

SEAT No. _____

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[91]

SARDAR PATEL UNIVERSITY

External Examination

M.Sc. Semester -III

Subject: PS03EMIC22/ PS03EBIC22/ PS03EBIT22 - Bioinformatics

Tuesday, 5th January, 2021

Time: 02:00 p.m. to 04:00 p.m.

Total marks: 70

Note: Figures to right side indicate marks.

[08]

Q.1

A. Choose the most appropriate alternative for the following questions:

1. The unit of classification of structure in SCOP is the protein _____.
A) Name
B) Orientation
C) Properties
D) Domain
E) None of Above
2. *Ab initio* Methods for protein structure prediction are considered as:
A) Template-Free Modeling
B) Free-Template Modeling
C) Template Modeling
D) All of above
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 a protein model evaluation tool.
A) CODA
B) GROMOS
C) PROCHECK
D) PRALINE
E) None of above.
6. The Protein Data Bank (PDB) is a database which does not contain three-dimensional structure of protein obtained by:
A) Computer Modeling
B) X-ray crystallography
C) Cryo-electron microscopy
D) NMR spectroscopy
E) None of Above

[]

[P.T.O.]

4. Write short note on Entrez and its role in the Bioinformatics Analysis.
 5. Explain motif & domain in context of protein structure.
 6. Explain dihedral angles present in the primary structure of protein.
 7. Explain different types of pairwise sequence alignment.
 8. Write short note on DDBJ and its importance in the Bioinformatics analysis.
 9. Explain various possible secondary structures of RNA.
- Q.3 Describe Dot Plot method for pairwise sequence alignment with example and discuss on various interpretation of it. [8]

OR

- Q3. Enlist various methods for protein secondary structure prediction and discuss the Chou Fasman method with necessary details. [8]
- Q.4 Discuss importance of RNA secondary structure prediction in biological analysis and describe circle plot method for RNA secondary structures prediction with example using given sequence ACGUGCCACGAUUCAACGUGGCACAG. [8]

OR

- Q4. Enlist various databases available for the protein classification based on structure. Describe various classification levels of SCOP database. [8]
- Q.5 Discuss various steps for homology protein modeling method to build 3D protein models and describe the SPDBV tool for protein modeling. [8]
- Q5. What is scoring matrices? Explain how the values in scoring matrix are derived by discussing value derivation method of PAM1 scoring matrix. [8]
- Q.6 Define phylogenetics analysis? Construct the phylogenetic tree by using UPGMA algorithm with given distance matrix. [8]

	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

OR

- Q6. Describe secondary structure of protein and discuss structural details of various types of helices found in protein. [8]

