Roll No: _____

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MSc Biochemistry, Semester III Examination, 2023

Paper Code: MBC 306
Paper Title: Bioinformatics

Time: 1½ h Max Marks: 30

Note: *This paper has 3 Sections, A, B, and C. Attempt all three sections. Section A: Answer all the questions; Section B: Answer any one; Section C: Answer all the questions, each question in this section has an internal choice*

Course/Program Learning Outcomes (CLO/PLO) and Blooms Taxonomy Levels (BTL):

CLO-1: Understand concepts; CLO-2: Systematically learn the processes; CLO-3: Gain knowledge of mechanism; CLO-4: Comprehend how things are integrated; CLO-5: Analyze and evaluate processes

SECTION A

Attempt All Questions
(1x6= 6 Marks)

Q. No. 1	COMMENT BRIEFLY ON THE FOLLOWING:	BTL	CLO	PLO
(a)	(i)After performing DNA/RNA sequencing of novel sequence region with identified function, where would be the most apt place to submit it for the public records? A) Genbank B) PDF C) Uniprot D) NCBI	2	2	3
	(ii)If you are asked to make a database search for similarity for any sequence with FASTA tag, which of the following symbols your query will bear and at which line? A) <, Last line B) $, Last line C) >, First line D) <, First Line	2	2	3

	(iii)Which of the following will be the most suitable to study the most divergent proteins: A) PAM 250 B) PAM 1 C) PAM 100 D) PAM80	4	5	2
	(iv)Which of the following compounds has desirable properties to become a drug? A) Fit drug B) Lead C) Fit compound D) All of the above	4	4	3
	(v)After crystallography study you got the 3-D strucutre of a protein. Which would be the most appropriate place to submit its 3-D Structure? A) NCBI B) UniProt C) Prosite D) PDB	3	3	2
	(vi)Which of the following are not the application of bioinformatics: A) Drug designing B) Data storage and management C) Understand the relationships between organisms D) None of the above	3	4	3

SECTION B

Attempt Any One

(1x12 = 12 Marks)

Q. No. 2	LONG ANSWER QUESTIONS	BTL	CLO	PLO
a)	Describe Global alignment with proper example and matrix illustration.	5	3	2
b)	Describe how BLAST works with step wise explanation and illustration of its various stages and components.	2	2	3

SECTION C

Attempt All Questions
(3x4 = 12 Marks)

Q. No. 3	SHORT ANSWER TYPE QUESTIONS	BTL	CLO	PLO
a)	Design the Dot matrix plot for any 2 sequences and explain all the possible analysis? **OR** Describe Multiple Sequence Alignment and its various possible applications.	3	2	2
b)	For the given ORF sequence, find 6 different translated frames **ATGCCAAGCTGAATAGC** **OR** What is molecular docking analysis and how it is done. Also name some software to perform that.	4	5	3
c)	For the given distance matrix, design the final Phylogenetic tree using UPGMA? **OR** Explain the triangle of primary nucleotide database with the diagram and explain its importance?	4	3	2

	A	B	C	D	E
B	2				
C	4	4			
D	6	6	6		
E	6	6	6	4	
F	8	8	8	8	8

END OF THE QUESTION PAPER