

Total No. of Pages : 02

M.Code : 71845

Max. Marks : 60

1. **SECTION-A is COMPULSORY** consisting of **TEN** questions carrying **TWO** marks each.
2. **SECTION-B** contains **FIVE** questions carrying **FIVE** marks each and students have to attempt any **FOUR** questions.
3. **SECTION-C** contains **THREE** questions carrying **TEN** marks each and students have to attempt any **TWO** questions.

1. Write briefly :

- Define SNP.
- What is whole genome shotgun sequencing?
- Define pseudogenes.
- What is the advantage of using fluorescent probes over radioactive probes in microarray analysis?
- What is the application of mass spectrometry in proteomics?
- What is the application of homology modeling in structural proteomics?
- What is the importance of databases of Protein-Protein interactions?
- What do you understand by eukaryotic clusters of orthologous groups (KOGs)?
- What were the goals of human genome project?
- What is the application of Nuclear Magnetic Resonance (NMR) spectroscopy in structural proteomics?

SECTION-B

2. Compare microarray based transcriptome analysis with proteome analysis approaches for studying global gene expression.
3. Describe RAPD analysis. Comment on its advantages and limitations.
4. With the help of suitable example write importance of comparative genomics of bacteria.
5. Discuss the printing technology for producing spotted arrays.
6. Write about a comparative genomics based method to study protein- protein interactions.

SECTION-C

7. Using schematic diagram, describe SAGE. Compare SAGE with microarray technology.
8. Describe 2D gel electrophoresis and its application in proteomics.
9. Describe AFLP with the help of schematic diagram.

NOTE : Disclosure of Identity by writing Mobile No. or Making of passing request on any page of Answer Sheet will lead to UMC against the Student.