

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -1 EXAMINATIONS-2025

M.Tech-II Semester (BT)

COURSE CODE (CREDITS): 14M11BT213 (3)

MAX. MARKS: 15

COURSE NAME: FUNCTIONAL GENOMICS

COURSE INSTRUCTOR: DR JATA SHANKAR

MAX. TIME: 1 Hour

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	Create common strategies/approaches/ signals used to predict genes in the newly sequenced genome of eukaryotic and prokaryotic organisms.	2
Q2	If the number of introns in a gene is 3 (three), how many possible isoforms in the genes are predicted, illustrate the combination of exon/intron in the gene isoforms. Give two examples of genes known to have isoforms	2.5
Q3	A less common type of skin cancer that is more likely to spread to other parts of the body. It is the most dangerous form of skin cancer and is responsible for most deaths from skin cancer. Describe the model organism (s) to study the skin cancer and why/associated gene (s).	2.5
Q4.	The complexity of an organism is a measure of how intricate or complicated it is. It's related to how well the organism can function in a complex environment. After analyzing the genomic data of the human genome or higher eukaryotes, describe the 2 (two) attributes for the genome complexity of the organism	2.5
Q5	The mitochondrial and nuclear gene expression processes are spatially separated. The genomes must communicate with each other to generate a coordinated gene response to various environmental cues. Give the descriptive genomic data of the mitochondrial and nuclear genome of humans.	2.5
Q6	Arabidopsis has been recognized as a model system because of its salient features, and powerful reverse and forward genetics. Evaluate the functional genomic data of the model organism applicable to study the plant system.	3