

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST-3 EXAMINATION-2023

M. Tech.-II Semester (BT)

COURSE CODE (CREDITS): 14M11BT213 (3)

MAX. MARKS: 35

COURSE NAME: FUNCTIONAL GENOMICS

COURSE INSTRUCTORS: DR. JATA SHANKAR

MAX. TIME: 2 Hours

Note: All questions are compulsory. Marks are indicated against each question in square brackets.

Q1. What is RNAi technology? Give account of silencing /microRNA? Why it is relevant in functional genomics study explain with suitable of miRNA in any model organism? 4 Marks [CO II]

Q2. The genomic organization varies across the organisms? Compare the gene density of *S. cerevisiae* vs human genome? 4 Marks [CO II]

Q3. Describe the normalization equation/step used in DNA microarray data. differentiate between pre- and post normalization data to obtain true biological data? 4 Marks [CO III]

Q4. Write on methodology (amplification and sequencing) of next generation Illumina sequencing, and their application in functional genomics study? 4 Marks [CO II & III]

Q5. There are different strategies that have developed in analysis of sequenced genome with respect to gene prediction, isoforms prediction. Describe different approaches used in gene identification of a gene from prokaryotic and eukaryotic genome? 4 Marks [CO I]

Q6. There are different important domains in the genomics have been developed. Explain the role of metagenomics from environmental prospective and/or pharmacogenomic relevant to pharmaceutical industry, with an example? [3.5 Marks] CO III

Q7. What is biomarker? Define the condition for a ideal biomarker? How it helps to identify the pathogen or an unhealthy condition, describe keeping COVID-19 pandemic as an example or in the cancer patients? 3.5 Marks [CO IV]

Q8. Write on following; 8 Marks- each carry 2 marks [CO I, II & III]

- Expressed sequence tags
- C_T Value or Absolute and relative quantification
- Oncogene
- Reverse genetics