JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATION- 2025

M.Sc.- II Semester (Biotechnology)

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

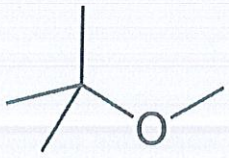
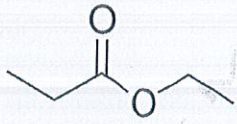
COURSE NAME: Protein Engineering

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

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

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

Q. No.	Question	Marks
Q1	How does the screening differ from the selection? What is the significance of high-throughput screening?	3
Q2	Name at least two computational tools used for the following? a) Protein sequence alignment b) Structure prediction c) Quality check of the predicted structures	3
Q3 a)	What do you understand by the Cell Surface Display method?	1
Q3 b)	What are the advantages of bacterial cell display over the phage display method?	2
Q3 c)	How the ribosome display method is different from the cell display method? Diagramatically illustrate the whole process of mutant selection from a library using the ribosome display method.	4
Q4 a)	What are the differences between sequence-based and structure-based protein analysis?	2
Q4 b)	How does structural analysis aid in designing enzymes with improved catalytic activity?	2
Q5 a)	What is Gigamatrix screening? What are the major steps involved in the Gigamatrix screening method?	3

Q5 b)	What are the key advantages of Gigamatrix technology over traditional screening methods in protein engineering?	**2**
Q6 a)	Which organism is known for expressing bacteriorhodopsin? What is the primary function of bacteriorhodopsin in microbial cells?	**2**
Q6 b)	What are the potential biotechnological applications of engineered bacteriorhodopsin?	**2**
Q7	Assess and explain the following structure for the number of signals in ^1H NMR. a)  b) 	**2**
Q8	Explain the significance of peptidomimetics in the context of research and development. Design any three peptidomimetics for bioactive hexapeptide KFLYKA.	**3**
Q9	A team of environmental scientists is working on developing a more efficient enzyme for plastic biodegradation. They focus on improving the activity of PETase, an enzyme known for breaking down polyethylene terephthalate (PET), commonly found in plastic bottles. However, the natural PETase has low efficiency and is unstable at industrial-scale temperatures. Given the limitations of natural PETase, analyze the advantages and drawbacks of using error-prone PCR vs. site-directed mutagenesis in evolving a more efficient enzyme. Additionally, discuss how computational methods like molecular dynamics simulations can complement laboratory experiments in directed evolution.	**4**