

- > KEEPING MOBILE PHONE/ANY ELECTRONIC GADGETS, EVEN IN 'OFF' POSITION IS TREATED AS EXAM MALPRACTICE
- > DON'T WRITE ANYTHING ON THE QUESTION PAPER

Answer ALL Questions
(10 X 10 = 100 Marks)

1. Elucidate on coding and non-coding DNA present in human chromosomes.
2. In eukaryotes how does protein(s) evolve? With an illustration explain the process and the significances.
3. a) Give an overview of Massively Parallel Signature Sequencing, an approach to analyse the level of expression of virtually all genes in a sample. [5]
b) Evaluate the reason that using a DNA microarray is more useful than performing a Northern blot. [5]
4. Discuss the tools and approaches you might use to retrieve following information about the protein tubulin.
a) Nucleic acid sequence
b) Expression studies
c) Protein sequence
d) Structure and comparative analysis
5. It is well established that a mutagen modifies the genome. State the consequences of the mutation and how can the mutations be studied using genomics tools?
6. a) Outline the reasons for using High-performance liquid chromatography (HPLC) with mass spectrometry (MS) for analysing proteins/peptides in biological samples. [4]
b) Outline the principles of High-performance liquid chromatography (HPLC) technique. [6]
7. Evaluate the advantages of stable isotope labelling by amino acids in cell culture (SILAC) a quantitative proteomics method over other isotope tagging approaches.
8. Explain the analytical workflow of Nanopore DNA sequencing technology.
- 9.a) Explain the yeast two hybrid system to test for the interactions of two proteins of interest (X and Y). Use a diagram and the terms "BAIT", "PREY" and "REPORTER" to aid your explanation.

OR

- 9.b) (i) Explain RNA editing [5]
(ii) What are the basic concepts of Phylogenetics [5]
- 10.a) Describe the basic principles of the ionisation process in electrospray ionisation (ESI) mass spectrometry.

OR

- 10.b) Briefly present the workflow for glycoproteomic analysis.

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