# Biology Fsc Part 1 Chapter 7 Online Test

| Sr | Questions | Answers Choice |
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| 1 | Ortholgs are. | A. Genes in same species<br>B. Humanhistone H1,1 and H1,2<br>C. Sequences in different species<br>D. Arise from same ancestralgene |
| 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<br>B. Proteomics<br>C. Bioinformatics<br>D. Biodynamics |
| 3 | the biologist compare proteins sturtures to unknown genes. | A. To assign possibel functions<br>B. To study novel proteins<br>C. To discover drugs<br>D. To make an act |
| 4 | The active site of enzyme is important is designing a drug, because. | A. It deterimines enzyme physiology<br>B. It is where a substrate binds<br>C. It provides informaton about drug<br>D. It is made up of lipids |
| 5 | Human histone H1,1 and Chimpanzee histone H1,1 are. | A. Ortholog<br>B. Paralog<br>C. Metalog<br>D. Algorithm |
| 6 | Protein misfolding is associaed with which of he following diseases. | A. Hypertension<br>B. Gout<br>C. Alzheimer's<br>D. Influenza |
| 7 | The database of nuclelotid sequences and supporting bibliographic annotations is. | A. Gen Bank<br>B. FASTA<br>C. BLAST<br>D. PDB |
| 8 | Which bioinforamtics tools acts like a Google Search for DNA sequences. | A. Photoshop<br>B. BLAST<br>C. PDB<br>D. Excel |
| 9 | What is primary role of computational biology | A. Using computer algorithms to analyze data<br>B. Identifying genetic multations<br>C. Studying protein functions<br>D. Analyzing the expression patterns |
| 10 | Generally, the functon of a protin depends on its | A. One dimensional structure<br>B. Two -dimentsional structue<br>C. Three- dimensional struture<br>D. Four-dimensional structure |
| 11 | The first step in x-ray crystallography experimetn is. | A. Compute an electron density<br>B. Build a odel of your molecule<br>C. Mesure a diffraction pattern<br>D. Grow a crystal |
| 12 | Which computational approach is used to predict protein stuture based on amino acid sequence. | A. Multiple sequence alignment<br>B. Homology modelling<br>C. Clustering analysis<br>D. BLAST Searches |
| 13 | Which of the followng is not the area in computationalbiology. | A. Genomics<br>B. Ergonomics<br>C. Proteomics<br>D. Bioinformatics |
| 14 | e/m is a link for. | A. GenBank<br>B. Em BL<br>C. PDP<br>D. DDBJ |
| 15 | How does strutual homology helps in drug designing. | A. By identifying similar protein structures for targeted drug binding.<br>B. By idntify homologus genes |

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| | | C. By providing aninsight into evolutionary relationships of genes<br>D. By gene sequencing |
| 16 | Whcih data base stores 3D strutures of macromolecules. | A. PDB<br>B. Ensembl<br>C. GenBank<br>D. BLAST |
| 17 | Which techniuqe is used to determine the 3D-struture of proteins. | A. Electron microscopy<br>B. Mass spectrometry<br>C. X-ray crystallography<br>D. spectromery |
| 18 | In x-ray diffraction technique, the diffraction pattern is used to. | A. Make good quality crystal<br>B. Creae a density map<br>C. Make density gradient<br>D. Diagnose disease |
| 19 | The tool used for sequene salignemnt in bioinformatics | A. FASTA<br>B. PDB<br>C. Gen Bank<br>D. Ensembl |
| 20 | What is the primary focus of strutural biology | A. Styding metabloic pathwarys<br>B. Determining 3D atomic level strutures of macromolecules<br>C. Gene seuencing<br>D. Gene expression |