Biology Fsc Part 1 Chapter 7 Online Test

Sr	Questions	Answers Choice
1	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
2	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
3	The limiation of homology modeling is	A. Depends on protein function B. Only specific for carbohydrates C. Requires a template struture with maximum similarities D. None of above
4	Which of the followng is not the area in computationalbiology.	A. Genomics B. Ergonomics C. Proteomics D. Bioinformatics
5	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
6	What is the primary focus of strutrual biology	A. Styding metabloic pathwarys B. Determining 3D atomic level strutures of macromolecules C. Gene seuencing D. Gene expression
7	Whcih data base stores 3D strutures of macromolecules.	A. PDB B. Ensembl C. GenBank D. BLAST
8	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
9	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
10	Sequencing, assembiling and analyzing he function and struture of genomes is studied in.	A. Bioniformatics B. Genomics C. Ptoteomics D. Strututal biology
11	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
12	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
13	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

14	The tool used for sequene salignemnt in bioinformatics	A. FASTA B. PDB C. Gen Bank D. Ensembl
15	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
16	the biologist compare proteins sturtures to unknown genes.	A. To assign possibel functions B. To study novel proteins C. To discover drugs D. To make an act
17	Human histone HI,` and Human histone H1,2 are.	A. Paralog B. Ortholog C. Metalog D. Both a and b
18	A researcher wants to search protein and nucleotide databases to identify sequee homology , which one is most approrjate to study.	A. Uni Port KB B. FASTA C. Gen Bank D. Swiss port
19	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
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