribosome display method?	2
Q4 a)	Why are amino acid sequence comparisons generally preferred over nucleotide sequence comparisons?	2
Q4 b)	Name two algorithms used for pairwise sequence alignment.	1
Q4 c)	What is CASP and why is it important?	2
Q5	A recombinant protein expressed in *E. coli* forms insoluble inclusion bodies. Propose an experimental workflow to obtain soluble and active protein.	2
Q6	Why is structure-based protein engineering considered superior to sequence-only approaches? Discuss the limitations of experimental	4

	structure determination methods.	
Q7	A protein sequence shares 45% identity with a known protein structure. Which structure prediction method would you choose and why?	2
Q8	Discuss the principles of rational design, directed evolution, and semi-rational design. Highlight their advantages, limitations, and typical applications.	6