3/21

1311E1114

Candidate's Seat No :_____

M.Sc. Sem.-3 Examination

501

CB

Time : 2-30 Hours] **November-2025** **[Max. Marks : 70**

Instructions:

All Questions are compulsory
Draw neat and labeled diagram wherever necessary

Q-1		**Write the following**	**14**
	(i)	Write in detail about central dogma of molecular biology.	7
	(ii)	Explain laser capture microdissection technique.	7
		OR	
	(i)	Explain genome mapping.	7
	(ii)	Write a note on genomic landscape of cancer.	7
Q-2		**Write the following**	**14**
	(i)	Describe the major goals of human genome project. Mention the techniques used to achieve these goals.	7
	(ii)	Discuss implications of the application of proteomic approach to cancer screening.	7
		OR	
	(i)	Discuss two types of human genomes.	7
	(ii)	Write a short note on significance of cancer genomics.	7
Q-3		**Write the following**	**14**
	(i)	Explain differences between MALDI-TOF and ESI techniques for proteomics study.	7
	(ii)	What are the applications of proteomics in cancer research? Describe clinical significance of proteomics in cancer.	7
		OR	
	(i)	Write a short note on challenges and limitations of 2D electrophoresis.	7
	(ii)	Explain: Role of proteomics in discovery of cancer biomarkers and its challenges.	7
Q-4		**Write the following**	**14**
	(i)	Describe about protein-protein interactions: The structure and systems approaches to analyze diverse genomic data.	7
	(ii)	Discuss the significance of applying serum and tissue proteomics in the understanding and detection of solid tumors.	7

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OR

(i) Discuss the principle and steps involved in two dimensional electrophoresis. 7

(ii) Explain the importance of proteomic study in breast cancer. 7

Q-5 **MCQs (Any seven out of twelve)** 14

1 **Which is the commonly used start codon?**

a UAA b UGA

c AUG d AGG

2 **According to human genome project, all humans are approximately _____ identical.**

a 99.9% b 70%

c 85% d 95%

3 **Proteins are synthesized on the surface of _____.**

a tRNA b snRNA

c mRNA d Ribosome

4 **Translational research refers to moving findings from _____.**

a Animals to humans b Bench to bedside

c DNA to RNA d Theory to law

5 **Mutation that alters the wild-type phenotype is called a _____.**

a Cross mutation b Forward mutation

c Reverse mutation d Neutral mutation

6 **A technique that identifies characteristic patterns of mutations left by different mutagenic processes on the genome is known as _____.**

a Genome sequencing b Cancer genomics

c Biomarker testing d Mutation signature

7 **Which labeling technique is used in quantitative proteomics?**

a PCR labelling b iTRAQ and SILAC

c Western blot d Sanger sequencing

8 **Onco-proteomics contributes to personalized medicine by _____.**

a Using one treatment for all b Identifying unique proteins profiles of patients

c Sequencing mitochondrial DNA d Measuring environmental exposures only

E1114-3

9 **Bioinformatics in proteomics is mainly used for _____.**

a Designing PCR primers

b Interpreting mass spectrometry data

c RNA splicing

d Chromosome banding

10 **In 1999, which country started Sanger Caner Genome Project?**

a Japan

b United States

c United Kingdom

d Canada

11 **Which step is NOT a part of a mass spectrometer?**

a Ionization

b Mass analyzer

c Detector

d DNA amplification

12 **The HUPO project is mainly focused on _____.**

a DNA sequencing standardization

b RNA interference therapies

c Genome editing tools

d Plasma proteome standardization