[944]   **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.*

Q.1   [08]

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

7. In classical genetics, _____ describes the physical co-localization of genetic loci on the same chromosome within an individual or species.
    A) Count   B) Map
    C) Synteny   D) Signature
    E) None of above.

8. The _____ is an extremely rare secondary structural element in proteins.
    A) π - helix   B) α helix
    C) 3_{10} helix   D) ϕ helix
    E) None of above.

B.   Answer the following questions in appropriate way: [16]

1. QSAR stands for :

2. ADMET stands for :

3. CASP stands for :

4. CDART stands for :

5. CFSSP stands for :

6. BLAT stands for :

7. A contig is a set of _____ DNA segments that together represent a consensus region of DNA.

8. The chain termination method of DNA sequencing "Sanger sequencing" can only be used for short DNA strands of _____ base pairs.

9. In bioinformatics, _____ refers to aligning and merging fragments from a longer DNA sequence in order to reconstruct the original sequence.

10. Transcriptomics is the study of the _____ using high-throughput methods.

11. _____ is an experimental tool that helps taxonomists to find closest database neighbors of submitted query sequences.

12. _____ is web-based sequence submission tool for one or a few submissions to the GenBank database, designed to make the submission process quick and easy.

13. Margaret Dayhoff developed the BLOSUM matrices in the year 1978.   [T/F]

14. PIR was established by NBRF in 1984.   [T/F]

15. The DNA Data Bank of Japan is a biological database that collects DNA sequences from only Japan.   [T/F]

16. The alignment procedure that tries to align regions with high level of matches without considering the alignment of rest of the sequences is Local alignment.   [T/F]

Q.2   Attempt _any seven out of nine_ form the following questions: [14]

1. Write short note on any one protein 3D visualization tools.

2. Write short note on transition and transversion substitution in nucleotide sequence alignment.

3. Explain Paralogous and Orthologus relationship.

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 detials. [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]

OR

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]

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[3]