

CBCS SCHEME

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BBT503

Fifth Semester B.E./B.Tech. Degree Examination, June/July 2026 Genomics, Proteomics and Bioinformatics

Time: 3 hrs.

Max. Marks: 100

*Note: 1. Answer any FIVE full questions, choosing ONE full question from each module.
2. M : Marks, L: Bloom's level, C: Course outcomes.*



Module – 1			M	L	C
Q.1	a.	Define Polymorphism. Explain the different types of polymorphisms found in genomes.	10	L1	CO1
	b.	Describe the principle and steps involved in the Sanger Dideoxy Method of DNA sequencing.	10	L2	CO1
OR					
Q.2	a.	Explain the principle of Next Generation Sequencing (NGS) and its advantages over traditional sequencing.	10	L1	CO2
	b.	Define Genome Annotation. Highlight its process and applications.	10	L2	CO1
Module – 2					
Q.3	a.	Elaborate on the general architecture of Prokaryotic and Eukaryotic genomes with suitable examples.	10	L2	CO1
	b.	Substantiate the use of bioinformatics tools like dbSNP for the detection of Single Nucleotide Polymorphisms (SNPs).	10	L3	CO2
OR					
Q.4	a.	Summarize the achievements and applications of the Human Genome Project.	10	L2	CO1
	b.	Comment on the role of molecular markers such as RFLP, RAPD and AFLP in genome mapping.	10	L4	CO3
Module – 3					
Q.5	a.	Define Proteomics. Elaborate on the methodology of two-dimensional PAGE in protein analysis.	10	L2	CO1
	b.	Describe mass spectrometry-based protein identification and the concept of peptide mass fingerprinting.	10	L2	CO2

OR

Q.6	a.	Discuss the yeast two-hybrid system and phage display technique used for studying protein-protein interactions.	10	L2	CO2
	b.	“Proteomics has vast applications in drug discovery and toxicology”. Justify.	10	L4	CO3

Module – 4

Q.7	a.	Enumerate major biological databases and describe the significance of NCBI and UniProt databases.	10	L2	CO1
	b.	Define Sequence Alignment. Deliberate on the working of BLAST with its different types.	10	L2	CO2

OR

Q.8	a.	Explain the progressive multiple sequence alignment and the principle of MUSCLE algorithm.	10	L1	CO2
	b.	Justify the need of phylogenetic tree construction methods – Distance based and character based. Substantiate on how bootstrapping validates results.	10	L4	CO3

Module – 5

Q.9	a.	Illustrate different computational methods used to detect promoters and transcription factor binding sites.	10	L3	CO2
	b.	Justify the role of structure prediction tools such as SOPMA and JPRED in secondary and tertiary protein structure prediction.	10	L4	CO3

OR

Q.10	a.	Outline the workflow of molecular docking. Describe in detail the most commonly used docking tools.	10	L2	CO3
	b.	Define Pharmacophore. Co-relate receptor mapping and QSAR approaches in drug design.	10	L3	CO2
