JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
TEST -3 EXAMINATION- Dec.2023
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)Marks are indicated against each question in square brackets.
(c) The candidate is allowed to make Suitable numeric assumptions wherever required for solving problems

Q.1 Do two of following questions **[4x2 = 8] Co -III, V**

a. Discuss functional modules and working of pET 11 expression vectors? Explain how gene expression is controlled in an uninduced and induced state. Draw a suitable diagram.
b. Expression vectors are available for providing purification or assay tags with recombinant protein. Explain the design of such expression vectors and the working principle of at least one such tag. Draw a Suitable labeled diagram to support your answer..
c. You are trying to express a gene from a eukaryotic organism as a recombinant protein in E.coli, but the label of expression of the gene is quite low. Assign at least three possible solutions to raise the accumulation of recombinant protein.

Q.2 **Co- IV,V**

a. What are gene libraries? Explain the concept of genomic and cDNA library? [3]
b. Calculate the minimum number of clones to be included in the genomic library of insert size of 20 kb and with 0.99 probability of finding any random clone ? Genome size of the target organism is 12Mbp. [4]

Q.3 **Co- IV, V**

a. Enlist the steps involved in construction of cDNA library? Discuss methods used to synthesize the second strand of cDNA in detail. [4]
b. Why are genomic libraries not so useful when we are interested in isolating a gene from a eukaryotic organism, but are very useful in case of a prokaryotic organism. Mention at least three abstract points in each argument. [4]

Q.4 **Co- IV**

a. Explain the principle and procedure of Sanger's original method of DNA sequencing? Give a contrasting comparison of output of the original and fully automated system. [4]
b. Describe three common steps of Next generation sequencing methods. Give a list of NGS platforms. How is the library prepared in case of the 454 NGS platform? [4]

Q.5 **Co- IV**

Enlist different types of gene transfer methods? Describe at least two of these focussing on principle, methodology and advantages and limitations? [4]

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