JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
TEST -2 EXAMINATIONS-2022
M.Sc-II Semester (BT)

COURSE CODE (CREDITS): 20MS1BT214 (2)
COURSE NAME: GENOMICS & PROTEOMICS
COURSE INSTRUCTOR: DR. JATA SHANKAR

MAX. MARKS: 25

MAX. TIME: 1 Hour 30 Min

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

Q1. In humans, a common polymorphism has been observed in tumor suppressor gene, discuss the cancer cases where the mutation is associated with cancer, not associated and associated non cancer cases? [2 marks]

Q2. The cancerous tissue contain hetrogenous cells with respect to mutations, unique pathology or unique drug response, Single Cell RNA sequencing could distinguish the expression of these cells, write the strategy for RNA sequencing and other applications? [2 marks]

Q3. If you have given a nucleotide sequence (1000b), the possible ORF is six, explain? [2 marks]

Q4. State a model organism applicable to functional genomics studies for cancer and why? [2 marks]

Q5 How SNPs are introduced in the genome? How does it affect function and structure of a gene encoding protein, explain? [2 marks]

Q6. Write on DNA sequencing technology? And how it influences the functional genomics studies? [2 marks]

Q7. The approximate no. of genes in human genome is around 20,000 to 25,000; calculate the gene density? [3 marks]

Q8. What is purpose of mapping query sequence read to the reference genome and how it helps to identify the open read frame? [3 marks]

Q9. Human genome project is the landmark in the science, what are the outcomes of the genome projects? What is VNTR, where do find the application of it? [3.5 marks[

Q10. In functional genomics, assigning coding sequenc in the genome project is important task? What basic strategies you would construct to distinguish prokaryotic vs eukaryotic genes? 3.5 marks