Biology Fsc Part 1 Chapter 7 Online Test

Sr	Questions	Answers Choice
1	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
2	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
3	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
4	Human histone H1,1 and Chimpanzee histone H1,1 are.	A. Ortholog B. Paralog C. Metalog D. Algorithm
5	Whcih field of biology helps in identifying genetic variations associated with diseases.	A. Strutural biology B. social biology C. Computational biology D. Biomathematics
6	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
7	Ortholgs are.	A. Genes in same species B. Humanhistone H1,1 and H1,2 C. Sequences in different species D. Arise from same ancestralgene
8	The database of nuclelotid sequences and supporting bibliographic annotations is.	A. Gen Bank B. FASTA C. BLAST D. PDB
9	Which computational approach is used to predict protein stuture based on amino acid sequence.	A. Multiple sequence alignment B. Homology modelling C. Clustering analysis D. BLAST Searches
10	Whcih data base stores 3D strutures of macromolecules.	A. PDB B. Ensembl C. GenBank D. BLAST
11	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
12	Protein misfolding is associaed with which of he following diseases.	A. Hypertension B. Gout C. Alzheimer's D. Influenza
13	The tool used for sequene salignemnt in bioinformatics	A. FASTA B. PDB C. Gen Bank D. Ensembl
14	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
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	Which techniuqe is used to determine the 3D-struture of proteins.	A. Electron microscopy B. Mass spectrometry C. X-ray crystallography D. spectromery
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 first step in x-ray crystallography is	A. Protine crystallization B. Production of a diffraction pattern C. Creating density map D. Determination of protin struture
19	The active site of enzyme is important is designing a drug, because.	A. It deterimines enzyme physiology B. It is where a substrate binds C. It provides informaton about drug D. It is made up of lipids
20	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