

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) dbSNP
- (b) VNTR
- (c) Co-immunoprecipitation
- (d) Gene fusion
- (e) Threading
- (f) PDB
- (g) NCBI genome
- (h) Mutation

(8x1½)

UNIT - I

II. Write a note on strategies used in identifying human disease genes.

(12)

- III. a) Discuss the construction of cytological maps.
b) Elaborate on any two SNP detection methods.

(2x6)

UNIT - II

- IV. a) Explain yeast 2 hybrid method for studying protein-protein interactions?
b) How is Mass spectrometry used to analyze proteins?

(2x6)

- V. a) How are phylogenetic profiles used for predicting protein-protein interactions?
b) Discuss the applications of phage Display.

(2x6)

UNIT - III

- VI. a) How is the problem of complexity, size and repeats in Eukaryotic genomes addressed during large genome alignments?
b) Discuss the analysis of transmembrane proteins. Explain any software used for the same.
- VII. Explain any one web based server and software used for genomics.

(2x6)

(12)

x-x-x