

[1917]

SARDAR PATEL UNIVERSITY**External Examination****M.Sc. (Microbiology) Semester -III****Subject: PS03EBIC22 - Bioinformatics****Monday, 29th October, 2018****Time: 02:00 p.m. to 05:00 p.m.****Total marks: 70****Note: Figures to right side indicate marks.****Q.1 Choose the most appropriate alternative for the following questions:****[8]**

1. Sequence submission tool of EBI database is _____.
 - A) Sakura
 - B) BankIt and Sequin
 - C) MSS
 - D) WebIn
 - E) None of Above
2. In PDB file format of protein, right handed alpha helix is denoted by number _____.
 - A) 5
 - B) 1
 - C) 3
 - D) 2
 - E) None of Above
3. _____ method predicts the evolutionary tree (or trees) that minimize the number of steps required to generate the observed variation in the sequences.
 - A) UPGMA
 - B) Maximum Parsimony
 - C) NJ
 - D) Maximum likelihood
 - E) None of Above
4. Which of these is not a primary database?
 - A) REBASE
 - B) DDBJ
 - C) PDB
 - D) GenBank
 - E) None of Above
5. _____ is induced electrical interactions which contribute significantly to conformational stability in the interior of the protein.
 - A) Hydrophilic interactions
 - B) Covalent interactions
 - C) Van der Waals interactions
 - D) Hydrophobic interactions
 - E) None of above.

B. Discuss the Chou Fasman method for protein secondary structure prediction. [6]

OR

B. Explain gene prediction. Discuss different parameters that helps in *in-silico* gene prediction process for eukaryotic organism. [6]

Q.5 A. Define phylogenetics analysis? Construct the phylogenetic tree by using UPGMA algorithm with given distance matrix. [6]

	A	B	C	D	E
A	0	22	39	39	41
B		0	41	41	43
C			0	18	20
D				0	10
E					0

B. Describe acquisition process of protein structure information from protein database by explaining UniProt database. [6]

OR

B. What is scoring matrices? Explain how the values in scoring matrix are derived by discussing value derivation method of PAM1 scoring matrix. [6]

Q.6 A. Give flow chart of drug discovery steps and discuss major six stages of drug discovery process. [6]

B. Describe protein structure alignment. Explain the how VAST tool aligns protein structure. [6]

OR

B. Explain secondary structure of protein and discuss about various types of helices found in protein structure. [6]



