

GUJARAT TECHNOLOGICAL UNIVERSITY**BE - SEMESTER-V (NEW) EXAMINATION – WINTER 2023****Subject Code:3150407****Date:11-12-2023****Subject Name:Fundamentals and Applications of Bioinformatics****Time:10:30 AM TO 01:00 PM****Total Marks:70****Instructions:**

1. Attempt all questions.
2. Make suitable assumptions wherever necessary.
3. Figures to the right indicate full marks.
4. Simple and non-programmable scientific calculators are allowed.

		MARKS
Q.1	(a) Compare Uniprot, swissprot and PIR.	03
	(b) Discuss protein structure databases.	04
	(c) Compare CATH and SCOP.	07
Q.2	(a) What are various features and functionality to use pymol? How can you visualise structural differences among homologous proteins using pymol.	03
	(b) Discuss a case study of a genomics research using any bioinformatics database for research.	04
	(c) Discuss Tools and databases used for CADD.	07
	OR	
	(c) Discuss application of python in bioinformatics.	07
Q.3	(a) Discuss score calculation in BLAST.	03
	(b) Compare FASTA and BLAST	04
	(c) Discuss application of multiple sequence alignment.	07
	OR	
Q.3	(a) What are various features of evolution of protein?	03
	(b) What are various benefits and application of molecular phylogeny?	04
	(c) Compare Various types of BLAST available at NCBI.	07
Q.4	(a) What is Next generation sequencing technology ?	03
	(b) What is QSAR?	04
	(c) Align given sequences and calculate score using Needleman Wunsch algorithm : Sequence 1: ACGTT Sequence 2: GCTA Explain method.	07
	OR	
Q.4	(a) What is ADME/T ?	03
	(b) What is use of QSAR in drug discovery?	04
	(c) Align given sequences and calculate score using Smith waterman algorithm : Sequence 1: ACGTT Sequence 2: GCTA. Explain method.	07
Q.5	(a) Draw and explain super secondary structures	03
	(b) Discuss case study regarding CADD.	04
	(c) How does pattern recognition play a crucial role in identifying and predicting genes within a DNA sequence?	07

OR

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| Q.5 | (a) Explain the terms : Domain, microarray, CATH | 03 |
| | (b) Compare cladogram and phylogram. | 04 |
| | (c) Discuss Hidden Markov models for gene prediction in detail | 07 |
