



LOYOLA COLLEGE (AUTONOMOUS), CHENNAI – 600 034

M.Sc. DEGREE EXAMINATION – BIOTECHNOLOGY

THIRD SEMESTER – NOVEMBER 2016

BT 3956 – FUNCTIONAL GENOMICS

Date: 11-11-2016

Dept. No.

Max. : 100 Marks

Time: 09:00-12:00

PART- A

Answer all the questions

I. Choose the correct answer

(5 × 1 = 5 Marks)

- Which among the following model organisms is a vertebrate?
a) *D. melanogaster* b) *Danio reiro* c) *S.cerevisiae* d) *E.coli*
- The following are used as substrates for microarray except
a) Silica b) Glass c) Nylon d) Quartz
- Which of the following uses Bridge PCR for amplification?
a) Pyrosequencing b) Sanger sequencing c) Illumina sequencing d) Em-PCR
- _____ is the process of identifying as many possible proteins in a test sample.
a) Mining b) Profiling
c) Protein network mapping d) Network expression
- Which among the following is NOT a reverse genetics approach?
a) RNAi b) Gene knockout c) Chemical mutagenesis d) Insertional mutagenesis

II State whether the following statements are True or False

(5 × 1 = 5 Marks)

- Molecular and genetic details of *C. elegans* is seen in FlyBase.
- Oligonucleotide arrays are more specific than cDNA arrays.
- Genome tiling arrays are used for genome wide mapping of RNA.
- The term proteome was coined by Marc Wilkins and colleagues.
- The primary miRNA is converted into pre miRNA by Dicer.

III Complete the following

(5 × 1 = 5 Marks)

- _____ is the genome browser at NCBI.
- _____ destroys the unused dNTPs in pyrosequencing.
- _____ is the study of the proteome, the protein complement of the genome.
- _____ is a common drug metabolizing enzyme.
- The size of miRNA transcript is _____.

IV. Answer the following, each within 50 words

(5 × 1 = 5 Marks)

- What are NATs?
- Give an example for a dye used in microarray.
- Mention the tag based technology used for RNA profiling.
- Write the principle of mass spectrometry?
- Define metabolomics.

PART - B

(5 × 8 = 40 Marks)

Answer the following, each within 500 words. Draw diagram wherever necessary.

21. a) Explain the four levels of annotation in model organisms.

OR

b) Draw the structure of an eucaryotic gene and mention any five properties that adds to the complexity of genome.

22. a) Write about facultative gene expression and constitutive gene expression.

OR

b) Employ a suitable PCR method for real time quantification of gene expression.

23. a) Compare Northern blot and reverse northern blot.

OR

b) Explain genome tiling microarray.

24. a) Elucidate with examples how online resources have enhanced the study of protein-protein interactions.

OR

b) Comment on the different techniques to study protein- protein interactions.

25. a) Write about gene silencing using antisense RNA.

OR

b) Compare the response of people to the Codeines and Imatinib.

PART - C

(2 × 20 = 40 Marks)

Answer any TWO of the following, within 1500 words. Draw diagram wherever necessary.

26. Elaborate on pyrosequencing and Illumina sequencing.

27. Write in detail about microarray technology and add a note on its applications.

28. Post-translational modification in proteins increase the functional diversity of the proteome. Discuss.

29. Explain in detail about siRNA and miRNA mediated RNA interference.
