D/L/TX

Reg. No: 22BBT0092

Final Assessment Test – November 2024

VIT
Vellore Institute of Technology

Course: BBIT303L - Genomics and Proteomics
Class NBR(s): 1226 / 1227
Time: Three Hours

Slot: D2+TD2
Max. Marks: 100

- 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. Compare and contrast the 1st, 2nd and 3rdgeneration genome sequencing technologies.

2. Interpret the role of integrating genetic and physical mapping processes for proper genome mapping.

3. Explain the major components of Mass spectrometer and how Tandem MS analysis is done.

4. Demonstrate the different types of functional roles played by stacking and separating gel in an SDS-PAGE. Explain DIGE.

5. Relate the role of Pharmacogenetics and Pharmacogenomics in analysis of clinical samples.

6. Differentiate between DNA microarrays and protein microarrays.

7. Describe the use of DNA and protein databases in genomics and proteomics studies.

8. Identify the use of ESI-MS, MALDI-TOF MS and MS-MS in proteome analysis.

9.a) Cancer biomarkers are significant for the diagnosis of various cancers. Design the experiment using genomics and proteomics tools to discover a novel biomarker for a new type of cancer.

OR

9.b) A survey analysis of infants from rural and urban populations identified the prevalence of different types of diseases. Rural infants show resistance to cold and cough, while urban infants have fewer diarrhoeal disorders. Develop a strategy to investigate these differences using genomics tools.

10.a) Explain the different tools used for quantitative proteomics.

OR

10.b) A biochemist has isolated two proteins P1 and P2 found to have a role in a metabolic pathway. How he will determine whether these proteins are interacting or not? What is the common approach to validate this protein-protein interaction?

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