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JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
TEST -2 EXAMINATIONS MARCH-2026
M.Tech-II Semester (BT)

COURSE CODE (CREDITS): 14M11BT213 (3) MAX. MARKS: 25
COURSE NAME: FUNCTIONAL GENOMICS
COURSE INSTRUCTOR: DR JATA SHANKAR MAX. TIME: 1 Hour and 30 minutes

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	Describe how DNA microarrays function in gene expression analysis, including the role of labelled targets, complementary hybridisation, and signal detection.	4
Q2	What is a Single Nucleotide Polymorphism (SNP)? Explain, with reference to the TP53 gene, how the identification and discovery of SNPs can be utilised to develop molecular markers for distinguishing between healthy and diseased individuals with different types of cancer.	4
Q3	Explain the principle of Restriction Fragment Length Polymorphism (RFLP). Describe the steps involved in conducting an RFLP analysis of a 900bp PCR product and the enzymes used to digest at 600bp. Discuss the significance of size in distinguishing homozygous, heterozygous, and homozygous mutant disease alleles.	4
Q4.	If the frequency of SNPs in a Genome is around 1 in 1000 bases, how many SNPs are present in human genomes?	4
Q5	Describe the principle and workflow of Illumina sequencing technology. It's based on the principle of "sequencing by synthesis. Explain the steps involved in amplification and sequencing in this NGS technology?	4
Q6	The Human Genome Project is regarded as a major scientific milestone in modern biology. Critically examine the key types of genomic data generated from this project. Further, define repetitive elements in the human genome and evaluate their functional significance. Using the estimated number of genes and total genome size, calculate the gene density and discuss its biological implications. Give also the role of VNTR as a biomarker in screening human subjects	5

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