Biology Fsc Part 1 Chapter 7 Online Test

Sr	Questions	Answers Choice
1	In x-ray diffraction technique, the diffraction pattern is used to.	A. Make good quality crystal B. Creae a density map C. Make density gradient D. Diagnose disease
2	If two proteins have strutural homology what can be inferred.	A. They likely share functional similarities B. They have identical DNA sequences C. They share orthologs D. Does not give clue about unknown gene
3	How did strutural biiology contribute to OVID-19 research.	A. By measuring blood sugar level B. By sequencing the human genome C. By determining 3D struture of spike protein D. By analyzing bacterial cell wall
4	Generally, the functon of a protin depends on its	A. One dimensional structure B. Two -dimentsional structue C. Three- dimensional struture D. Four-dimensional structure
5	Orthology differ from paraalogs in	A. Orthologs arie from speciation paralogs from gene duplication B. Orthoogs arise form gene duplication and paralogs frm specieation C. Orthologs have idential genetic sequence D. Both a and c
6	Which one of the following is a sequene alignemnt tool that compares a query sequence to a database of sequences.	A. FASTA B. BLAST C. BEMBL D. PDB
7	the strutual studies of enzyme HIV-Lreverse transcriptase have identified its.	A. Polymerase domain B. RNase H Domain C. Nuclease domain D. All of above
8	The database of nuclelotid sequences and supporting bibliographic annotations is.	A. Gen Bank B. FASTA C. BLAST D. PDB
9	Mapping the entire set of proein produced by an organism and to understaind their interactions and rule in cellular process, is achieved in.	A. Genomics B. Proteomics C. Bioinformatics D. Biodynamics
10	What is sequence homology.	A. Similarity in sequences due to shared ancestry B. 3D-strutre of proteins due to shared ancestry C. Large scale study of proteins D. none of above
11	Which of the followng is not the area in computationalbiology.	A. Genomics B. Ergonomics C. Proteomics D. Bioinformatics
12	The place on a disease causing molecule where a drug can work are called.	A. Drug targets B. Off targests C. Counter target D. Active
13	A researcher is studying a newly discoverec protin. Linked to a rare diseaes. The protein's sequene shows no match inBLAST, the next possible step is	A. Modigy protin sequenfe B. Check for struutal homology using PDB C. Reanalyze the protin struture

		D. Gofor x-ray crystallography
14	How does strutual homology helps in drug designing.	A. By identifying similar protein structures for targeted drug binding. B. By idntify homologus genes C. By providing aninsight into evolutionary relationships of genes D. By gene sequencing
15	What is primary role of computational biology	A. Using computer algorithms to analyze data B. Identifying genetic multations C. Studying protein functions D. Analyzing the expression patterns
16	The first step in x-ray crystallography experimetn is.	A. Compute an electron density B. Build a odel of your molecule C. Mesure a diffraction pattern D. Grow a crystal
17	The proetin domains are.	A. Functional and stuctural units within protein B. Secondary strutural elemetns C. Linear sequences of amino acids D. Specific regions for post translational modification
18	The field that uses computional tools to anayze biologicla data is.	A. quantum physics B. Geography C. Geo Physics D. Computational biology
19	Which bioinforamtics tools acts like a Google Search for DNA sequences.	A. Photoshop B. BLAST C. PDB D. Excel
20	Protein misfolding is associaed with which of he following diseases.	A. Hypertension B. Gout C. Alzheimer's D. Influenza