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Barasat, Kolkata -700125

BRAINWARE UNIVERSITY

Term End Examination 2021 - 22

Programme – Bachelor of Technology in Computer Science & Engineering

Course Name – Biology

Course Code - BSC(CSE)701

(Semester VII)

Time : 1 Hr.25 Min.

Full Marks : 70

[The figure in the margin indicates full marks.]

Group-A

(Multiple Choice Type Question)

1 x 70=70

Choose the correct alternative from the following :

- (1) Amino acid are linked together by
 - a) Glycosidic bond
 - b) peptide bond
 - c) Di ester bond
 - d) phosphate bond
- (2) A multi subunit protein have
 - a) quaternary structure
 - b) tertiary structure
 - c) secondary structure
 - d) primary structure
- (3) Hydrophobic side chain generally present in
 - a) Outer Periphery region
 - b) hydrophobic sidechain do not form bond
 - c) Core region
 - d) randomly assorted
- (4) An example of protein engineering is
 - a) Co-vaccine
 - b) Covisheald
 - c) Humulin
 - d) BT- cotton
- (5) Basic amino acid is
 - a) Glutamic acid
 - b) Aspartic acid
 - c) Arginine,
 - d) Glycine
- (6) Primary structure of Protein involved
 - a) Right hand twisted rotation
 - b) Peptide bond formation
 - c) beta sheet formation
 - d) metal ion involvment
- (7) Which of the following is not true about secondary protein structure?
 - a) The hydrophilic/hydrophobic character of a amino acid residues is important to secondary structure.
 - b) The ability of peptide bonds to form intramolecular hydrogen bonds is important to secondary structure
 - c) The alpha helix, beta pleated sheet and beta t
 - d) The steric influence of amino acid residues i

urns are examples of protein secondary structure. s important to secondary structure.

(8) A structure that has hydrogen bonds between polypeptide chains arranged side by side is

- a) Primary structure
- b) α -helix
- c) β -pleated sheets
- d) Tertiary structure

(9) Identify the amino acids containing nonpolar, aliphatic R groups

- a) Phenylalanine, tyrosine, and tryptophan
- b) Lysine, arginine, histidine
- c) Glycine, alanine, leucine
- d) Serine, threonine, cysteine

(10) Which of the following factors is not responsible for the denaturation of proteins

- a) Heat
- b) Charge
- c) pH change
- d) Organic solvents

(11) A nucleoside consists of

- a) Nitrogenous base
- b) Purine or pyrimidine base + sugar
- c) Purine or pyrimidine base + phosphorous
- d) Purine or pyrimidine base + sugar + Phosphorous

(12) The nitrogenous base not present in DNA structure

- a) Guanine
- b) adenine
- c) thiamine
- d) uracil

(13) A dipeptide has

- a) 2 amino acids and 1 peptide bond
- b) 2 amino acids and 3 peptide bond
- c) 2 amino acids and 2 peptide bond
- d) 3 amino acids and 2 peptide bond

(14) Which of the following bonds are broken during DNA replication?

- a) hydrogen bonds between bases
- b) phosphodiester bonds
- c) covalent bonds between bases
- d) ionic bonds between bases and phosphate groups

(15) How many base pairs are there in one full turn of the B-DNA double helix?

- a) 4
- b) 10
- c) 16
- d) 64

(16) Who is credited with discovering the structure of DNA?

- a) Crick and Neck
- b) Watson and Crick
- c) Watson and Franklin
- d) Holmes and Watson

(17) Replication occurs once every cell generation during

- a) S phase
- b) T phase
- c) C phase
- d) A phase

(18) Synthesis of RNA from DNA is

- a) Transcription
- b) Translation
- c) Metabolism
- d) Reduction

(19) At the physiological pH, the DNA molecules are;

- a) Positively charged
- b) Negatively charged
- c) Amphipathic
- d) Neutral

(20) DNA replication is

- a) Conservative
- b) Non-conservative
- c) Semi-conservative
- d) None

- (21) Unwinding of DNA is done by
a) Helicase
c) Exonuclease
- (22) Which of the following RNAs bind to an amino acid?
a) mRNA
c) rRNA
- (23) Which of the following RNAs binds to large subunit of ribosome
a) mRNA
c) rRNA
- (24) Protein synthesis process are known as
a) Transcription
c) translation
- (25) Synthesis of DNA from RNA is known as
a) Reverse transcriptase
c) Reverse Replication
- (26) DNA dependent DNA polymerase
a) responsible for replication
c) responsible for translation
- (27) How many bones are present in our body
a) 206
c) 106
- (28) Humerous is the part of
a) Upper arm
c) Upper leg
- (29) we received pulse in
a) vein only
c) artery and vein both
- (30) Salivary gland mostly present in
a) Stomach
c) Mouth
- (31) Gaseous exchange is take place in
a) Nostril
c) Alveoli
- (32) Tricuspid valve is present in
a) between Left auricle and left ventricle
c) between two auricle
- (33) The largest lymph gland is
a) Splen
c) Tonsil
- (34) Blood is produced from
a) Kidney
c) Bone marrow
- (35) The master gland are
b) ligase
d) Topoisomerase
b) tRNA
d) hnRNA
b) tRNA
d) hnRNA
b) Replication
d) Reverse transcription
b) Reverse transcription
d) Reverse Translation
b) responsible for transcription
d) none of them
b) 306
d) 602
b) Lower Arm
d) Lower Leg
b) artery only
d) none of them
b) Oesophagus
d) Intestine
b) Skin
d) bronchai
b) between right auricle and riht ventricle
d) between two ventricle
b) Liver
d) Gastric gland
b) Liver
d) Brain

- a) Pituitary
b) Hypothalamas
c) Pancreous
d) adrenal
- (36) The Emergency hormone adrenaline is released from
a) Pituitary
b) Hypothalamas
c) Pancreous
d) adrenal
- (37) The unit of Kidney is known as
a) nephron
b) Neuron
c) Epithelial cell
d) Epididymis
- (38) The cell formed after fusion of sperm and ovum is known as
a) Embryo
b) Blastula
c) Zygote
d) Infant
- (39) Bioinformatics is the subject comprising
a) Biology and IT
b) Biology and computer science
c) Biology, computer science and IT
d) None of them
- (40) The first secondary database developed was
a) PRINT
b) PROSITE
c) PIR.
d) .PDB
- (41) Which of the following scientists created the first Bioinformatics database?
a) Dayhoff
b) Pearson
c) Richard Durbin
d) Michael.J.Dunn
- (42) The human genome contains approximately _____.
a) 6 billion base pairs
b) 5 billion base pairs
c) 3 billion base pairs
d) 4 billion base pairs
- (43) The first molecular biology server expasy was in the year _____.
a) 1992
b) 1993
c) 1993
d) 1995
- (44) The identification of drugs through the genomic study is called _____.
a) Genomics
b) Pharmacogenomics
c) Pharmacogenetics
d) Proteomics
- (45) The process of finding the relative location of genes on a chromosome is called _____.
a) Gene tracking
b) Genome walking
c) Genome mapping
d) Chromosome walking
- (46) The computational methodology that tries to find the best matching between two molecules, a receptor and ligand are called _____.
a) Molecular fitting
b) Molecular matching
c) Molecule affinity checking
d) Molecular docking
- (47) Which of the following are not the application of bioinformatics?
a) Drug designing
b) Data storage and management
c) Understand the relationships between organisms
d) None of the above
- (48) The stepwise method for solving problems in computer science is called _____.
a) Flowchart
b) Algorithm
c) Procedure
d) Procedure

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- (49) The computer simulation refers to _____.
- a) Dry lab
 - b) Invitro
 - c) In silico
 - d) Invivo
- (50) GeneBank, a nucleotide sequence database is maintained by
- a) DDBJ
 - b) NCBI
 - c) EMBL
 - d) CSIR
- (51) The information retrieval tool for NCBI Gene Bank is -
- a) Entrez
 - b) SeqIn
 - c) Text Search
 - d) STAG.
- (52) The vector used for Human genome project are
- a) BAC
 - b) ECORI
 - c) BAMHIII
 - d) Ti Plasmid
- (53) Gene bank Include
- a) Only DNA sequence
 - b) Potein level expression
 - c) information about the locus name, length of the sequence,
 - d) None of them
- (54) Identify Incorrect statement, Algorithms can be represented:
- a) as pseudo codes
 - b) as syntax
 - c) as programs
 - d) as flowcharts
- (55) Two sequences are said to be homologous if:
- a) they have diverged from a common ancestor.
 - b) their alignments share 30% identity or more.
 - c) they belong to the same fold family.
 - d) they have converged to share similar functional properties.
- (56) What is a fingerprint?
- a) A protein family discriminator built from a set of regular expressions.
 - b) A protein family discriminator built from a set of conserved motifs.
 - c) A cluster of protein sequences gathered from a BLAST search.
 - d) A cluster of protein sequences gathered from a FASTA search.
- (57) Well-conserved regions in multiple sequence alignments:
- a) reflect areas of structural importance.
 - b) reflect areas of functional importance
 - c) reflect areas of both functional and structural importance.
 - d) reflect areas of both functional and structural importance.
- (58) Why are colour schemes important in creating and analysing sequence alignments?
- a) They look pretty
 - b) To make clearer printouts and presentations
 - c) To allow you to distinguish conserved residues and residue groups more easily
 - d) To allow you to detect active sites of proteins
- (59) Coordinates for known protein structures are housed in?
- a) CATH
 - b) SCOP
 - c) PDBsum
 - d) PDB
- (60) Adaptive grids change automatically based on _____
- a) flow field gradients
 - b) time rate of change of the flow properties
 - c) grid gradients
 - d) time rate of change of the grid points
- (61) Double-helical structure of DNA is analysed by Data obtained from which techniques?
- a) Electrophoresis
 - b) Chromatography

- c) X-ray crystallography
- (62) Comparative genomics is used for study in
- a) between differences in species
b) Relation between two species
c) similarity between two species
d) Genome study for one individual
- (63) Next-generation sequencing technology is primarily applied for
- a) Gene therapy
b) Pharmacoeconomics study
c) Target-oriented drug therapy
d) None of them
- (64) Phylogenetic tree is employed for study of
- a) Mutation
b) Drawing
c) Environmental relationships among species variation
d) Evolutionary relationships among various biological species
- (65) For making a Phylogenetic Tree, we prefer data obtained from
- a) DNA micro array
b) m-RNA
c) Protein Data Base
d) None of them
- (66) Close relation between species is focused on
- a) Rooted tree
b) Unrooted tree
c) Phylogenetic tree
d) Living tree
- (67) Distant relation between species is focused on
- a) Rooted tree
b) Unrooted tree
c) Phylogenetic tree
d) Living tree
- (68) The radial structure is generally observed in
- a) Rooted tree
b) Unrooted tree
c) Phylogenetic tree
d) Living tree
- (69) "Rooted bifurcating"-This term is used to denote
- a) two descendants arising from each interior node
b) two descendants arising from different nodes
c) two descendants arising from different species
d) None of them
- (70) The branch point denotes
- a) divergence event
b) Convergence event
c) Multivergence event
d) No eventual significance

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