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22BTP208N

PSG COLLEGE OF ARTS & SCIENCE
(AUTONOMOUS)

MSc DEGREE EXAMINATION MAY 2025
(Second Semester)

Branch – **BIOTECHNOLOGY**

OMICS TECHNOLOGY

Time: Three Hours Maximum: 75 Marks

SECTION-A (10 Marks)
Answer **ALL** questions
ALL questions carry **EQUAL** marks (10 × 1 = 10)

Module No.	Question No.	Question	K Level	CO
1	1	Which of the following is true about eukaryotic genomes? a) They are generally larger than prokaryotic genomes. b) They contain only coding DNA. c) They are found in the cytoplasm. d) They lack introns.	K1	CO1
	2	What type of DNA is amplified in RAPD analysis? a) mRNA b) Genomic DNA c) cDNA d) Ribosomal RNA	K1	CO1
2	3	Which method is commonly used to analyze gene expression in bacterial pathogens? a) Southern blotting b) Northern blotting c) Microarray analysis d) Western blotting	K1	CO2
	4	Select one limitation of RAPD markers is: a) They are highly reproducible. b) They can be affected by PCR conditions. c) They require expensive reagents. d) They provide quantitative data.	K2	CO2
3	5	What is a common application of FRET in biological research? a) Protein sequencing b) Studying protein-protein interactions c) DNA amplification d) RNA quantification	K1	CO3
	6	What does the term "resolution" refer to in mass spectrometry? a) The ability to quantify the concentration of analytes b) The ability to distinguish between ions with very close mass-to-charge ratios c) The total time taken for the analysis d) The maximum number of ions detected	K1	CO3
4	7	Ubiquitination is a post-translational modification primarily associated with which cellular process? a) Protein synthesis b) Protein degradation c) Protein folding d) Protein trafficking	K2	CO4
	8	In proteomics, the identification of low-abundance proteins is often challenging due to __________. a) High-throughput sequencing technologies b) Mass spectrometry limitations c) The simplicity of protein interactions d) The abundance of genomic data	K2	CO4
5	9	Which of the following methods is commonly used for predicting protein functions based on sequence similarity? a) Molecular dynamics simulations b) Homology modeling c) Gene ontology annotation d) Phylogenetic profiling	K2	CO5
	10	Which of the following tools is commonly used for visualizing protein interaction networks? a) BLAST b) Cytoscape c) Clustal Omega d) STRING	K2	CO5

Cont...

SECTION - B (35 Marks)

Answer **ALL** questions
ALL questions carry **EQUAL** Marks (5 × 7 = 35)

Module No.	Question No.	Question	K Level	CO
1	11.a.	Explain the organization of eukaryotic genomes in terms of genes and regulatory elements.	K2	CO1
		(OR)		
	11.b.	Illustrate the applications of VNTR analysis in forensic science.		
2	12.a.	Construct and Discuss the key differences between the comparative genomics of bacteria and eukaryotes.	K3	CO2
		(OR)		
	12.b.	Explain the process of STR typing using PCR and its applications.		
3	13.a.	Explain the principle of protein microarrays and their applications in biomedical research.	K3	CO3
		(OR)		
	13.b.	Explain the principle of peptide mass fingerprinting (PMF), advantages, and limitations.		
4	14.a.	Categorize the challenges associated with studying post-translational modifications (PTMs) in the fields of bioinformatics.	K4	CO4
		(OR)		
	14.b.	What is metabolomics, and how does it contribute to our understanding of biological systems, health, and disease?		
5	15.a.	List out the techniques commonly used in genetic interactomics.	K4	CO5
		(OR)		
	15.b.	Categorize and define Cytoscape, and its key features for protein interaction network visualization.		

SECTION -C (30 Marks)

Answer **ANY THREE** questions
ALL questions carry **EQUAL** Marks (3 × 10 = 30)

Module No.	Question No.	Question	K Level	CO
1	16	Categorize the principle , mechanism and application of RFLP.	K4	CO1
2	17	Inspect and describe the process of using a DNA microarray for gene expression profiling and applications .	K4	CO2
3	18	Explain the principle of Surface Plasmon Resonance (SPR) and its applications in biosensing.	K5	CO3
4	19	Interpret the experimental and computational methods used in protein chip technology and significance .	K5	CO4
5	20	Elaborate the primary methods used in text mining to identify protein-protein interactions, and how do they function?	K6	CO5

Z-Z-Z

END