U.S.N.										

B.M.S.College of Engineering, Bengaluru-560019

Autonomous Institute Affiliated to VTU

June 2025 Semester End Main Examinations

Programme: B.E. **Semester: VI**

Branch: Biotechnology **Duration: 3 hrs.**

Course Code: 23BT6PCGAP / 22BT6PCGAP **Max Marks: 100**

Course: Genomics & Proteomics

Instructions: 1.Answer any FIVE full questions, choosing one full question from each unit.
2. Missing data, if any, may be suitably assumed.

Important Note: Completing your answers, compulsorily draw diagonal cross lines on the remaining blank pages. Revealing of identification, appeal to evaluator will be treated as malpractice.

		UNIT - I	*CO*	*PO*	Marks
1	a)	Define the C-value and C-value paradox. Explain the significance of Cot curve.	*CO1*	*PO1*	**10**
	b)	Illustrate how the shotgun sequencing approach was utilized in sequencing large genomes like that of humans. Differentiate between shotgun & clone contig approaches.	*CO1*	*PO1*	**10**
		OR			
2	a)	List the steps involved in next-generation sequencing (NGS) and differentiate between first, second, and third-generation sequencing methods.	*CO1*	*PO1*	**10**
	b)	Describe a scenario where Nanopore sequencing would be more advantageous than traditional NGS techniques. Write the principles and functions of Nanopore sequencing with neat figure.	*CO1*	*PO1*	**10**
		UNIT - II			
3	a)	Explain the importance of sequence alignment tools in genome mapping and annotation.	*CO 2*	*PO2*	**10**
	b)	Apply double digestion and partial digestion techniques to construct a restriction map of a hypothetical plasmid.	*CO 2*	*PO2*	**10**
		OR			
4	a)	Describe the principle and application of FISH and its amplified variants in genome mapping.	*CO 2*	*PO2*	**7**
	b)	Demonstrate how software tools assist in aligning sequences and visualizing mapped regions of a genome.	*CO 2*	*PO2*	**7**

		c)	Analyze the steps in generating a genome-wide map using a combination of restriction mapping and FISH.	*CO 2*	*PO2*	**6**
			UNIT - III			
	5	a)	Explain the role of microRNAs, shRNAs, and piRNAs in post-transcriptional gene regulation	*CO2*	*PO1*	**10**
		b)	Compare and contrast RFLP, RAPD, and AFLP in terms of reproducibility, sensitivity, and ease of use.	*CO 2*	*PO2*	**10**
			OR			
	6	a)	How SNPs are detected and their significance in disease association studies.	*CO2*	*PO1*	**10**
		b)	Develop the pipeline for an RNA-seq experiment to identify differentially expressed genes with neat illustrations.	*CO2*	*PO2*	**10**
			UNIT - IV			
	7	a)	How mass spectrometry helps in peptide mass fingerprinting and protein identification.	*CO 3*	*PO5*	**8**
		b)	Compare and contrast the advantages and limitations of gel-based versus gel-free proteomics approaches.	*CO3*	*PO1*	**8**
		c)	Critically evaluate the role of proteomics in biomarker discovery and disease diagnostics.	*CO3*	*PO1*	**4**
			OR			
	8	a)	Apply the principles of soft ionization MS to determine protein expression in a given sample.	*CO3*	*PO1*	**10**
		b)	Propose an integrated proteomics pipeline for studying drug response in cultured mammalian cells using radio isotope labelling.	*CO3*	*PO2*	**10**
			UNIT - V			
	9	a)	How yeast two-hybrid systems help identify protein–protein interactions.	*CO4*	*PO2*	**10**
		b)	Develop suitable label free method to determine protein –ligand interaction.	*CO4*	*PO2*	**10**
			OR			
	10	a)	How immunoprecipitation followed by mass spectrometry can be used for interaction studies.	*CO4*	*PO2*	**10**
		b)	Analyze the limitations of protein microarrays and distinguish various types of protein arrays.	*CO4*	*PO2*	**10**

****