Biology Fsc Part 1 Chapter 7 Online Test

Sr	Questions	Answers Choice
1	e/m is a link for.	A. GenBank B. Em BL C. PDP D. DDBJ
2	The tool used for sequene salignemnt in bioinformatics	A. FASTA B. PDB C. Gen Bank D. Ensembl
3	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
4	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
5	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
6	Human histone Hl,` and Human histone H1,2 are.	A. Paralog B. Ortholog C. Metalog D. Both a and b
7	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
8	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
9	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
10	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
11	The field that uses computional tools to anayze biologicla data is.	A. quantum physics B. Geography C. Geo Physics D. Computational biology
12	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
13	Whcih field of biology helps in identifying genetic variations associated with diseases.	A. Strutural biology B. social biology C. Computational biology D. Biomathematics
14	A genome browser prividing infomation on genome sequenes, gene models and comparatie	A. Ensembl B. Gen Bank

	genomics for various species is.	C. FASTA D. BLAST
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	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
17	Sequencing, assembiling and analyzing he function and struture of genomes is studied in.	A. Bioniformatics B. Genomics C. Ptoteomics D. Strututal biology
18	The database of nuclelotid sequences and supporting bibliographic annotations is.	A. Gen Bank B. FASTA C. BLAST D. PDB
19	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
20	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