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SARDAR PATEL UNIVERSITY

M. Sc. Integrated Biotechnology, Eight Semester Examination

Day and Date: Monday, 16-04-2018

Time: 02:00 Pm to 5:00 pm

Paper Code and Subject: PS08CIGGB3/ PS08CIGIB3/ PS08CIGMB3, 'O'mics

Total Marks: 70

Q-1 Multiple choice questions (**All are compulsory**). [8x1=8]

(i) In the Sanger method, the DNA sequence can be read directly from the gel
a) Randomly b) From the largest to the smallest fragments
c) From the smallest to the largest fragments d) None of the above

(ii) Which sequences remain as donor sequences at exon-intron boundaries?
a) AG b) GA c) GC d) AC

(iii) The first genomes sequenced via shotgun sequencing methods were
a) *Homo sapiens* and *Mus musculus* b) *Plasmodium vivax* and *Plasmodium falciparum*
c) *Haemophilus influenzae* and *Mycoplasma genitalium* d) All of the above

(iv) What is used for development of physical map of an organism?
a) RFLP b) Restriction mapping c) FISH d) RAPD

(v) Which is an *in-vivo* method for protein-protein interaction study?
a) Far-western analysis b) Solid-phase ELISA c) Yeast 2-hybrid system d) None of above

(vi) At certain pH environments isoelectric point affects the
a) solubility of molecule b) solubility of solvent
c) temperature d) density of molecule

(vii) Which of the following is **untrue** about SAGE?
a) This approach is much more efficient than the EST analysis
b) This approach is quite less efficient than the EST analysis
c) It uses a short nucleotide tag to define a gene transcript
d) It allows sequencing of multiple tags in a single clone

(viii) Expressed sequence tags (ESTs)
a) Are random genomic sequences b) Are usually larger than 2000 bp
c) Are cDNA sequences d) Can be used as genome markers

Q-2 Answer the following questions in short. (**Any Seven**) [7x2=14]

(i) What do you mean by codon bias?

(ii) What do you mean by CpG mutation rate?

(iii) Write a note on Homeobox.

(iv) Why assembly of draft genome sequence is important.

(v) Give the importance of shot gun sequencing.

(vi) Give the importance of adenosine phosphosulfate (APS) and Luciferase in Pyrosequencing.

(vii) Enlist advantages of STS over FISH and Restriction Mapping.

(viii) Write basic principle and applications of mass spectrometry.

(ix) Write a note on EST library

P.T.O

Q-3 (A) Discuss Maxam and Gilbert method of sequencing giving its advantages and disadvantageous. [06]

(B) Explain the principle and workflow of microarray technique. [06]

OR

(B) Give a detailed account on C-value paradox, C-value enigma and Exon-Intron boundaries. [06]

Q-4 (A) Discuss the strategies involved in human genome sequencing. [06]

(B) Explain BAC library construction in detail. [06]

OR

(B) Discuss the Gene content of the human genome in detail. [06]

Q-5 (A) Discuss identification and analysis of protein by 2D electrophoresis. [06]

(B) Give significance of study of protein-protein interaction. Explain yeast-two-hybrid system. [06]

OR

(B) Explain MALDI-TOF in detail. [06]

Q-6 (A) Discuss the principle and method of SAGE technique for measuring differential gene expression. What are the current applications of SAGE? [06]

(B) Explain the method and importance of Whole transcriptome shotgun sequencing (*WTSS*) or RNA sequencing method. What are the advantages and disadvantages of these techniques? [06]

OR

(B) Define metabolomics and give an overview of Human metabolome project. [06]

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