QP Code: RA22BTECH404	Reg.						AR 21/22
	No						

Gandhi Institute of Engineering and Technology University, Odisha, Gunupur (GIET University)



B. Tech (Sixth Semester) Examinations, April 2025

21BBTPC36002 / 22BBTPC36002 - Bioinformatics

(Biotechnology)

>	(Biotecimology)						
Ti	me: 3 hrs	aximum	: 70 Ma	arks			
	Answer ALL questions						
ъ.	(The figures in the right-hand margin indicate marks)		1035				
$PART - A (2 \times 5 = 1)$							
Q.1. A	answer ALL questions		CO#	Blooms Level			
b. (What are the submission tools of Gen Bank? What are the data not accepted by Ger Convert the given molecular marker into MSA CCYGIFVL	ı Bank	CO1	K1			
7	CCGIFVL		CO2	K2			
S	SCYGIFVLSG						
A	ACGIFVLSG						
c. E	Explain the option of BLAST and FASTA		CO2	K1			
d. V	d. What is phylogenetic? How many rooted and unrooted trees can be obtained using 7 OUT.						
e. I	Draw the flow chart of molecular docking		CO4	K1			
$PART - B ag{15 x 4} =$							
Answ	er All the questions	Marks	CO#	Blooms			
2. a.	Explain the layer of PIR database	8	CO1	Level K1			
	•	o 7	CO1	K2			
b.	Write the storing and retrieving method of EMBL database (OR)	,	COI	KΖ			
c.	Write retrieving method and submission tools of PDB database	8	CO1	K2			
d.	Write the storing method and submission tools of DDBJ database	7	CO1	K2			
3.a.	Find the optimal alignment and alignment score between two sequence GCATGCA and GATTACA by using Needleman-Wunch algorithm (Assume Match= 1, Mismatch = -1 and Gap= -1)	8	CO2	K2			
b.	Expand BLOSUM. Find the BLOSUM value of all amino acid of the given block GGI TGM SGM	7	CO2	K2			
	SGW GGM						
	(OR)						
c.	Find the optimal alignment and alignment score between two sequence GGATCGA and GAATTCAGTTA (Assuming match = 5, Mismatch = -3 and gap = -4) By using Smith -Waterman algorithm.	8	CO2	К2			
d.	Define PAM. Find the PAM value of all amino acid of the given MSA ACGCTAFKI GCGCTAFKI	7	CO2	K2			

GCGG GCGG ASGG ACAG	CTGF CTLF CTAF CTAF	KI KI KL KL	netic 1	tree by	v usin	o NJ method	8	CO3	K2
						J			
Α	11								
			1.2						
D					10				
Е									
b. Suppose there are 20,000aminoacid in the database of which 2000 are serin and there are 5000 amino acids in helical conformation of which 500 are serin. calculate the type of information						7	CO3	K2	
							0	CO4	К2
							٥	CO4	ΝZ
							7	CO4	К2
distance method									
ADIKLAAIKL									
ADSKLAAIKA									
KILA	SDPQ	WE							
. Explain the computational method of Drug design						8	CO5	K2	
b. Explain different windows of Cn 3D						7	CO5	K2	
					(OR)			
c. Explain molecular Dynamic Simulation. Write the process of study the dynamic						8	CO5	K2	
behaviour of protein by AMBER package.									
d. How do you predict the 3D structure of proteins by homology modelling End of Paper							7	CO5	K2
	GCGG GCGG ASGG ACAG Desig A B C D E Supporthere calcul Find to seque Which distant ADIK ADSE KILA Expla Expla Expla Expla	GCGCTGF GCGCTLF ASGCTAF ASGCTAF ACACTAF Design a ph A A B C D E Suppose the there are 5 calculate the find the not sequence 26 Which two distance me ADIKLAA ADSKLAA KILASDPC Explain the Explain diff Explain mo behaviour of	A B A 22 B C D E Suppose there are there are 5000 a calculate the type Find the no. of vasequence 26 using Which two sequed distance method ADIKLAAIKL ADSKLAAIKA KILASDPQWE Explain the comp Explain different Explain molecula behaviour of protests.	GCGCTGFKI GCGCTLFKI ASGCTAFKL ACACTAFKL Design a phylogenetic to A B C A 22 39 B 41 C D D E D D D D D D D D D D D D D D D D	GCGCTGFKI GCGCTLFKI ASGCTAFKL Design a phylogenetic tree by ABCOTAFKL Design a phylogenetic tree by BUTCOTAFKL DESIGN ABCOTAFKL DESIGN ABCOTAFKL DESIGN ABCOTAFKL ACACTAFKL DESIGN ABCOTAFKL ALIENDAL ASSTRATE ACACTAFKL ACACTAFKL DESIGN ABCOTAF ACACTAFKL ALIENDAL ASSTRATE ALIENDAL ASSTRATE ACACTAFKL ACACTAFKL ALIENDAL ASSTRATE ALIENDAL ASSTRATE ACACTAFKL ACACTAFKL ALIENDAL ASSTRATE ALIENDAL ASSTRATE ALIENDAL A	GCGCTLFKI ASGCTAFKL ACACTAFKL Design a phylogenetic tree by using ABCDEA BCDEA BCDDEA B	GCGCTGFKI GCGCTLFKI ASGCTAFKL Design a phylogenetic tree by using NJ method A B C D E A 22 39 39 41 B 41 41 43 C 18 20 D 10 E Suppose there are 20,000aminoacid in the database of which 2000 are serin and there are 5000 amino acids in helical conformation of which 500 are serin. calculate the type of information (OR) Find the no. of valid shift of the given Test sequence- 31415926535 and patten sequence 26 using Rabin Krap algorithm Which two sequence are very closed to each other justify it by using Hamming distance method ADIKLAAIKL ADSKLAAIKA KILASDPQWE Explain the computational method of Drug design Explain different windows of Cn 3D (OR) Explain molecular Dynamic Simulation. Write the process of study the dynamic behaviour of protein by AMBER package. How do you predict the 3D structure of proteins by homology modelling	GCGCTLFKI ASGCTAFKL ACACTAFKL Design a phylogenetic tree by using NJ method A B C D E A 22 39 39 41 B	GCGCTLFKI ASGCTAFKL ACACTAFKL Design a phylogenetic tree by using NJ method A B C D E A 22 39 39 41 B 41 41 43 C 18 20 D 10 E Suppose there are 20,000aminoacid in the database of which 2000 are serin and there are 5000 amino acids in helical conformation of which 500 are serin. calculate the type of information (OR) Find the no. of valid shift of the given Test sequence- 31415926535 and patten sequence 26 using Rabin Krap algorithm Which two sequence are very closed to each other justify it by using Hamming which two sequence are very closed to each other justify it by using Hamming of the stance method ADIKLAAIKL ADSKLAAIKA KILASDPQWE Explain the computational method of Drug design Explain different windows of Cn 3D (OR) Explain molecular Dynamic Simulation. Write the process of study the dynamic behaviour of protein by AMBER package. How do you predict the 3D structure of proteins by homology modelling 7 CO5