USN | 1 A Y 2 2 B T 0 1 5 | **BBT503**

Fifth Semester B.E./B.Tech. Degree Examination, Dec.2024/Jan.2025
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.	Comparatively discuss the various types of Polymorphisms found in genomes. Elaborate on the methods used to identify them.	10	L1	CO1
	b.	Substantiate the steps involved in Sanger's dideoxy sequencing method.	10	L1	CO1
		OR			
Q.2	a.	Elaborate the methodology and salient steps involved in Pyrosequencing.	10	L1	CO1
	b.	Discuss the relevance of dbSNP and dbEST in genome annotation and analysis.	10	L1	CO1
		Module – 2			
Q.3	a.	Deliberate on the characteristics and significance of mitochondrial genomics.	10	L2	CO2
	b.	Elaborate the steps involved in DNA micro array experiment. Comment on the work – flow in the analysis of micro array data.	10	L2	CO2
		OR			
Q.4	a.	Substantiate the utilities of genome databars of model organisms, with relevant examples. Comment on the tools used for comparative genome analysis.	10	L2	CO2
	b.	Highlight the importance of RNAi tool in the study of functional genomics. Comment on the steps involved with an appropriate case study.	10	L3	CO2
		Module – 3			
Q.5	a.	Substantiate that 2D – Gel electrophoresis is a valuable technique to study PTMs in proteomics.	10	L2	CO2
	b.	Justify the relevance of automated tools and techniques in proteomics work flow with suitable examples.	10	L2	CO2
		OR			
Q.6	a.	Substantiate the need for Y2H methods in the study of protein – protein interaction. Comment on the application of reverse Y2H system.	10	L2	CO2
	b.	Elaborate the role of MALDI – Tof as a potential tool in the investigation of peptide mass finger printing.	10	L2	CO2

		Module – 4			
Q.7	a.	Justify the importance of PDB as a resourceful database in Bioinformatics exercises, with a case study.	10	L1	CO3
	b.	Highlight the significance of Gen Bank and Swissprot databases in Bioinformatics exercises, with examples.	10	L1	CO3
		OR			
Q.8	a.	What is BLAST? Elaborate the steps involved and the utility of the tool in searching for relevant homologs.	10	L1	CO3
	b.	Discuss the popular tree building methods involved in the phylogenetic analysis of molecular sequences.	10	L2	CO3
		Module – 5			
Q.9	a.	Comment on the tools used in analysis of functional sites of Eukaryotic Genomes.	10	L2	CO3
	b.	Justify the need for the design of primers via appropriate tools. Substantiate the factors considered in the computational design of primers.	10	L3	CO3
		OR			
Q.10	a.	Elaborate the steps involved in the 3D structure modeling of receptors using the homology based approaches.	10	L3	CO3
	b.	What is Molecular docking? Detail the steps involved in the study of Ligand – receptor interactions via appropriate tools.	10	L3	CO3

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