

Biology Fsc Part 1 Chapter 7 Online Test

Sr	Questions	Answers Choice
1	The field that uses computational tools to analyze biological data is.	A. quantum physics B. Geography C. Geo Physics D. Computational biology
2	Human histone H1, and Human histone H1,2 are.	A. Paralog B. Ortholog C. Metalog D. Both a and b
3	The limitation of homology modeling is	A. Depends on protein function B. Only specific for carbohydrates C. Requires a template structure with maximum similarities D. None of above
4	The place on a disease causing molecule where a drug can work are called.	A. Drug targets B. Off targets C. Counter target D. Active
5	The tool used for sequence alignment in bioinformatics	A. FASTA B. PDB C. Gen Bank D. Ensembl
6	Which of the following is not the area in computational biology.	A. Genomics B. Ergonomics C. Proteomics D. Bioinformatics
7	The protein domains are.	A. Functional and structural units within protein B. Secondary structural elements C. Linear sequences of amino acids D. Specific regions for post translational modification
8	Which one of the following is a sequence alignment tool that compares a query sequence to a database of sequences.	A. FASTA B. BLAST C. BEMBL D. PDB
9	A researcher wants to search protein and nucleotide databases to identify sequence homology, which one is most appropriate to study.	A. Uni Port KB B. FASTA C. Gen Bank D. Swiss port
10	Which computational approach is used to predict protein structure based on amino acid sequence.	A. Multiple sequence alignment B. Homology modelling C. Clustering analysis D. BLAST Searches
11	the biologist compare proteins structures to unknown genes.	A. To assign possible functions B. To study novel proteins C. To discover drugs D. To make an act
12	Which bioinformatics tool acts like a Google Search for DNA sequences.	A. Photoshop B. BLAST C. PDB D. Excel
13	How did structural biology contribute to COVID-19 research.	A. By measuring blood sugar level B. By sequencing the human genome C. By determining 3D structure of spike protein D. By analyzing bacterial cell wall
14	A researcher is studying a newly discovered protein. Linked to a rare disease. The protein's sequence shows no match in BLAST, the next possible step is	A. Modify protein sequence B. Check for structural homology using PDB C. Reanalyze the protein structure D. Go for x-ray crystallography

15	The database of nucleotide sequences and supporting bibliographic annotations is.	<p>A. Gen Bank</p> <p>B. FASTA</p> <p>C. BLAST</p> <p>D. PDB</p>
16	Orthology differ from paralogues in	<p>A. Orthologs arise from speciation paralogues from gene duplication</p> <p>B. Orthologs arise from gene duplication and paralogues from speciation</p> <p>C. Orthologs have identical genetic sequence</p> <p>D. Both a and c</p>
17	The structural studies of enzyme HIV-1 reverse transcriptase have identified its.	<p>A. Polymerase domain</p> <p>B. RNase H Domain</p> <p>C. Nuclease domain</p> <p>D. All of above</p>
18	If two proteins have structural homology what can be inferred.	<p>A. They likely share functional similarities</p> <p>B. They have identical DNA sequences</p> <p>C. They share orthologues</p> <p>D. Does not give clue about unknown gene</p>
19	What is the primary focus of structural biology	<p>A. Studying metabolic pathways</p> <p>B. Determining 3D atomic level structures of macromolecules</p> <p>C. Gene sequencing</p> <p>D. Gene expression</p>
20	What is sequence homology.	<p>A. Similarity in sequences due to shared ancestry</p> <p>B. 3D-structure of proteins due to shared ancestry</p> <p>C. Large scale study of proteins</p> <p>D. none of above</p>