

**University of Mumbai**  
**Examination 2020 under cluster 4 (PCE)**

Program: BE Biotechnology

Curriculum Scheme: Rev2016

Examination: Third Year Semester V

Course Code: BTC501 and Course Name: Bioinformatics

Time: 1 hour

Max. Marks: 50

Note to the students: - All the Questions are compulsory and carry equal marks.

Q1.	Which of the following is wrong about National Biomedical Research Foundation/Protein Information Resource Sequence Format?
Option A:	Sequences retrieved from the PIR database are not in this compact format, but in an expanded format with much more information about the sequence
Option B:	The NBRF format is similar to the FASTA sequence format but with significant differences
Option C:	This is different than PIR format
Option D:	The first line includes an initial ">" character followed by a two-letter code such as P for complete sequence or F for fragment, followed by a 1 or 2 to indicate type of sequence, then a semicolon, then a four- to six-character unique name for the entry
Q2.	How many different types of chemical treatments are required in Maxam-Gilbert method?
Option A:	1
Option B:	2
Option C:	3
Option D:	4
Q3.	Which of the following is incorrect about evolution?
Option A:	The macromolecules can be considered molecular fossils that encode the history of millions of years of evolution
Option B:	The building blocks of these biological macromolecules, nucleotide bases, and amino acids form linear sequences that determine the primary structure of the molecules
Option C:	DNA and proteins are products of evolution
Option D:	The molecular sequences barely undergo changes
Q4.	The format of an entry in the SwissProt protein sequence database is very similar to the
Option A:	DDBJ Format
Option B:	NCBI Format

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Option C:	Genbank Format
Option D:	EMBL format
Q5.	Which tool can be used for viewing molecular structures and animating molecular trajectories?
Option A:	Chimera
Option B:	Qmol
Option C:	Arguslab
Option D:	ChemSketch
Q6.	Which of the following is untrue about the PRSS program?
Option A:	It stands for Probability of Random Shuffles
Option B:	It is a web-based program that can be used to evaluate the statistical significance of DNA or protein sequence alignment
Option C:	It first aligns two sequences using the Needleman-Wunsch algorithm and calculates the score
Option D:	It holds one sequence in its original form and randomizes the order of residues in the other sequence.
Q7.	Which of the following is not correct about the $\beta$ -sheet?
Option A:	A $\beta$ -sheet is a fully extended configuration built up from several spatially adjacent regions of a polypeptide chain
Option B:	Each region involved in forming the $\beta$ -sheet is a $\beta$ -strand
Option C:	The $\beta$ -strand conformation is pleated with main chain backbone zigzagging and side chains positioned on same sides of the sheet
Option D:	$\beta$ -Strands are stabilized by hydrogen bonds between residues of adjacent strands
Q8.	Which one of the following tools can be used for both modeling the protein and structure visualization?
Option A:	Swiss-PDB Viewer
Option B:	Qmol
Option C:	RasMol
Option D:	ChemSketch

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Q9.	What is meant by ADME in pharmacokinetics?
Option A:	Affinity, dosage, marketing, efficacy
Option B:	Absorption, distribution, metabolism, excretion
Option C:	Agonism, dependence, mobility, efficiency
Option D:	Antagonism, deficiency, mean, efflux
Q10.	Which of the following is not correct about the stabilizing Forces?
Option A:	Protein structures from secondary to quaternary are maintained by noncovalent forces
Option B:	They include electrostatic interactions but not van der Waals forces, and hydrogen bonding
Option C:	Electrostatic interactions are a significant stabilizing force in a protein structure
Option D:	Electrostatic interactions occur when excess negative charges in one region are neutralized by positive charges in another region
Q11.	Which of the following is not correct about the Coils and Loops?
Option A:	They are regular structures
Option B:	They are irregular structures
Option C:	The loops are often characterized by sharp turns or hairpin-like structures
Option D:	If the connecting regions are completely irregular, they belong to random coils
Q12.	Which of the following terms is used to describe a drug that has the same effect on a receptor as the endogenous chemical messenger?
Option A:	agonist
Option B:	antagonist
Option C:	partial agonist
Option D:	inverse agonist
Q13.	Which one of the following is a command based offline tool for molecular structural visualization?
Option A:	ChemSketch
Option B:	QMol

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Option C:	RasMol
Option D:	PyMol
Q14.	Which of the following statements best describes pharmacokinetics?
Option A:	the study of how drugs reach their target in the body and how the levels of a drug in the blood are affected by absorption, distribution, metabolism and excretion.
Option B:	the study of how drugs can be designed using molecular modelling based on drug's pharmacophore.
Option C:	the study of how a drug interacts with its target binding site at the molecular level to produce a particular pharmacological effect.
Option D:	the study of which functional groups are important to a drug's activity, and the identification of a pharmacophore.
Q15.	Which of the following is incorrect regarding sequence homology?
Option A:	Two sequences can homologous relationship even if have do not have common origin
Option B:	It is an important concept in sequence analysis
Option C:	When two sequences are descended from a common evolutionary origin, they are said to have a homologous relationship
Option D:	When two sequences are descended from a common evolutionary origin, they are said to share homology
Q16.	Which of the following is not correct about the $\alpha$ -Helices?
Option A:	An $\alpha$ -helix has a main chain backbone conformation that resembles a corkscrew
Option B:	Nearly all known $\alpha$ -helices are right handed, exhibiting a leftward spiral form
Option C:	Nearly all known $\alpha$ -helices are right handed, exhibiting a rightward spiral form
Option D:	In right handed helix, there are 3.6 amino acids per helical turn
Q17.	In Stanford University/Intelligenetics Sequence Format At the end of the sequence
Option A:	0 is placed if the sequence is linear, and a 1 if the sequence is circular
Option B:	1 is placed if the sequence is linear, and a 2 if the sequence is circular
Option C:	1 is placed if the sequence is linear, and a 0 if the sequence is circular
Option D:	2 is placed if the sequence is linear, and a 1 if the sequence is circular

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Q18.	Homology modeling can be done using
Option A:	Swiss-PDB Viewer
Option B:	Qmol
Option C:	RasWin
Option D:	Babel
Q19.	The principle of Sanger's method relies on
Option A:	Use of chemicals for base specific cleavage
Option B:	Use of dNTPs for chain termination
Option C:	Use of ddNTPs for chain termination
Option D:	Use of for P32 chain termination
Q20.	Which of the following is incorrect regarding pair wise sequence alignment?
Option A:	The most fundamental process in this type of comparison is sequence alignment
Option B:	It is an important first step toward structural and functional analysis of newly determined sequences
Option C:	This is the process by which sequences are compared by searching for common character patterns and establishing residue-residue correspondence among related sequences
Option D:	It is the process of aligning multiple sequences
Q21.	The samples in Sanger's method after reaction are separated using
Option A:	AGE
Option B:	PAGE
Option C:	PFGE
Option D:	2-D gel electrophoresis
Q22.	Which of the following is wrong about FASTA Sequence Format?
Option A:	The FASTA sequence format includes a comment line identified by a ">" character in the first column followed by the name and origin of the sequence

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Option B:	The FASTA sequence format includes the sequence in standard one-letter symbols
Option C:	This format provides a very convenient way to copy just the sequence part from one window to another because there are no numbers or other nonsequence characters within the sequence
Option D:	The presence of '*' is not quite essential for reading the sequence correctly by some sequence analysis programs
Q23.	Which of the following is wrong about Genetics Computer Group Sequence Format?
Option A:	Earlier versions of the Genetics Computer Group (GCG) programs require a unique sequence format and include programs that convert other sequence formats into GCG format
Option B:	Information about the sequence in the GenBank entry is not included but the line information is carried out
Option C:	If one or more sequence characters become changed through error, a program reading the sequence will be able to determine that the change has occurred because the checksum value in the sequence entry will no longer be correct
Option D:	Lines of information are terminated by two periods, which mark the end of information and the start of the sequence on the next line
Q24.	Guanine specific cleavage in Maxam-Gilbert method is done by using
Option A:	formic acid
Option B:	hydrazine
Option C:	Dimethyl sulphate
Option D:	piperidine
Q25.	Which of the following is incorrect regarding pair wise sequence alignment?
Option A:	The most fundamental process in this type of comparison is sequence alignment
Option B:	It is an important first step toward structural and functional analysis of newly determined sequences
Option C:	This is the process by which sequences are compared by searching for common character patterns and establishing residue-residue correspondence among related sequences
Option D:	It is the process of aligning multiple sequences

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<b>Question</b>	<b>Correct Option (Enter either 'A' or 'B' or 'C' or 'D')</b>
Q1.	C
Q2.	A
Q3.	D
Q4	D
Q5	B
Q6	C
Q7	C
Q8.	A
Q9.	B
Q10.	B
Q11.	A
Q12.	A
Q13.	C
Q14.	A
Q15.	A
Q16.	B
Q17.	B

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Q18.	A
Q19.	C
Q20.	D
Q21.	B
Q22.	D
Q23.	B
Q24.	C
Q25.	D