

SEAT No. \_\_\_\_\_

No. of Printed Pages: 03

[40 &amp; A-28]

**SARDAR PATEL UNIVERSITY****External Examination****M.Sc. (Microbiology) Semester -IV****Subject: PS04EMIC02 - Bioinformatics****Friday, 13<sup>th</sup> April, 2018****Time: 10:00 a.m. to 01:00 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 GenBank database is \_\_\_\_\_.  
 A) BankIn and Bankout  
 B) BankIt and Sequin  
 C) Entrez  
 D) SubmitIt  
 E) None of Above
2. In GCG format of nucleotide sequence, nucleotide sequence starts with \_\_\_\_\_.  
 A) Start  
 B) SEQ  
 C) Origin  
 D) SQ  
 E) None of Above
3. According to IUPAC Nucleotide base code for c or g or a; i.e. not t is represented by \_\_\_\_\_ letter.  
 A) b  
 B) d  
 C) v  
 D) e  
 E) None of Above
4. According to IUPAC-IUB Joint Commission on Biochemical Nomenclature glutamic acid is represented by \_\_\_\_\_ letter.  
 A) K  
 B) G  
 C) E  
 D) M  
 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.
6. \_\_\_\_\_ may not be an indicator of an evolutionary relationship.  
 A) Sequence similarity  
 B) Genome similarity  
 C) Structural similarity  
 D) All of Above  
 E) None of Above

C.P.T.O.)

7. The primary sequence of a protein is called as \_\_\_\_\_.  
 A) Consensus B) Conformation  
 C) Configuration D) Conservation  
 E) None of above.
8. The \_\_\_\_\_ is an extremely rare secondary structural element in proteins.  
 A)  $\pi$  - helix B)  $\alpha$  helix  
 C)  $3_{10}$  helix D)  $\phi$  helix  
 E) None of above.

**Q.2 Attempt any seven of the following questions:**

**[14]**

1. Explain different types of Gap penalties for pairwise sequence alignment.
2. Write short note on Neural Networks and its use in Bioinformatics.
3. Write short note on genebank database and its detailed file format.
4. Write short note on gene prediction.
5. Write short note on secondary databases of bioinformatics.
6. Explain dihedral angles present in the primary structure of protein.
7. Explain importance of IC 50 value in drug designing.
8. Explain Quantitative structure-activity relationship models (QSAR models).
9. Write short note on Transcriptomics.

**Q.3 A. Discuss on Dot Plot method of pairwise sequence alignment with example.**

**[6]**

**B. Enlist and describe various types of BLAST programme available for sequence alignment.**

**[6]**

**OR**

**B. Describe local and global alignment algorithm for pairwise sequence alignment.**

**[6]**

**Q.4 A. Describe the protein structure prediction and usefulness of Ramachandran plot in protein structure evaluation.**

**[6]**

**B. Define and explain Sensitivity and Specificity for measuring sequence detection efficiency.**

**[6]**

**OR**

**B. Explain gene prediction. Discuss different parameters that help in the gene prediction for eukaryotic organism.**

**[6]**

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

	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 [6]  
explaining UniProt database.

OR

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

- Q.6 A. Explain any one maskless photodeprotection technology for construction of oligonucleotide [6]  
microarray synthesis.

- B. Explain primary, secondary, and tertiary protein structure with diagrams. [6]

OR

- B. Give flow chart of drug discovery pipeline and discuss major areas of interest in process of [6]  
drug discovery.

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