U.G. 6th Semester Examination-2021

Molecular Biology & Biotechnology

[HONOURS]

Course Code : MBBT-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 following: 2×5=10

   a) What is the role of dimethyl sulphate and hydrazine in Maxam-Gilbert method of sequencing?

   b) Mention few automations of Sanger method of DNA sequencing.

   c) What is the application of FASTX-Toolkit and Fast QC?

   d) Describe the principle of peptide sequencing by Edman degradation.

   e) State the significance of Ramachandran plot in validation of three dimensional structure of proteins.

   f) What is Two-dimensional difference gel electrophoresis (2D DIGE)?

   g) State the role of salt bridges in stabilization of the protein structure.

   h) Proteomic profiles reflect cellular responses to genomic, epigenomic, and environmental alterations. Explain.

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

   a) Define the following terms with respect to assembly of sequences: i) N50 ii) Q-score iii) FASTQ format iv) k-mer size v) Contig 1+l+l+1+1

   b) Explain the principle and process of Pyrosequencing. What is the importance of dATPαS in Pyrosequencing? 3+2

   c) Explain the two parameters used for separation of proteins in a 2D gel. The 2D gel profile of a normal cell and a cancer cell from the same tissue is provided. Can you identify the potential oncoproteins and tumour suppressor proteins? Explain. 2+3

   d) Specifically mention the bonds and interactions involved in secondary, tertiary and quaternary structure of proteins. The solubility of a protein reduces if the pH of the buffer is close to the pl of the protein. Explain. 3+2

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

a) Name one sequence assembly software that is used to assemble the read sequences into complete sequence. Explain the algorithm used by the software to assemble large number of read sequences. Differentiate between whole genome shotgun sequencing and hierarchical shotgun sequencing approach mentioning their advantages. 1+4+5

b) Differentiate (with example) between i) Web-based genome browser and Stand alone application ii) Multiple species genome browser and Species specific genome browser. Write the significance of Ensembl genome browser. What is the full form of i) MGI ii) TAIR iii) SGD iv) ZFIN 2+3+3+2

c) In a SEC column calibrated by globular proteins, a 25 kDa protein should have an elution volume of ~85 ml. However, this 25 kDa protein is eluting at ~80 ml corresponding to a molecular weight of 33 kDa. What can you infer about the shape of the protein? How can you use sedimentation analysis to determine the physiological states (dimer, oligomer, etc.) of proteins and protein-protein interaction? What is the role of SDS, β-ME/DTT and heating in SDS PAGE? In spite of availability of Native PAGE protein markers, Native PAGE is not an authentic technique for determination of molecular weight of proteins. Explain. 2+3+3+2

d) Why peptide sequencing by mass spectrometry is prefered over traditional techniques of protein sequencing? The peptide mass fingerprint generated from a protein does not show any match in the database. What approach would you adapt to sequence the protein and why? Explain the working principle and entire process of De novo peptide sequencing using mass spectrometric data. 2+3+5

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