SARDAR PATEL UNIVERSITY EXAMINATION

DATE -04/04/19

DAY- Thursday

TIME 10:00 TO 1:00 pm

Course- US06CBNF06

SUBJECT: BIOINFORMATICS

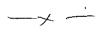
CLASS- T.Y.B.Sc VI Sem

TITLE-Structural Bioinformatics & RDBMS-II

TOTAL MARKS: 70

Q1-	Answer the following Multiple Choice Questions:	10]
1]	Profile is prepared using PSI-BLAST in a) Chou Fasman b) GOR c) PSIPRED d) PHD	
2]	Coordinates for known protein structures are housed in? a) CATH b) SCOP c) PDBsum d) PDB	
3]	Which server is used to compare three-dimensional protein structures? a) DALI b)FSSP c) SCOP d) CATH	
4]	Which one of the following tools can be used for both modeling the protein structure visualization? a) Swiss-PDB Viewer b) QMol. c) RasMol. d) ChemSketch.	1 and
5]	The window size in GOR method is a) 15 b) 17 c) 13 d) none	
6]	The address field of an index is called) Index
7]	The statement containing subquery is called statement. a) Parent b) Primary c) child d) main	
8]	The concept of joining multiple tables is called a) Cross joins b) Outer join c) Edit join d) Inner join	
9]	To reduce redundant data to the minimum possible and object is create ca a) Views b)Synonym c) Sequences d) Indexes	lled a
10]	The function returns an integer value corresponding to the UserID of currently logged in. a) ROWID b) USER c) UID d) ROWNUM	of the user

Q2—Answer the Short Questions: (attempt any TEN) [20] [] Why Ramachandran plot is important. 2] Give abbreviation of GOR, CATH, SCOP, and PDB. 3] Explain protein and concept of protein secondary structure prediction 4] Differentiate between Chou fasman and GOR method. 5] Give the important features of PSI-PRED. 6] Define transmembrane and its importance. 7] What are unique indexes? 8] What is a privilege? List the object privileges. 9] Explain the use of rollback. 10] Explain self-join in brief with example. 11] List all Character functions & Number Functions available in oracle. 12] List different privileges that can be granted to a user. Describe in detail about ANN algorithm and its utility in bioinformatics. Q31 [10] Discuss any two methods for protein secondary structure prediction. Q3] [10] Write in detail about the method and importance of homology modeling. Q41 [10] OR Discuss the concept and method of any tool for protein structure comparison. Q41 [10] What is index? How various types of indexes are created? Explain with syntax with Q5] [10] example. OR i) What is use of sequences? Explain creating & dropping it with example. Q5] [05] ii) What is view? Why it is created, explain it syntax & example [05] Q6] i) Explain INNER join and OUTER join in detail. [05] li)List all Aggregate functions available in oracle and explain any one of them with [05] appropriate syntax and example.



Q6] List different types of index files and explain how to create index files with example.

OR

[10]