U.G. 6th Semester Examination - 2022

Molecular Biology and Biotechnology

[HONOURS]

Course Code : MBBT-H-602-T-CCR-14

(Genomics & Proteomics)

Full Marks : 40 Time : $2\frac{1}{2}$ Hours

The figures in the right-hand margin indicate marks. Candidates are required to give their answers in their own words as far as practicable.

1. Answer any **five** of the following : 2×5=10

   a) How will you close a sequence gap and a physical gap in whole genome shotgun sequencing?

   b) Name two algorithms that can be applied for assembly of reads into complete sequence.

   c) Write the full form of: ENCODE, TAIR, MGI, SGD.

   d) Explain the terms: Comparative genomics and Meta-genomics.

   e) Why does a protein tend to precipitate near its iso-electric pH?

   f) How could you rupture the hydrophobic interactions in a protein?

   g) What are the demerits of Edman degradation as a method of protein sequencing?

   h) Differentiate Structural proteomics from Functional proteomics.

2. Answer any **two** of the following: 5×2=10

   a) Explain Maxam Gilbert method of DNA sequencing. What are its disadvantages? 3+2

   b) Differentiate species specific database from global genome browser. Mention the features of UCSC, ENSEMBL genome browser and NCBI genome browser. 2+3

   c) Describe the process of Peptide Mass Fingerprinting.

   d) Differentiate Domains from Motifs in a protein structure. What are the patterns of hydrogen bonding in different secondary structural element of a protein? $2\frac{1}{2}+2\frac{1}{2}$

3. Answer any **two** of the following: 10×2=20

   a) What is chromosome walking? Explain how probe hybridization and PCR can be used as methods for chromosome walking. Describe the process of pyrosequencing. 2+4+4

b) What parameters must be checked for selection of fragments during sequence assembly? A sequence fragment is having a low overall Q-score, but there are multiple fragments with same sequence in the population of fragments. Under what circumstances will you select this fragment for assembly? How will you filter reads of correct sequence from a population of correct and incorrect sequence reads? Name two software used for trimming and filtering reads.

$2\frac{1}{2}+2\frac{1}{2}+3+2$

c) How can you analyze the proteome of a normal cell and a cancer cell using 2D gel electrophoresis? What is the significance of this analysis in clinical research? Explain the process of *de novo* sequencing of proteins using mass spectrometry. 4+2+4

d) Describe the principle of separation of proteins in SDS PAGE. Size Exclusion Chromatography is a separation and an analytical technique. Explain. What are the applications of analytical ultracentrifugation? 3+4+3

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