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Biology Fsc Part 1 Chapter 7 Online Test

Sr	Questions	Answers Choice
1	Human histone HI,` and Human histone H1,2 are.	A. Paralog B. Ortholog C. Metalog D. Both a and b
2	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
3	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
4	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
5	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
6	A genome browser prividing infomation on genome sequenes, gene models and comparatie genomics for various species is.	A. Ensembl B. Gen Bank C. FASTA D. BLAST
7	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
8	The field that uses computional tools to anayze biologicla data is.	A. quantum physics B. Geography C. Geo Physics D. Computational biology
9	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
10	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
11	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
12	e/m is a link for.	A. GenBank B. Em BL C. PDP D. DDBJ
13	Which techniuqe is used to determine the 3D-struture of proteins.	A. Electron microscopy B. Mass spectrometry C. X-ray crystallography D. spectromery
14	Sequencing, assembiling and analyzing he function and struture of genomes is studied in.	A. Bioniformatics B. Genomics C. Ptoteomics D. Strututal biology

15	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
16	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
17	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
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	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
20	Ortholgs are.	A. Genes in same species B. Humanhistone H1,1 and H1,2 C. Sequences in different species D. Arise from same ancestralgene