

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST-3 EXAMINATION-2023

M. Sc.-II Semester (BT)

COURSE CODE (CREDITS): 20MS1BT214 (2)

MAX. MARKS: 35

COURSE NAME: GENOMICS AND PROTEOMICS

COURSE INSTRUCTORS: DR. JATA SHANKAR

MAX. TIME: 2 Hours

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

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Q1. Describe the methodology for Sanger's sequencing technology or Illumina sequencing technology? Provide application of sequencing DNA in human health? 4marks [CO I]

Q2. If you have been provided with genomic facilities and mice oligo-chip (DNA microarray), how to proceed to identify the differential expressed gene in Cancerous mice while comparing with that to in a normal mice model in a defined studies? 4 marks [CO II]

Q3. What is SNP? How SNPs are introduced in the genome? Give a suitable example where screening of SNP in a gene is crucial for prescribing a drug for the treatment of Cancer? 4 marks [CO II]

Q4. Post-translational modification is important for eukaryotic protein to perform biological functions. what are these modifications in the proteins? How you are going to differentiate the glycosylated and phosphorylated proteins from the given sample? 4 marks [CO II]

Q5. Describe protein array/chip that helped functional proteomics studies, explain with suitable example on protein-ligand interactions or protein-protein interactions? Or describe the method 'MALDI TOF' for the identification of the proteins? What are the protein databases for the protein identification? 4 marks [CO II]

Q6. Yeast two hybrid system is a successful technique to study protein-protein interaction, describe the technique with example how two proteins interact in the yeast model system? 5 marks [CO II]

Q7. Write on following: 10 marks (each carry 2.5 marks) [CO I & CO II]

- a. Lipidomics
- b. Forward and reverse genetics or 16S rRNA
- c. Biomarker
- d. Genetic information of mitochondrial genome or nuclear genome