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	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
3	e/m is a link for.	A. GenBank B. Em BL C. PDP D. DDBJ
4	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
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	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
7	A genome browser priviging infomation on genome sequenes, gene models and comparatie genomics for various species is.	A. Ensembl B. Gen Bank C. FASTA D. BLAST
8	Whcih data base stores 3D strutures of macromolecules.	A. PDB B. Ensembl C. GenBank D. BLAST
9	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
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	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
12	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
13	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
14	Which of the followng is not the area in computationalbiology.	A. Genomics B. Ergonomics C. Proteomics

15	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
16	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
17	The database of nuclelotid sequences and supporting bibliographic annotations is.	A. Gen Bank B. FASTA C. BLAST D. PDB
18	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
19	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
20	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