JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
TEST -3 EXAMINATION- 2025
B.Tech-V Semester (BT)

COURSE CODE (CREDITS): 1811BT512 (4) **MAX. MARKS: 35**
COURSE NAME: Genetic Engineering
COURSE INSTRUCTORS:Dr Anil Kant **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 (c) Use of Calculator is allowed.*

Q.No	Question	CO	Marks
Q1	a.Explain following terms: i) primary library ii) amplified library iii) minimum (golden) tillage path iv) genome coverage v) inclusion bodies b.Demonstrate your understanding about the concept of genomic DNA library and cDNA library.	Co-I	2.5x2=5
Q2	**Do any three of following** a.Explain how the choice of promoters affect the level of recombinant protein expression? Write briefly about given inducible promoters (2-3line only), i) lac, ii) trp, iii) tac, iii) λPL, T7 focusing on their induction / repression compounds. b.Draw and describe the workflow for purification of a recombinant protein tagged with maltose binding protein tag? c.Give at least two examples along with the mechanism of action, of i) purification tags ii) dual purpose tags iii) development of purification and solubilization tags (Lu et al.1996, Smith et al 1998). d.Discuss how the nature of protein affects the level of recombinant protein expression. Include stability of protein, protein folding, location of protein and suggested solutions to overcome the problems associated with these aspects.	Co-4	3x3=9
Q3	a. Discuss the factors and on which minimum number of clones to be maintained in the library depends. Calculate the minimum number of clones required in a gene library of *rice*? Given genome size $5.7x10^2$ MB, fragment size 40 KB, desired probability of finding the fragment 0.99 b. Explain the methods used for DNA fragmentation in construction of genomic DNA libraries? What are limitations of enzymatic methods and how are these limitations obviated? c. Let you be interested in identifying and isolating a gene from a cDNA expression library. Briefly outline the logic and procedure you will use to screen the library, following two situations i) An antibody	Co-3,4	4x3=12 **P.T.O**

	is available which binds with protein encoded by gene ii) Some sequence information of the gene is available.		
Q4	a. State the principle of Sanger's dideoxynucleotide method. Mention modifications which lead to i) Computer based base calling ii) application of higher voltage for electrophoresis. b. Explain the three common steps of next generation sequencing platforms. Discuss library preparation and clonal amplification in case of 454 sequencing with diagrams. c. How whole genomes can be sequenced, as DNA sequencing read length is too small? Describe hierarchical approach of whole genome sequencing in detail?	Co-3	3x3=9