Register Number.....

M.TECH. DEGREE EXAMINATIONS:OCTOBER /NOVEMBER - 2008

Third Semester

BIOTECHNOLOGY

P07BTE34 Genomics and Proteomics

Time: Three Hours **Maximum Marks: 100**

Answer All Questions:-

Part A (20x1= 20 Marks)

1. The first genome to be completely sequenced is

   A) E. coli B) Bacteriophage C) H. influenzae D) Drosophila

2. Yeast genome contains
   A) 25,000 genes B) 10,000 genes C) 6,000 genes D) 30,000 genes

3. The first multi cellular animal genome completely sequenced was
   A) Drosophila B) human C) Mouse D) C. elegans

4. The least frequent SNPs found in Human genome by the SNP Consortium is

   A) Noncoding 5'UTR
   B) Coding, nonsynonymous, non conservative
   C) Coding, nonsynonymous, conservative
   D) Coding synonymous

5. Choose the odd technique out

   A) Hybridization mapping B) optical mapping C) radiation hybrid mapping
   D) Happy mapping

6. Reverse genetics is

   A) Genes for which function is unknown are deliberately mutated and introduced into host to study the effect
   B) Identifying mutant phenotypes and finding the gene by mapping
   C) Random mutagenesis by physical or chemical mutagens
   D) Studying present day findings of genetics followed by Mendelian findings

7. The maximum size of DNA that can be resolved in PFGE is
   A) 100Kb B) 1000 kb C) 1Mb D) 10MB

8. DNA Sequencing method which exploits hybridization technique is

   A) Sangers dideoxy method B) microarray
   C) pyrosequencing D) chemical method

9. mRNA quantification by sequencing is followed in

   A) EST B) cDNA array C) SAGE D) Differential Display

10. Megaclone is
    A) YAC
    B) BAC with high insert capacity
    C) Clone obtained from Megalovirus
    D) glass beads with unique anti tags in MPSS technique.

11. Neural network method of gene prediction tool is

A) FGENEH B) GENESCAN C) GRAIL D)GENIE

12. Choose the wrong statement regarding Differential display PCR

A) Aids in finding genes expressed at specific tissues
B) Could display the mRNA which is unique for a development stage
C) up regulated and down regulated genes for any disease condition can be studied
D) Genes with codon bias can be identified

13. Which statement does not correlate to proteomics

A) system biology B) individual proteins
C) protein complex mixtures D) partial sequence analysis

14. In MS-MS analysis, Neutral lose of ammonia shows a difference of
A) 18u B) 17u C) 5u D) 28u

15. The snapshot of the proteome is obtained from

A) MUDPIT B) 2DSDSPAGE C) MALDI-TOF D) ESI-MS

16. Parent ion scanning mode is

A) scan-collision-select B) scan -No collision-RF
C) select-collision-scan D) RF-No collision-scan

17. Rolling disk method is followed in

A) Image analysis B) spot detection C) gel matching D) image processing

18. Which technique can not be used for protein interaction studies?

A) Co-immunoprecipitation B) Yeast two hybrid system
C) cytogenetic analysis D) Fluorescence resonance Energy Transfer

19. Choose the odd one out
A) Leptin B) glycosyl phosphatidyl inositol
C) N-linked Glycans D) O-linked Glycans

20. Phosphorylation in peptides can be detected by

A) MS/MS mode B) precursor ion scanning
C) Neutral loss scan D) PSD-MALDI

Part B (5x16=80 Marks)

21. A). Write briefly about the importance, genome size, gene content and striking features of genome sequencing projects of a model plant, animal and fungi namely Arabidopsis, Drosophila and Yeast respectively (16 marks)

OR

21. B) (i) Describe Celera Genomics's Shotgun sequencing strategy of HGP (8 marks)

(ii) Which method of sequencing is used in an automated sequencer? Compare Sanger method and Maxum Gilbert method of sequencing (8 marks)

22. A) Describe clone by clone approach for sequencing a complete eukaryotic genome

(i) Genetic map, and physical map generation strategies to be followed (8 marks)

(ii) contigs development and filling gap strategies (8 marks)

OR

22. B) (i) What is a STS marker? How they can be assembled in a map discuss minimum two strategies to order/ arrange them if they are from different YAC clones. (8 marks)

(ii) Describe the FISH technique for identification of chromosome and mapping of human genes (8 marks)

23. A) (i) Mention two gene prediction programs and explain the algorithms used in prediction of eukaryotic genes (8marks)

(ii) Explain Differential Display PCR technique Step by step by a flow chart and its applications (8 marks)

OR

23. B) (i) How SAGE analysis is performed? What is the advantage over DDPCR? (8marks)

(ii) What is functional genomics? Disscuss two approaches to annotate a completely sequenced genome by this approaches. (8 marks)

24. A) (i) What is Mass spectrometry? How a proteome is analyzed using MALDI-TOF analyzer (8marks)

(ii) Why the 2D SDS PAGE is considered "the proteomics tool" even after 5 decades after its invention? Discuss. (8 marks)

OR

24. B) Explain ESI-MS with the five modes of operation using triple quadrupole equipment (16 marks)

25. A) (i) How phosphor peptides are isolated and enriched? Describe the methods (8 marks)

(ii) What are the post translational modifications observed in a functional protein? Discuss its significance in cell metabolism (8 marks)

OR

25. B) (i) What are glycoproteins? How they are identified? What is the functional significance of glycosylation ? (8 marks)

(ii) Elaborate on the methods to analyze the phosphorylated amino acids (8 marks)

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