BIRLA INSTITUTE OF TECHNOLOGY, MESRA, RANCHI
(MID SEMESTER EXAMINATION)

CLASS: BTECH   SEMESTER: V
BRANCH: Biotechnology   SESSION: MO/2022

SUBJECT: BE316 BIOINFORMATICS ALGORITHM

TIME: 2 HOURS   FULL MARKS: 25

INSTRUCTIONS:
1. The total marks of the questions are 25.
2. Candidates attempt for all 25 marks.
3. Before attempting the question paper, be sure that you have got the correct question paper.
4. The missing data, if any, may be assumed suitably.
5. Tables/Data hand book/Graph paper etc. to be supplied to the candidates in the examination hall.

				CO	BL
Q1	(a)	What is KEGG database? Give example.	[2]		
Q1	(b)	Describe CATH database with example.	[3]		
Q2	(a)	What is the characteristics DBMS should have?	[2]		
Q2	(b)	What is database 3-tier architecture? Describe with diagram.	[3]		
Q3	(a)	State about binary search and its importance.	[2]		
Q3	(b)	Describe with diagram about merge sorting.	[3]		
Q4	(a)	What is Back tracking paradigms?	[2]		
Q4	(b)	State about BLAST algorithm to align two sequences.	[3]		
Q5	(a)	What is the difference between sequence and molecular file format.	[2]		
Q5	(b)	Do global alignment for the following two sequences, TTAGGC and TAAGGT where match=1, mismatch=0 and gap=-1.	[3]		

:::::: 15/10/2022 ::::::M