JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST-3 EXAMINATIONS-MAY 2025

M.Sc-II Semester (BT)

COURSE CODE (CREDITS): 20MS1BT214 (2) MAX. MARKS: 35

COURSE NAME: GENOMICS & PROTEOMICS

COURSE INSTRUCTOR: DR. JATA SHANKAR 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	Demonstrate the principle and methodology of protein-protein interaction analysis on a chip-based platform? Explain how this technique is used to detect and quantify interactions between specific proteins, including its advantages, limitations, and applications in biomedical research.	5
Q2	Provide a comprehensive explanation of how protein-protein interactions can be studied using the yeast two-hybrid (Y2H) system. Describe the molecular principles underlying this technique, including the roles of the DNA-binding domain and activation domain of a transcription factor in the reconstitution of transcriptional activity. Discuss how bait and prey constructs are designed and introduced into yeast cells, and how the interaction between proteins is detected and measured.	5
Q3	Describe the DNA microarray or DNA chip and its major characteristics. Provide the workflow of DNA Microarray to differentiate lung cancer and non-cancer transcriptome	5
Q4	Describe in detail how differentially expressed proteins in lung cancer cells can be identified in comparison to normal lung cells using a proteomics-based approach. Outline the key steps involved in sample preparation, protein extraction, digestion (e.g., trypsinisation), and peptide separation. Explain the role of mass spectrometry in protein identification and quantification, with specific emphasis on time-of-flight (TOF) mass spectrometry.	5
Q5	Give insight into the human genome project with an emphasis on the estimated number of genes, genome size and gene density and compare with a prokaryotic organism such as *E. coli*	5
Q6	Draw the difference between Sanger's sequencing and the mechanism used by next-generation sequencing, such as pyrosequencing, and their major applications where Sanger sequencing finds limitations	5
Q7	Explain the efficacy of drugs such as Gefitinib depends on the genotype of the *EGFR* gene of individuals/Cancer patients. Describe the criteria that a medical practitioner prescribes the drug who are likely to benefit	5