B.Sc. BIOTECHNOLOGY
SIXTH SEMESTER
GENOMICS AND PROTEOMICS
BBT-602
[USE OMR SHEET FOR OBJECTIVE PART]

SET
B

Duration: 3 hrs.

Full Marks: 70

(**Objective**)

Time: 30 mins.

Marks: 20

Choose the correct answer from the following:

1×20=20

1. Following is/are example of web based server and software for genome analysis:
   a. VISTA
   b. Ensemble
   c. Neither a nor b
   d. Both a and b

2. Proteins, on reaction with strong acids or bases results in:
   a. Protonation
   b. Deprotonation
   c. Both a and b
   d. Neither a nor b

3. Reduction to sulphydryl groups of proteins occurs in the presence of:
   a. Ethanol
   b. B-mercaptoethanol
   c. Detergents
   d. None of the above

4. Occurrence of electrostatic attraction between molecules of proteins resulting in the formation of a precipitate takes place in:
   a. Isoelectric precipitation
   b. Above pI
   c. Below pI
   d. None of the above

5. In α-helix, each residue is related to the next one by a rise of:
   a. 1.2 Å
   b. 1.7 Å
   c. 1.4 Å
   d. 1.5 Å

6. Amino acid residues present in turns:
   a. Glycine and Aspertate
   b. Leucine and Proline
   c. Leucine and Valine
   d. Glycine and Proline

7. In SDS-PAGE, SDS act as a:
   a. Reducing agent
   b. Disulphide breakpoint
   c. Charging agent
   d. All of the above

8. Example of porous beads is/are:
   a. Sepharose
   b. Dextran
   c. Polyacrylamide
   d. All of the above

9. In mass-spectrometry, in velocity selector region, the strength of magnetic field is.......... the strength of electric field.
   a. Equal to
   b. Greater then
   c. Smaller then
   d. None of the above

10. In 2D-PAGE, the anode of the IPG strip is dipped in:
    a. Triethanol amine
    b. Phosphoric acid
    c. Sodium hydroxide
    d. None of the above

11. The term 'Genomics' was coined by:
    a. Thomas Raderick
    b. Nethen Wright
    c. Jessy Ross
    d. None of the above

12. Functional genomics includes:
    a. Forward genetics
    b. Reverse genetics
    c. Both a and b
    d. Only a

13. Chemical sequencing is another name of:
    a. Sanger's sequencing
    b. Maxam-Gilbert sequencing
    c. Automated DNA sequencing
    d. None of the above

14. Oxygen at position 3 is absent in:
    a. Pyro sequencing
    b. Maxam-Gilbert sequencing
    c. Sanger's sequencing
    d. None of the above

15. In pyrosequencing, light is given by the final product:
    a. Sulfurylase enzyme
    b. Luciferase enzyme
    c. ATP
    d. Luciferin

16. Most commonly used short segment DNA sequencing is:
    a. Pyro sequencing
    b. Maxam-Gilbert sequencing
    c. Sanger's sequencing
    d. Automated DNA sequencing

17. Contigs are:
    a. Short DNA fragments
    b. Long DNA fragments
    c. Single broken nucleotides
    d. None of the above

18. BACs are used in:
    a. Shotgun sequencing
    b. Clone contig method
    c. Pyrosequencing
    d. None of the above

19. Example of genome assembly tool:
    a. Phrap
    b. Phred
    c. Assembler 2.0
    d. All of the above

20. Programme used to find overlapping regions among fragments and to align them is:
    a. GelMerge
    b. GelAssemble
    c. GelView
    d. GelDisassemble

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(Descriptive)

Time : 2 hr. 30 mins.   Marks : 50

[Answer question no.1 & any four (4) from the rest]

1. Explain Maxam-Gilbert and Sanger's method of DNA sequencing with   5+5=10
   proper diagram.

2. Write short notes on: 5+5=10
   a) Pyrosequencing
   b) Shotgun sequencing

3. Elaborate with examples web based servers and softwares for genome   10
   analysis.

4. Write a note on selected model organisms of Genomes and databases.   10

5. What is Edman's degradation? Explain with proper diagram.   10

6. Differentiate between SDS-PAGE and Native PAGE. Write down the   10
   advantages and disadvantages.

7. Explain 2D-PAGE with sample preparation, solubilization, reduction,   10
   resolution and reproducibility.

8. What is mass-spectrometry based method of protein identification?   10

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