

Time allowed: 3 Hours

Max. Marks: 60

**NOTE:** Attempt five questions in all, including Question No. I which is compulsory and selecting atleast one question from each Unit.

x-x-x

I. Answer briefly:-

- a) Homology modelling
- b) Gene Neighbourhood
- c) VISTA
- d) Nonsense mutation
- e) Microsatellites
- f) STRING
- g) Molecular Interactions
- h) TGGE

(8x1½)

**UNIT - I**

- II. Discuss any two techniques used for Genetic mapping. (12)
- III. a) Write a note on the history and milestones of the Human Genome Project.  
b) Explain the relationship between SNP and disease giving suitable example. (8,4)

**UNIT - II**

- IV. Explain the principle and applications of Phage Display. (12)
- V. a) Discuss any one database of protein-protein interactions.  
b) How are phylogenetic profiles and gene fusion used for predicting pathways and interactions? (5,7)

**UNIT - III**

- VI. a) How are Hydropathy plots used for analysis of membrane proteins?  
b) Explain the process of fold recognition for predicting protein structures. (2x6)

P.T.O.

(2)

- VII. a) How is BLASTZ used for large genome alignments?
- b) Write a note on the problem of complexity and repeats in large genome alignments. (2x6)

x-x-x