JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST-3 EXAMINATION-2024

M. Tech.-I Semester (BT)

COURSE CODE (CREDITS): 13M11BT114 (3) MAX. MARKS: 35

COURSE NAME: HIGH THROUGHPUT TECHNOLOGIES

COURSE INSTRUCTORS: DR. JATA SHANKAR MAX. TIME: 2 Hour

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

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

Q. No.	**Questions**	**Marks**
Q1	a. Explain the principle behind the yeast two-hybrid system. How does it allow for the detection of protein-protein interactions? b. What are the main advantages and limitations of using the yeast two-hybrid system for studying protein-protein interactions?	2.5 2.5
Q2	Explain with examples behind identifying glycosylated and phosphorylated proteins in a given protein sample. Create a strategy to identify the glycosylated and phosphorylated protein in a given protein sample.	4
Q3	Explain DNA microarray technology to study the expression profile of drug-treated *E. coli* vs *E. coli* cells	4
Q4	What are different strategies to immobilize the protein to construct a protein array to study the large-scale protein-protein interaction studies	3
Q5	What is a protein array/chip, and how has it contributed to the widespread adoption of the technology in functional proteomics research? Provide a relevant example of protein-protein interactions.	4
Q6	Design the experiment to identify the 90-100 k Dalton protein to get a lead biomarker in the cancer tissue. Explain the "MALDI TOF" method used for protein identification. What are some of the protein databases commonly used for this purpose?	5
Q7	Notes on a. Chip Seq technology b. Normalization method in DNA microarray c. Sequence-based metagenomics d. Illumina sequencing	 2.5 2.5 2.5 2.5