JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATIONS-MAY 2026

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	Why are dideoxynucleotides (ddNTPs) called chain terminators in Sanger sequencing? Explain with a suitable diagram	4
Q2	Explain how genetic variations in patients influence the therapeutic efficacy of targeted anticancer drugs such as gefitinib, with reference to EGFR mutations, mechanisms of drug resistance, and the role of pharmacogenomics in personalised medicine. Explain the pharmacogenomics terms responder and non-responder.	4.5
Q3	Describe the DNA microarray (DNA chip) and its major characteristics. Explain the workflow of DNA microarray analysis used to differentiate the transcriptome profiles of lung cancer and normal (non-cancerous) tissues	4.5
Q4	Explain the principle of protein–protein interaction analysis using a protein array with suitable examples. Describe the methodology and major applications of protein arrays in studying protein interactions.	4.5
Q5	Describe the steps involved in a DNA microarray experiment and discuss how gene expression data are analysed (normalisation steps) and interpreted if genome-wide analysis is of cancer vs non-cancerous tissue.	4.5
Q6	Discuss the relationship between Phred scores 20 and 30 and sequencing error rates?	5
Q7	Short question a. MALDI-ToF b. Gene density of the yeast genome c. Tumour suppressor gene 'TP53' d. System biology	8