



LOYOLA COLLEGE (AUTONOMOUS), CHENNAI – 600 034

M.Sc. DEGREE EXAMINATION – BIOTECHNOLOGY

THIRD SEMESTER – APRIL 2017

BT 3956- FUNCTIONAL GENOMICS

Date: 24-04-2017
09:00-12:00

Dept. No.

Max. : 100 Marks

PART – A

Answer ALL the Questions

I. Choose the correct answer

(5 x 1 = 5 Marks)

- Which of the following has largest genome?
a. Human b. *E.coli* c. *Pisum sativum* d. *Amoeba dubia*
- Which method is used for quantification of RNA?
a) Microarray b) RT-qPCR
c) Mass Spectrometry d) Northern Blotting
- _____ is the proteomic approach to determine how proteins interact with each other in living systems.
a) Mining b) Profiling c) Protein network mapping d) None of the above
- Which of the following uses antibodies to study proteins?
a) SPR b) FRET c) Mass Spectrometry d) Pull down assay
- Which among the following technique was used to study β globin gene?
a) RNAi b) Gene knockout c) Chemical mutagenesis d) Insertional mutagenesis

II. State whether the following are true or false

(5x1=5 Marks)

- Esterase is used to degrade the excess nucleotide bases
- Operons are not found in eucaryotes
- MPSS is a tag based technology.
- RNAi is a post transcriptional process.
- snRNAs are small nucleolar RNAs.

III. Complete the following

(5 x 1 = 5 Marks)

- The number of genes in yeast is _____.
- The company that introduced photolithography for making arrays was _____.
- Cy 5 gives _____ fluorescence
- In MS, the greater the m/z ratio, the _____ the speed of the ions
- Long ds RNA are cleaved by _____.

IV. Answer the following, each within 50 words

(5 x 1 = 5 Marks)

- What is C value paradox?
- Define metabolic profiling?
- Mention a tag based technology for transcriptomics

19. State any one advantage of dye flip in microarray.
20. What is pharmacodynamics?

PART - B

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

(5 x 8 = 40 Marks)

21. (a) Comment on Yeast and *E.coli* as model organisms
OR
(b) Discuss the complexities of eucaryotic genome.
22. (a) Employ a technique to estimate DNA during PCR.
OR
(b) Compare SAGE and MPSS.
23. (a) Employ a technique to estimate DNA during PCR.
OR
(b) Differentiate between cDNA array and oligonucleotide array.
24. (a) Elucidate with examples how online resources have enhanced the study of protein-protein interactions.
OR
(b) Review about the different types of protein-protein interactions.
25. (a) Briefly explain gene knockout through homologous recombination.
OR
(b) Outline the steps involved in metagenomics.

PART - C

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

(2 x 20 = 40 Marks)

26. Write in detail about gene expression study using microarray technology.
27. Elaborate on pyrosequencing and ion torrent sequencing.
28. Describe in detail any four experimental techniques to study protein-protein interaction
29. Explain in detail about any two reverse genetics approach.

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