Total No. of Questions : 3]

SEAT No. :

P1748

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[5132]-401
M.Sc.
BIOTECHNOLOGY
BT-401: Genomics and Proteomics
(2013 Pattern) (Credit System) (Semester-IV)

Time : 3 Hours] ***[Max. Marks : 50***

Instructions to the candidates:

1) ***All questions are compulsory.***
2) ***Figures to the right indicate full marks.***
3) ***Neat labelled diagrams must be drawn wherever necessary.***

Q1) Attempt any four of the following: **[20]**

a) With a representative example of model organism. Explain the concept of genome at chromosome level.

b) Explain any one next generation sequencing method for analysis of whole genome.

c) Give the strategic method for cDNA library construction. Does it differ in prokaryotes & Eukaryotes?

d) Explain the principle and working of RNA Microarray.

e) Write notes on:

i) Zenicogenomis.

ii) Gene annotation.

Q2) Attempt any four of the following: **[20]**

a) Discuss the advantages and limitations of expressional Proteomics.

b) Explain the application of MALDI-TOF in proleomic study.

c) Describe the Bait approach to study the protein-protein interaction.

d) Give the principle and working of protein microarray.

e) Explain how 2D electrophoresis is helpful in comparative proteomic study.

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Q3) Attempt any one of the following: **[10]**

a) What are the strategies needed to integrate genomic and proteomic studies aiming to understand health and diseased states in humans? Explain with examples.

b) Give the importance of databases in-omic studies. Explain important tools with appropriate examples.

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