

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATIONS-APRIL 2025

M.Sc-II Semester (BT)

COURSE CODE (CREDITS): 20MS1BT214 (2)

MAX. MARKS: 25

COURSE NAME: GENOMICS & PROTEOMICS

COURSE INSTRUCTOR: DR. JATA SHANKAR

MAX. TIME: 1 Hour 30 Min

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 | The choice of a model organism is fundamental to successful research. Describe a model organism to study lung cancer genomics, specifying with a selection of an oncogene and why? | 3 |
| Q2 | Describe how the genes of the patients affect the effectiveness of medications like omeprazole or codeine, or warfarin. Explain the pharmacogenomics terms responder and non-responder. | 3 |
| Q3 | What is the best way to characterize 16SRNA's function in metagenomics? What does the term "unculturable microorganisms" mean in the context of metagenomics project analyses? | 3 |
| Q4 | Pyrosequencing is a technique for sequencing DNA in real time by detecting light signals. It works on the premise of "sequencing by synthesis." Describe the chain of reactions involved in pyrosequencing and its numerous uses. | 3 |
| Q5 | Give insight into the human genome project with an emphasis on estimated genes, genome size, genes encoding protein and gene density? | 4 |
| Q6 | Draw parallels between Sanger's sequencing and the mechanism used by next-generation sequencing such as ILLUMINA (NGS). | 4 |
| Q7 | Define a. Phred score b. Transcriptome c. Transcript d. Proteome e. Coding vs non-coding region in the genome | 5 |