## Exam.Code:0442 Sub. Code: 3511

## 1058

## M.Sc. (Bio-Informatics) Fourth Semester MBIN-8017: Genomics and Proteomics – II

## Time allowed: 3 Hours

#### Max. Marks: 60

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

x-x-x

- I. Answer the following:
  - a) What is a hydropathy plot?
  - b) Differentiate between PFAM types?
  - c) Name 2 softwares for whole genome alignment?
  - d) What is the application of Phage display?
  - e) Name any two protein interaction databases?
  - f) Give full forms of RFLP and RAPD.
  - g) Name any disease associated with SNPs.
  - h) Which organization/s played a pivotal role in the HGP? (8x1<sup>1</sup>/<sub>2</sub>)

### <u>UNIT – I</u>

| II.  | a) What are SNPs? How are they detected?                        |         |
|------|---|---------|
|      | b) Compare and contrast physical and genetic maps.              | (8,4)   |
| III. | Write notes on the following:-                                  |         |
|      | a) AFLP   |         |
|      | b) Polymorphism and Mutations                                   |         |
|      | c) SNP database   | (6,4,2) |
|      | <u>UNIT – II</u>  |         |
| IV.  | a) How is MS used to characterize proteins and their complexes? |         |
|      | b) How is Yeast two hybrid system used to detect PPI?           | (2x6)   |
| v.   | Write notes on the following:-                                  |         |
|      | a) FRET   |         |
|      | b) GST pull down assay  |         |
|      | c) STRING database  | (3x4)   |
|      | c) STRING database  | (3x4)   |
|      |   |         |

# (2)

# <u>UNIT – III</u>

- VI. a) Discuss any one online tool for genome analysis.
  - b) Write a note on homology based protein tertiary structure prediction. (2x6)
- VII. a) Compare and contrast SCOP and CATH.

Departure departure de

b) What strategy is used by MUMMER for aligning large genomes? (2x6)

#### x - x - x