JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -1 EXAMINATIONS-FEB 2026

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	Explain the complexity of the human genome. Provide key data related to the human genome and calculate the gene density of the human genome	2.5
Q2	If the Phred quality score is 30 for Sample A in a sequencing length of 1 billion base pairs, determine the error rate in Sample A.	2.5
Q3	Explain the principle and steps involved in the Sanger method of DNA sequencing. Illustrate how sequence information is generated	2.5
Q4	Illustrate and explain the differences in genome organisation between a prokaryotic genome (*E. coli*) and the human genome	2.5
Q5	Discuss the advantages of physical mapping. Describe Expressed Sequence Tags (ESTs) and Genome Survey Sequences (GSS)	2.5
Q6	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?	2.5

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