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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	Mapping the entire set of proein produced by an organism and to understaind their interactions and rule in cellular process, is achieved in.	A. Genomics B. Proteomics C. Bioinformatics D. Biodynamics
3	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
4	The field that uses computional tools to anayze biologicla data is.	A. quantum physics B. Geography C. Geo Physics D. Computational biology
5	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
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	Which of the followng is not the area in computationalbiology.	A. Genomics B. Ergonomics C. Proteomics D. Bioinformatics
8	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
9	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
10	Which techniuqe is used to determine the 3D-struture of proteins.	A. Electron microscopy B. Mass spectrometry C. X-ray crystallography D. spectromery
11	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
12	Whcih data base stores 3D strutures of macromolecules.	A. PDB B. Ensembl C. GenBank D. BLAST
13	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
14	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
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 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
17	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
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 tool used for sequene salignemnt in bioinformatics	A. FASTA B. PDB C. Gen Bank D. Ensembl
20	Human histone H1,1 and Chimpanzee histone H1,1 are.	A. Ortholog B. Paralog C. Metalog D. Algorithm