JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -1 EXAMINATIONS-FEB 2025

M.Sc-II Semester (BT)

COURSE CODE (CREDITS): 20MS1BT214 (2) MAX. MARKS: 15

COURSE NAME: GENOMICS & PROTEOMICS

COURSE INSTRUCTOR: DR. JATA SHANKAR MAX. TIME: 1 Hour

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	Central Dogma States that the flow of information is unidirectional (DNA → mRNA → Protein) with few exceptions, Describe the conceptual rationale that led to this (central dogma) hypothesis by Francis Crick in 1956	2
Q2	The Phred score is a measure of how likely it is that a base was called incorrectly during DNA sequencing. If the Phred scores of the DNA sequence Sample-1 and Sample-2 are Q20 and Q30, respectively, analyse the quality of the sequence read or error rate. Which one is better in terms of the quality of the sequences?	3
Q3	Describe the mechanism of traditional DNA sequence methodology and how it differs from next-generation sequencing technology such as sequencing by synthesis (Illumina Seq.)	3
Q4	Explain the dissociation kinetics. How it explains the complexity of the eukaryotic genome. Give genomic data (estimated genome size and gene number) in *Escherichia coli* and human genome	2.5
Q5	Describe the details of insight into Highly repetitive sequence, Moderately repetitive and Unique sequences in the human genome	2
Q6	Pyrosequencing is a DNA sequencing method that sequences DNA in real time by detecting light signals. It's based on the principle of "sequencing by synthesis. Write the cascade of reactions involved in pyrosequencing and their various applications pyrosequencing in genomics	2.5