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# B.M.S. College of Engineering, Bengaluru-560019

Autonomous Institute Affiliated to VTU

## August 2024 Supplementary Examinations

**Programme: B.E.**

**Branch: Biotechnology**

**Course Code: 19BT6DCGAP**

**Course: Genomics and Proteomics**

**Semester: VI**

**Duration: 3 hrs.**

**Max Marks: 100**

**Instructions:** 1. Answer any FIVE full questions, choosing one full question from each unit.  
2. Missing data, if any, may be suitably assumed.

### UNIT - I

1 a) This method of sequencing is considered to be revolutionary and sequencing of large-scale genomes can be done in no time. Identify the method and elaborate the technique with principle and a neat illustration. **06**

b) All species have fixed DNA content yet some organisms of similar type have different amount of DNA. What is this phenomenon is called? Define the term and provide reasons for the discrepancy. **06**

c) Develop a suitable method for sequencing a mammalian genome by next gen sequencing method. write its principle and steps involved with a neat labelled diagram. **08**

### UNIT - II

2 a) Construct a DNA map using the following information  
A DNA was digested with Sal1 and HhaIII . Following are digested fragments. Sal1 - 1.8kb, 0.25kb, 2.3kb for Hha1- 0.7, 2.1, 1.55 kb. For double digestion-0.75, 0.25, 1.1, 1.2, 0 and 0.7 kb fragments were resulted. Draw illustrations for each combination and construct a final map. **07**

b) Develop a genetic map using the following information. Indicate position of each gene and direction of transfer from the bacterial conjugation experiments **07**

Hfr1		Hfr2		Hfr3	
miy	10 min	sow	5 min	mic	5 min
sow	20 min	miy	15 min	tod	20 min
raj	35 min	chr	30 min	nub	30 min
nub	40 min	sha	40 min	raj	35 min
tod	50 min	mic	50 min	sow	50 min
mic	65 min	tod	65 min	miy	60 min
sha	75 min	nub	75 min	chr	75 min

**Important Note:** Completing your answers, compulsorily draw diagonal cross lines on the remaining blank pages. Revealing of identification, appeal to evaluator will be treated as malpractice.

c) Chromosomes can be painted and gene expression can be visualized. Identify the method behind this. write its principle and steps involved briefly with a neat illustration. 06

**OR**

3 a) Develop rules and principles to discover genes from the large genome raw sequence with neat illustrations 08

b) List any four types of molecular markers and explain each very briefly 06

c) Junk DNA is misnomer and it is very important. Justify this statement by providing reasons 06

**UNIT - III**

4 a) Design strategies for determining the function of a gene with neat illustrations 08

b) Develop suitable strategies for measuring gene expression. With a neat diagram explain one strategy in detail 08

c) classify various types of non-coding RNAs. Write very briefly about microRNAs 04

**UNIT - IV**

5 a) Design a strategy to purify recombinant proteins in a single step. With a suitable diagram outline the procedure. Give two examples of suitable tags for purification. 10

b) Develop a gel free strategy that involves tagging to analyse all Protein expression from more than two samples. Write the method to use and its applications with a neat illustrations. 10

**OR**

6 a) Design a gel-based strategy for identification of differentially expressed proteins from two or samples. Also write briefly about its variant method. 10

b) Develop a strategy for analysing protein expression on large scale using a soft ionization technique. Write principle behind the method and its applications with a neat illustrations. 10

**UNIT - V**

7 a) Outline procedure for invitro, label free method for protein interaction with a neat diagram. 08

b) Design a strategy for analyzing the in vivo protein -protein interactions. Write the detailed steps with a neat illustrations and various types of the method. 08

c) Compare and contrast DNA and protein arrays. 04

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