

2018

BIOTECHNOLOGY

BIT: 402

COMPUTATIONAL BIOLOGY

Full Marks: 80

Time: 3 hours

The figures in the margin indicates full marks for the questions :

1. Find out the correct answer of the following questions (*any five*):
1x5=5
 - a. Which of the following amino acids is least mutable according to the PAM scoring matrix?
 - i. Alanine
 - ii. Glutamine
 - iii. Methionine
 - iv. Cysteine
 - b. In a position-specific scoring matrix, the column heading can have the 20 amino acids, and the rows can represent the residues of a query sequence. Within the matrix, the score for any given amino acid residue is assigned based on :
 - i. A PAM or BLOSUM matrix
 - ii. Its frequency of occurrence in a multiple sequence alignment
 - iii. Its background frequency of occurrence
 - iv. The sum of its neighboring amino acids
 - c. The main difference between Pfam-A and Pfam-B is that :
 - i. Pfam-A is manually curated and Pfam-B is automatically curated
 - ii. Pfam-A uses hidden Markov models while Pfam-B does not.
 - iii. Pfam-A provides full length protein alignments while Pfam-B aligns protein fragments

- c. Local and Global Energy Minimization method
 - d. Molecular Mechanics and *ab initio* method for molecular modelling
 - e. Ligand based and Structure based Drug Designing
5. Describe *any two* from the following : 8x2=16
- a. Describe the experimental procedure and merits of NMR and X-ray crystallography in terms of determination of protein structure. 4+4=8
 - b. State the structural features of alpha helix and beta sheet. Compare parallel and anti parallel strand. 4+4=8
 - c. What is super secondary structure? Mention two different super secondary structures? Mention in which type of proteins they are observed and their functional importance. 2+2+2+2=8
6. Describe *any two* from the following : 12x2=24
- a. Discuss the protein secondary structure prediction methods. How prediction accuracy is compared? 10+2=12
 - b. How different types of trans-membrane protein structures are predicted? Describe with illustrations. 10+2=12
 - c. Describe the homology modeling method of protein tertiary structure prediction. 12
 - d. Describe the methods for protein-protein structure prediction by highlighting the tools used. 12