

TEST -2 EXAMINATIONS-2023

B. Tech V-Semester (BT)

COURSE CODE (CREDITS): 18B1WBT532 (3)

MAX. MARKS: 25

COURSE NAME: COMPARATIVE AND FUNCTIONAL GENOMICS

COURSE INSTRUCTOR: DR. JATA SHANKAR

MAX. TIME: 1 Hour 30 minutes

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*Note: (a) All questions are compulsory.*

*(b) Marks are indicated against each question in square brackets.*

*(c) The candidate is allowed to make Suitable numeric assumptions wherever required for solving problems*

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Q1. How does Illumina sequencing technology fit into the realm of next-generation sequencing, and how does it work to analyze the genome wide gene expression analysis transcriptomics study? [3 marks] CO I

Q2. Describe a detailed explanation of the mechanism and methodology underlying Sanger's DNA sequencing technology?" [3 marks] CO I

Q3. What is the estimated genome size of Human and *Saccharomyces cerevisiae* genome, and how many protein-encoding genes are believed their genome? [3 marks] CO I

Q4. Explain the concept of sequence and function based metagenomics. Provide a suitable example to illustrate this concept. Additionally, elaborate on how microbes contribute to maintaining inorganic and organic in the environment? [3 marks] CO III

Q5. If you have been provided with DNA microarray facility, how do you proceed to identify the gene expression pattern in drug-resistant *E. coli* in comparison to drug-sensitive *E. coli*? In addition illustrate the equation to normalize the microarray data? [3 marks] CO II

Q6. Notes on the following (2.5 marks each) CO I & II

a. What are the basic characteristics of DNA microarray that enable the technology to study whole genome expression profiling?

b. Oncogene

c. Application of pyrosequencing?

d. Human microbiome project?