22BTU520N

PSG COLLEGE OF ARTS & SCIENCE
(AUTONOMOUS)

BSc DEGREE EXAMINATION MAY 2026
(Fifth Semester)

Branch: **BIOTECHNOLOGY**

GENOMICS AND PROTEOMICS

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	A technique that uses restriction enzyme cleavage sites as DNA markers to detect polymorphisms is known as: A. SNP B. RFLP C. AFLP D. SAGE	K1	CO1
	2	Compare Genetic Mapping and Physical Mapping based on the distance unit they report. A. Both report relative distance in centimorgans (cM). B. Genetic mapping reports base pairs (bp); physical mapping reports cM. C. Genetic mapping reports relative distance (cM); physical mapping reports absolute distance (bp). D. Both report absolute distance in base pairs (bp).	K1	CO1
2	3	Which of the following model organisms is a nematode whose complete cell lineage has been mapped? A. *Drosophila melanogaster* B. *Saccharomyces cerevisiae* C. *Mus musculus* D. *Caenorhabditis elegans*	K2	CO2
	4	Distinguish between a BAC library and a YAC library in terms of insert capacity. A. YACs hold smaller inserts (up to 50 kb). B. YACs hold much larger inserts (up to 1,000 kb) than BACs. C. BACs can only hold cDNA, while YACs hold genomic DNA. D. BACs and YACs have the same capacity, but different hosts..	K2	CO2
3	5	The fragmentation of peptides into smaller ions within a mass spectrometer, a key step for sequencing, is often achieved using A. Electrospray Ionization (ESI) B. Collision-Induced Dissociation (CID) C. Matrix-Assisted Laser Desorption/Ionization (MALDI) D. Time-of-Flight (TOF)	K2	CO3
	6	Explain why proteins are treated with SDS and heat before separation in SDS-PAGE. A. To make them fluorescent for detection. B. To separate them by their pI. C. To denature them and give them a uniform negative charge, allowing separation primarily by mass. D. To digest them into smaller peptides.	K2	CO3

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4	7	The comprehensive study of all small-molecule metabolites within a biological system at a specific time is termed A. Transcriptomics B. Genomics C. Proteomics D. Metabolomics	K2	CO3
	8	Outline the use of Phage Display Screening in proteomics. A. For determining the mass of peptides. B. For separating proteins based on size. C. For identifying novel protein-protein interaction partners or ligands by selection. D. For quantifying mRNA expression levels.	K2	CO3
5	9	Which enzyme family is known for its high genetic variability, making it a critical focus in pharmacogenomics for drug metabolism? A. Restriction Endonucleases B. RNA Polymerases C. Cytochrome P450 (CYP) enzymes D. DNA Ligases	K2	CO4
	10	Summarize the main goal of Target Identification and Validation in drug discovery A. To optimize the drug dosage for individual patients. B. To confirm that a specific gene or protein is causally involved in the disease and is a viable site for drug action. C. To mass-produce the drug compound. D. To perform clinical trials on the new drug.	K2	CO4

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.	Compare the utility of Cytogenetic mapping with Radiation Hybrid (RH) mapping in genomics.	K1	CO1
		(OR)		
	11.b.	Illustrate the process of 16S r-RNA typing for the identification of microbes.		
2	12.a.	Model the procedure of comparative genomics to discover evolutionary relationships between model organisms.	K2	CO2
		(OR)		
	12.b.	Apply your knowledge of sequencing techniques to explain the differences and similarities between SAGE and differential display proteomics in terms of their goals.		
3	13.a.	Analyze the steps of LC/MS-MS (Liquid Chromatography-Mass Spectrometry/Mass Spectrometry) and infer how this combined technique identifies complex protein mixtures.	K2	CO3
		(OR)		
	13.b.	Examine the technique of Phage Display Screening and determine its significance in the study of protein-protein interactions.		
4	14.a.	Analyze the core objectives of structural proteomics and interpret how it contributes to drug design.	K2	CO3
		(OR)		
	14.b.	Examine the process of PCR directed protein arrays and outline their specific advantages over traditional expression-based protein microarrays.		

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5	15.a.	Relate the principles of pharmacogenomics to the challenges in drug efficacy and safety, explaining how it leads to more effective drug development.	K3	CO4
		(OR)		
	15.b.	Construct a plan for using High Throughput Screening (HTS) to identify potential drug leads from a large compound library.		

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	Analyze the process of Pedigree Analysis in humans. Examine the concept of gene duplication and infer its role in the evolution of new gene functions.	K1	CO1
2	17	Examine the utility of five key Model Organisms *(E.coli, S.cerevisiae, C.elegans, Drosophila, Musmusculus, or A.thaliana)* and analyze their specific contributions to genomics research.	K2	CO2
3	18	Analyze the different Mass Spectrometry techniques (MALDI-TOF and LC/MS-MS) and examine their specific uses in proteomics for protein sequencing and identification.	K2	CO3
4	19	Analyze the principles of transcriptomics (mRNA's in a cell, expression profiling) and determine how this data can be integrated with proteomics (protein expression) to provide a complete biological picture.	K2	CO3
5	20	Examine the development process of personalized medicine based on Pharmacogenetics. Interpret how this approach moves beyond the "one-size-fits-all" model of drug therapy.	K3	CO4

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