SC

SEAT No.\_\_\_\_

[25]

No. of Printed Pages: 03

## SARDAR PATEL UNIVERSITY

## **External Examination**

M.Sc. (Biochemistry) Semester -IV Subject: PS04EBIC09 - Bioinformatics Tuesday, 17th April, 2018

		Tuesday, 17th	April, 2018	
N	Tim lote:	ne: 10:00 a.m. to 01:00 p.m. Figures to right side indicate marks.		Total marks: 70
Q.1	Cho	oose the most appropriate alternative for the fo	llowing questions:	[8]
	1.	Sequence submission tool of EMBL-EBI d		
		<ul><li>A) EBIin</li><li>C) EMBLin</li><li>E) None of Above</li></ul>	B) BankIt and Sequin D) Webin	
	2.	In FASTA format of nucleotide sequence,	nucleotide sequence starts	with
·		<ul><li>A) Start</li><li>C) Origin</li><li>E) None of Above</li></ul>	B) SEQ D) SQ	
	3.	According to IUPAC Nucleotide base cletter.	ode for c or t or a; i.e. n	ot g is represented by
		<ul><li>A) b</li><li>C) v</li><li>E) None of Above</li></ul>	B) h D) e	
	4.	In the standard genetic code,	is not a ston codon in PN	IA coguence
		A) UAC	B) CAA	A sequence.
		C) UCA E) None of Above	D) All of Above	
	5.	is induced electrical interaction	s which contribute signific	antly to conformational
		stability in the interior of the protein.	. 0	is contoniadonal
		A) Hydrophilic interactions	B) Covalent interaction	ons .
		C) Van der Waals interactions	D) Hydrophobic inter	ractions
		E) None of above.		
	6.	may not be an indicator of	f an evolutionary relationsl	nip.
		A) Sequence similarity	B) Genome similarity	_
		C) Structural similarity	D) All of Above	
		E) None of Above		

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	7.	The primary sequence of a protein is called A) Consensus	as B) Conformation			
		C) Configuration	D) Conservation			
		E) None of above.	-			
	8.	In secondary structure of prot	oin 30 a a recidues per turn is present			
	v.	A) $\pi$ - helix	B) α helix			
		C) 3 <sub>10</sub> helix	D) $\phi$ helix			
		E) None of above.				
Q. <b>2</b>	Atte	empt <u>any seven</u> of the following questions:		[14]		
	1.	Explain different types of scoring matrix for pairwise sequence alignment.				
	2.	Write short note on genebank database and its detailed file format.				
	3.	Write short note on primary databases of bioinformatics.				
	4.	Write short note on sequential steps of microarray experiment.				
	5.	Write short note on Neural Networks and its use in Bioinformatics.				
	6.	Explain dihedral angles present in the primary structure of protein.				
	7.	Write short note on microarray spotting by robotic technique.				
	8.	Explain Quantitative structure-activity relationship models (QSAR models).				
4	9.	Explain importance of IC 50 value in drug desig	ning.			
Q.3	A.	Discuss on Dynamic programming method of pairwise sequence alignment. By using dynamic programming calculate the scoring table and give the back track line by taking +2 for match, -2 for mismatch, -1 for gap.  Seq1. A C G G C G Seq2. A C T G G				
	В.	Enlist and describe various types of BLAST prog	gramme available for sequence alignment.	[6]		
		C	R			
	В.	Describe multiple sequence alignment and discr	uss about motifs and domains.	[6]		
Q.4	A.	Define and explain overprediction and under p	rediction events in exon intron detection.	<b>[6]</b>		
	В.	•	usefulness of Ramachandran plot in protein	[6]		
		structure evaluation.				
		, C	PR			
	В.	Discuss on RNA secondary structure prediction	and its various algorithms.	[6]		

- Q.5 A. Define scoring matrices of sequence alignment. Explain how the values in scoring matrix are [6] derived by discussing value derivation steps for PAM1 scoring matrix.
  - B. Describe acquisition process of protein structure information from protein database by [6] explaining UniProt database.

OR

B. Define phylogenetics analysis? Construct the phylogenetic tree by using UPGMA [6] algorithm with given distance matrix.

	Α	В	С	D	Е
Α	0	22	39	39	41
В		0	41	41	43
С			0	18	20
D				0	10
Ε					0

- Q.6 A. Give flow chart of drug discovery pipeline and discuss major areas of interest in process of [6] drug discovery.
  - B. Explain chemical deprotection technology for construction of oligonucleotide microarray [6] synthesis.

OR

B. Explain primary protein structure analysis parameters of Protparam tool.

[6]

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