

Seat No.: _____

Enrolment No. _____

GUJARAT TECHNOLOGICAL UNIVERSITY

BE – SEMESTER- V EXAMINATION-SUMMER 2023

Subject Code: 3150407

Date: 27/06/2023

Subject Name: Fundamentals and Applications of Bioinformatics

Time: 02:30 PM TO 05:00 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) Explain secondary structure of turn and its types.	03
	(b) Discuss and draw structures of super secondary structures.	04
	(c) Give alignment of the following sequence using dot matrix - ATGCATT ATTCATA Assume values: 2 for match, -1 for mismatch, 1 for gap	07
Q.2	(a) What is the meaning of fold in SCOP database.	03
	(b) Compare BLAST and FASTA	04
	(c) Discuss structure based drug designing methodology and various tools.	07
	OR	
	(c) Explain working and application of of HMM.	07
Q.3	(a) Discuss features of NAD bininding sites.	03
	(b) How do proteins evolve new function?	04
	(c) Differentiate between needleman-wunsch and smith-waterman algorithm	07
	OR	
Q.3	(a) Differentiate between primary database and secondary database	03
	(b) Key point summery of evolution of globins.	04
	(c) Summerise various gene prediction methods.	07
Q.4	(a) Explain the method of phylogenetic analysis.	03
	(b) Are homology modeling and similarity search samel? Justify your answer.	04
	(c) Compare various next generation sequencing techniques.	07
	OR	
Q.4	(a) What are the gene prediction techniques?	03
	(b) Explain that with giving example of tools used for the gene prediction techniques	04
	(c) Give a brief idea about microarrays. Explain the workflow with neat diagram	07
Q.5	(a) Explain the three fuctions that can be carried out by pymol.	03
	(b) What is microarray technique and how it is useful?	04
	(c) If you are given with an unlabelled protein sequence and 3D structure,	07

how will you determine the structure? Explain your workflow and justify.

OR

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|------------|------------|--|-----------|
| Q.5 | (a) | What is multiple sequence alignment useful for ? | 03 |
| | (b) | What are lipinski's five rules to predict toxicity ? | 04 |
| | (c) | What is biopithon ? what are its applications in bioinformatics? | 07 |
