KUMARAGURU college of technology
character is life

Register Number: ……..

B.TECH DEGREE EXAMINATIONS: NOV 2015

(Regulation 2009)

Seventh Semester

BIOTECHNOLOGY

BTY211: Genomics & Proteomics

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

Answer all the Questions:-

PART A (10 x 1 = 10 Marks)

1. Which one is the limitation of clone by clone approach of genome sequencing
   a) Sequencing b) Assembly of repeat sequences
   c) need for a genetic/physical map d) cost
2. Reverse genetics is _____
   a) Identifying gene function from mutants b) Identification of mutants
   c) gene knock out and function determination d) identification of natural gene mutants and genes
3. Which is not a PCR based Marker
   a) AFLP b) STS
   c) RFLP d) SSR
4. The finest resolution of a physical map is _____
   a) 0.1cM b) 1Mb
   c) 1kb d) nucleotide
5. A genetic map is developed by _____
   a) RH mapping b) Recombination frequency
   c) FISH d) Chromosomal walking
6. Capillary electrophoresis followed in automated sequencing because _____
   a) Slab gels very short b) Four color dyes can be used for dideoxy mixes
   c) Radio label has to be used d) End labeling of primer is possible
7. Write the correct statement about microarray
   a) Absolute quantification of mRNA b) SNP and Expression analysis possible

c) Differential display is not possible
d) Since two hybridization is performed error level is high

8. Choose an odd statement about SAGE Technique
   a) Differentiation of transcriptomes
   b) Sequencing involved so absolute quantification
   c) Hybridization involved so relative quantification
   d) Number of transcripts present and quantity of each transcripts ismeasured

9. Cathodic drift results in _____
   a) Electrendosmotic flow
   b) SCA which are not fixed
   c) Loss of basic proteins in gradient beyond pH7
   d) Immobiline

10. Proteomics is_____
   a) another term for genomics in human
   b) study of proteins produced by a particular gene
   c) study of collection of proteins by a particular cell
   d) proof for single gene codes for single protein

PART B (10 x 2 = 20 Marks)

11. Differentiate EST and STS markers.
12. Describe chromosomal walking briefly.
13. Mention the role of padlock probes in gap filling.
14. Identify a chromosome separation technique and its principle.
15. Justify the superiority of Sanger sequencing over chemical method.
16. Outline the shotgun strategy of genome sequencing.
17. Compare subtractive hybridization and DDRT-PCR.
18. Define “Synteny” in comparative genomics.
19. Justify why 2D-SDS PAGE is referred as snapshot of proteome.
20. Survey the protein stains available .

PART C (5 x 14 = 70 Marks)

21. a) What is the present understanding on the relationship between genome size, complexity of genome, organism, and number of genes. Answer with few salient findings in genome projects.

(OR)

b) What is HGP? Narrate the history and important techniques used in the project.

22. a) Sketch the conversion of a genetic map to physical map using RH mapping and restriction mapping techniques.

(OR)

b) Give a detailed note on the various techniques used in joining contigs in physical mapping?

23. a) Compare the two strategies adopted in sequencing the Human genome project and discuss their advantages and limitations.

(OR)

b) Elaborate on the modern DNA sequencers and next generation sequencing methods.

24. a) Compare the two microarray platforms of gene expression and SNP analysis and spell out their significance.

(OR)

b) Narrate the steps in SAGE technique and comment on the superiority over microarray method of transcriptome analysis

25. a) Demonstrate how the 2D-SDS PAGE technique can be exploited as a proteome analysis tool

(OR)

b) Classify the various modes of operation of ESI-MS TQ instrument to analyse a proteome and the post translational modifications.

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