

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
TEST -3 EXAMINATIONS MAY-2026

M.Tech-II Semester (BT)

COURSE CODE (CREDITS): 14M11BT213 (3)

MAX. MARKS: 35

COURSE NAME: FUNCTIONAL GENOMICS

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	Explain the principle, methodology, and applications of Sanger sequencing. How does chain termination enable DNA sequence determination?	4
Q2	Describe the principle and procedural steps involved in pyrosequencing. How is nucleotide incorporation detected in this technique?	4.5
Q3	What are Single Nucleotide Polymorphisms (SNPs) and point mutations? If the frequency of SNPs in the human genome in an Indian population is approximately 1 per 2000 base pairs, estimate the total number of SNPs present in the human genome	4.5
Q4.	Explain how genetic variations among patients influence the therapeutic efficacy and safety of the anticancer drug Gefitinib. Discuss the major pharmacodynamic factors involved in its mechanism of action, therapeutic response, and risk of adverse effects.	4.5
Q5	What is the underlying principle of Serial Analysis of Gene Expression (SAGE), and what are the major procedural steps involved in this technique? Additionally, how does SAGE enable the comparative analysis of gene expression profiles between cancerous and non-cancerous lung tissue samples	4.5
Q6	Compare the reliability of sequencing reads having Phred scores of Q10, Q20, Q30 and Q40	5
Q7	Short notes on a. Biomarker b. qRT-PCR c. RNAi d. Gene density human genome	8