



AJEENKYA

D Y PATIL UNIVERSITY

End Term Examinations (December 2018)

School : School of Engineering **Program:** M.Tech. Bioengineering (Biotech)

Course: Genomics and Proteomics **Course Code:** BEN512

Semester: I **Max Marks:** 20 **Duration (mins) :** 60

Note : Attempt all questions. Each carry one mark.

Q1. Which of following vector was extensively used in human genome project?

- a) YAC b) Cosmid
- c) Plasmid d) a and b

Q2. The study of full complement of proteins expressed by a genome is called

- a) Proteome b) Proteomics
- c) Genomics d) Protein formation

Q3. The effects of protein on an entire organism is described in?

- a) Phenotypic function b) Cellular function
- c) Molecular function d) Structural genomics

Q4. The precise biochemical activity of a protein is described in?

- a) Phenotypic function b) Cellular function
- c) Molecular function d) Structural genomics

Q5. Sequencing of genomic DNA is included in?

- a) Phenotypic function b) Cellular function
- c) Molecular function d) Structural genomics

Q6. The goal of structural proteomics project is

- a) To crystallize and determine the structure of as many proteins as possible, in many cases with little or no existing information about protein function
- b) To identify and sequence of all the genes present in the human body
- c) To introduce new genes to human beings
- d) To remove disease causing genes from humans

Q7. Collection of microscopic DNA spots attached to solid surface are

- a) Ortholog b) Synteny
- c) Paralog d) Microarray?

Q8. A cDNA library:

- a) Can also be called an expressed sequence tag (EST) library.
- b) Consists of coding sequences from genes that are expressed.
- c) Is specific to the set of conditions under which the original mRNA was generated.
- d) All of these e) None of these.?

Q9. The technique of subtractive hybridization allows identification of genes that are selectively activated under a certain set of conditions.

- a) True b) False?
- c) all d) None

Q10. Which of these might be an advantage to genetic testing of individuals via microarrays?

- a) Many different potential mutations in a single gene could be tested at once.
- b) Expression patterns of many different genes can be analyzed simultaneously.
- c) Microarray analysis can provide information on relative levels of expression of particular genes.
- d) All of these e) None of these?

Q11. The two most common processes that lead to production of multiple functional proteins from the same DNA sequence are:

- a) RNA editing and alternative splicing.
- b) Protein folding and posttranslational covalent modifications.
- c) Alternative splicing and posttranslational covalent modifications.
- d) Posttranslational covalent modification and transcriptional regulation.
- e) RNA editing and base modification.

Q12. In two dimensional gel electrophoresis:

- a) Different forms of the same protein will tend to migrate at the same position.
- b) Up to about a hundred different proteins can be distinguished from each other.
- c) Proteins with similar functions will be located near each other.
- d) All of these.
- e) None of these.?

Q13. Tandem mass spectrometry can be used to determine the specific amino acid sequence of a protein

- a) True
- b) False
- c) All of above
- d) None of above

Q14. Functional protein microarrays can identify protein functions only if their sequence is known.

- a) True
- b) False?
- c) All of above
- d) None of above

Q15. How many potential open reading frames are present in a DNA sequence?

- a) One
- b) Three
- c) Six
- d) More than Six
- e) None of these:

Q16. A computer program must be written in a specific language in order for the computer to understand what needs to be done.

- a) True
- b) False?
- c) All of above
- d) None of above

Q17. Which of these would not be an example of sequence element?

- a) A recognition site for binding of a particular transcription factor.
- b) A restriction endonuclease cut site.
- c) An open reading frame.

d) A stop codon.?

Q18. In an analysis of eukaryotic gene, you identify several nonoverlapping open reading frames, but they are not all in the same frame. Which explanation makes the most sense?

- a) By random chance, a second reading frame within the gene also has an open reading frame.
- b) This gene includes introns which are not multiples of three.
- c) This is a mutant allele that has had several small insertions.
- d) All of these.?

Q19. Identification of a gene that does not fit the typical patterns for eukaryotic gene structure would not have a dramatic effect on bioinformatics.

- a) True
- b) False?
- c) All of above
- d) None of above

Q20. Secondary structure of RNA molecules:

- a) Depends on complementary base pairing.
- b) Is generated by covalent bonding between sections of the RNA molecule.
- c) Can be described as interactions between portions of the backbone of the molecule.
- d) Does not have an impact on function of the molecule.?