JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT **TEST -3 EXAMINATION- 2024**

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. Use of calculators is allowed.

Marks **Ouestion** Q.No a. Let your task is to express a recombinant protein in E. coli. During the cour 6 Q1 of experimentation it is observed that recombinant protein is forming insoluble inclusion bodies. On the basis of your understanding, discuss three possible methods that can be adopted to obviate this problem. b. Recognise that the nature of recombinant proteins is significant for a high level of expression? Include following points in your discussion with suitable examples i) Stability of protein and how stability can be increased ii) location of protein and how protein location can be modulated (signal peptides) iii) Protein folding and course of action if protein folding is important for a functional recombinant protein. Enlist at least three purification tags and assay tags for recombinant proteins Ш 0.2 along with their affinity molecules/ligands. Diagrammatically show how a recombinant protein having polyhistidine tag or maltose binding tag can be Why was the Maxam Gilbert method of DNA sequencing called a DNA 6 Q.3 degradation method of sequencing. Decipher the sequence DNA fragment on the basis of the outcome of the band profile depicted in the image given obtained in Maxam Gilbert method of DNA sequencing. Mentioned three points why the method is not used now. b. Briefly explain the Principle and enzyme reaction cascade of pyrosequencing chemistry of DNA sequencing? Explain the factors which dictate the minimum number of clones to be maintained in a gene library. Q.4 b) Calculate the minimum number of clones required in a gene library of D. melanogaster, having genome size 1.2 x 10⁵ kb. The fragment size in the library should be 20 kb, it should have a probability of 0.99 for finding a random fragment in it. c) Appraise the concept, advantages and applications of cDNA library?

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0.4	Give an account of methods used to screen gene libraries. Prepare an outline of	IV	6
Q.4	Give an account of methods used to solve a gene to identify a gene clone from the		
	the procedure in case any two of following cases to identify a gene clone from the		
1	library when given information is available about it. i) Partial sequence	1	
	information is available ii) Protein encoded by it and antibody against it available		
ļ	initialization is available by 1 forcing the control of the function are	1	
Ì	iii) Function conferred by gene is known and mutant for that function are		
ļ	available but no other information is available		
	Briefly answer the following questions.	I&V	4
Q.5	Briefly answer the following questions.		
}	a. Genetic engineering is not only a product oriented technology but also a tool	M.	
	in research and diagnosis. Justify		
ļ	b. Name and explain the modification in sangers sequencing procedure which		
	D. Ivalite and explain the measurement of the state of th		ì
	lead to sequencing PCR reaction in single tube		
	c. Let a DNA molecule be constructed with the following features. Would these	ſ	
	be called recombinant DNA or not? Give a key reason for your choice in case		
		ł	Ì
	of every option.		
	a. Consist of two DNA fragments from different sources, totable to	1	
	replicate in any host.		
	b. One DNA fragment from natural host and one synthetic DNA		
	fragment, able to replicate in a appropriate host		
	fragment, able to replicate in a appropriate host		
	d. Aparsie about two tools or techniques which you him were most important		
	for the advent of genetic engineering. Mention reasons for your answer	<u> </u>	J
	Mark Mark		
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