

**M.Sc. I Semester Degree Examination, April/May - 2024**
Skill Enhancement Courses (SEC)**MICROBIOLOGY****802C : Bioinformatics for Microbiology**

Time : 1 Hour

Maximum Marks : 30

1. The Term Bioinformatics was coined by_____.
(A) J.D. Watson (B) Pauline H Ogeweg
(C) Margaret Dayhoff (D) Frederic Sanger
2. Protein database is a :
(A) Information of proteins (B) Function of proteins
(C) Introduction of proteins (D) Structure of proteins
3. Global alignment is based on :
(A) Sequences which are of same length
(B) Sequences which are suspected to have similarity
(C) Sequences which are dissimilar
(D) All of the above
4. CENSOR tool is used for :
(A) Masking symbols (B) Cutting sequence
(C) Identifying sequence (D) Editing sequence
5. Clustal W is used for :
(A) Single sequence alignment (B) Homologous sequence alignment
(C) Multiple sequence alignment (D) None of the above
6. FASTA was developed by :
(A) Watson and Crick (B) Lipman and Pearson
(C) Needleman-Wunsch (D) None of the above
7. Antiviral molecule to collect database is :
(A) Avpdp (B) DRAMP
(C) CRAMP (D) Gene Bank
8. Molecular modelling and docking is used for :
(A) Function based drug design (B) Molecule based drug design
(C) Structure based drug design (D) None of the above



9. Micro array technique is used for :
(A) Interpreting data of only DNA (B) Interpreting data of only protein
(C) Interpreting data of only RNA (D) All of the above
10. Study of Genomics is :
(A) Study of genes and their interaction
(B) Study of gene function
(C) Study the structure of gene
(D) None of the above
11. Bacterial nucleotide sequence is analysed by :
(A) 16 sRNA (B) 80 sRNA
(C) 18 sRNA (D) None of the above
12. Primer is :
(A) Short single-stranded nucleic acid
(B) Multiple-stranded nuclei acid
(C) Double-stranded nucleic acid
(D) All of the above
13. Expasy :
(A) Enzyme pathway analysis system
(B) Expert protein analysis system
(C) Endonuclease protein analysis system
(D) None of the above
14. Computer simulation refers to :
(A) Dry lab (B) In silico (C) Wet lab (D) In vitro
15. Expand PDB :
(A) Protozoan Database (B) Peptide Database
(C) Protein Database (D) Protein-peptide Database
16. KEGG :
(A) Kyoto Encyclopedia of Gene and Genomes
(B) Keto Encyclopedia of Gene and Genomes
(C) Kent Encyclopedia of Gene and Genomes
(D) None of the above
17. The term "transcriptomics" refers to the study of :
(A) DNA sequences (B) Protein structures
(C) RNA molecules (D) Genetic mutations



18. The study of the three-dimensional structure of proteins is known as :
(A) Proteomics (B) Genomics
(C) Structural biology (D) Transcriptomics
19. Small cDNA sequence that represents a unique segment of an active gene is called :
(A) SNPs (B) ESTs (C) SnRNAs (D) Contings
20. Genes of same species, similarly related to each other are _____.
(A) Ortholog (B) Synteny (C) Paralog (D) Microarray
21. What is microbiome ?
(A) A group of parasites (B) Micro-organism in an environment
(C) A tiny bio-dome (D) None of the above
22. Which of the following is an example of Homology and similarity tool ?
(A) BLAST (B) RasMol (C) EMBOSS (D) PROSPECT
23. Which of the following are not the application of bioinformatics ?
(A) Drug designing
(B) Data storage and management
(C) Understand the relationship between organisms
(D) None of the above
24. The stepwise method for solving problems in computer science is called as :
(A) Flowchart (B) Algorithm (C) Procedure (D) Sequential design
25. In which year did the SWISSPROT protein sequence database begin ?
(A) 1988 (B) 1985 (C) 1986 (D) 1987
26. Identification of drugs through genomic study is called as :
(A) Genomics (B) Pharmacogenomics
(C) Pharmacogenetics (D) Cheminformatics
27. NCBI stands for :
(A) National Centre for Biology (B) National Centre for Biotechnology
(C) National Centre for Biochemistry (D) None of the above
28. RNA copies of active protein-coding genes are called :
(A) Transcriptome (B) Genomics (C) Genetics (D) Evolution
29. ANN refers to :
(A) Asian news network (B) Artificial neural networks
(C) Artificial newton network (D) All the above
30. Molecular visualization software is :
(A) Chimera (B) Primer (C) Python (D) C++



