Gujarat Biotechnology Research Centre

Computational BT

Application No: ____________________________

This question booklet contains 28 pages

Time: 2 Hours
Total Marks: 200
Total Questions: 200

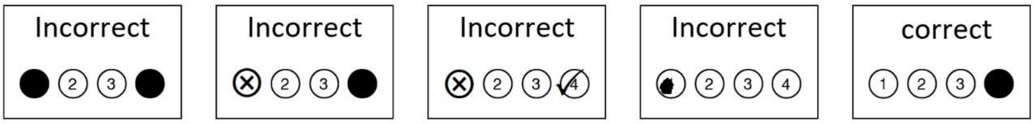
Candidate Signature : ....

Invigilator Signature : ....

Instructions for Candidate

---

1. This question booklet contains 200 questions.
2. Each correct answer carries 1 mark.
3. Every attempted question with incorrect answer shall carry a negative mark of 0.25.
4. Use only Black Ball Point Pen to darken the appropriate circle in OMR.
5. Please darken the complete circle.
6. Darken ONLY ONE CIRCLE for each Question as shown below:



7. Answer once marked cannot be changed.
8. Please do not make any stray marks on the Question Booklet.
9. Rough works must be done on the blank page of Question Booklet.
10. Mark your answer in the appropriate space in the Answer Sheet against the Number corresponding to the question.
11. The Candidate has to submit Question booklet and OMR response sheet to the invigilator on conclusion of examination.

1 Which taxon is Smallest, Mutable, and having animal with Interbreeding capability and similar morphology?
(A) Species
(B) Genus
(C) Family
(D) Order

2 Which structure appear first during embryo development?
(A) Yolk Plug
(B) Archenteron
(C) Notochord
(D) Blastocoel

3 The enzyme which removes hydrogen from the substrate is known as:
(A) Oxido-Reductase
(B) Dehydrogenase
(C) Hydrogenase
(D) Hydrolysis

4 Which of the following sets is not co enzyme?
(A) NAD, FAD, ATP
(B) NAD, NHDP,FMN
(C) Fe, Cu, Zn
(D) V, Ca, Mg

5 Which of the following methods does not require any carrier or channel for transport of substances?
(A) Secondary active transport
(B) Facilitated diffusion
(C) Simple diffusion
(D) Primary active transport

6 Which type of movement occurs when Na/K pump is used?
(A) Na ions moves out of the cell and Kions move in
(B) K+ ion moves out of cell and Na ion move in
(C) Both Na and Kions ions move inside the cell
(D) Both Na and Kions move out of the cell

7 Which of the following is correct for the partial pressure of oxygen in alveoli?
(A) Less than carbon dioxide
(B) Less than the blood
(C) More than the blood
(D) Equal to that of the blood

8 Correct sequence of urine formation is
(A) Filtration, reabsorption, secretion
(B) Secretion, reabsorption, filtration
(C) Reabsorption, secretion, filtration
(D) Reabsorption, filtration, secretion

9 Monocytes differentiate into which kind of phagocytic cells?

(A) Neutrophil
(B) B-cell
(C) Macrophage
(D) T-cell

10 Which of the following polypeptide is important for the expression of MHC I on the cell membrane?

(A) Interferons
(B) B2-Microglobulin
(C) Lymphokines
(D) Interleukins

11 Which of the following type of vaccine did the Moderna and Pfizer-BioNtech companies designed for COVID-19?

(A) Toxoid Vaccine
(B) Subunit Vaccine
(C) mRNA Vaccine
(D) Vector Borne Vaccine

12 In Ramachandran plot, which amino acid is allowable in non-allowable region?

(A) Tyr
(B) Gly
(C) Cys
(D) Leu

13 When the two sequences have substantial regions of similarity, many dots line up to form contiguous _______ lines.

(A) crossings on
(B) horizontal
(C) diagonal
(D) vertical

14 What does C-value in genome denotes?

(A) Qualitative traits
(B) Phenotypic variation
(C) Amount of DNA present in the genome
(D) Genetic disorders

15 Which of the following factors is not responsible for the denaturation of proteins?

(A) Heat
(B) Charge
(C) pH change
(D) Organic solvents

16 Which of the following is accountable for specifying the 3D shape of a protein?

(A) The peptide bond
(B) The amino acid sequence
(C) Interaction with other polypeptides
(D) Interaction with molecular chaperons

17 Which of the following is the first protein sequenced by Frederick Sanger?

(A) Hemoglobin
(B) myoglobin
(C) insulin
(D) myosin

18 Phylogenetic relationship can be represented by

(A) Data retrieving tool
(B) Gene Bank
(C) Dendrogram
(D) Data search tool

19 Which are the commonly used vectors for human genome sequencing?

(A) Expression vector
(B) BAC vectors
(C) T/C cloning vector
(D) T-DNA

20 Which of the following is not a part of downstream processing?

(A) Separation
(B) Preservation
(C) Purification
(D) Expression

21 Which one of the following features distinguishes between gymnosperms & angiosperms?

(A) Seed formation
(B) Vascular tissues
(C) Seed cover
(D) Gamete production

22 Mycorrhizae are the example of symbiotic relationships between

(A) Algae and fungi
(B) Root and fungi
(C) Bacteria and root
(D) Bacteria and fungi

23 You are isolating DNA from bacteria, which of the following enzymes is not used in the isolation process?

(A) Lysozyme
(B) Ribonuclease
(C) Deoxyribonuclease
(D) Protease

24 Which of the following is called as dideoxynucleotide chain termination method?

(A) Sanger Method
(B) Maxam Gilbert method
(C) Edman's method
(D) Automated Sequencing method

25 Which is the recommended way of freezing animal cells?

(A) Freeze as rapidly as possible
(B) Freeze slowly, at about 1 degree per minute
(C) Freeze sequentially with some time interval
(D) Keep at -20°C for long time

26 ABC transporters falls in to the category of?

(A) Passive diffusion
(B) Facilitated diffusion
(C) Active transport
(D) Group translocation

27 Which of the following is the site where tRNA donates its amino acid to growing polypeptide chain?

(A) mRNA Binding site
(B) A site
(C) P site
(D) E site

28 An intermediate that connects TCA cycle with Urea cycle is __________

(A) Fumarate
(B) Aspartate
(C) Bicarbonate
(D) Oxaloacetate

29 Even though methionine is a sulphur containing amino acid, why it cannot develop disulfide bond as cysteine does?

(A) More hydrophobic than cysteine
(B) Sterically larger than cysteine
(C) Less reactive than cysteine
(D) Polarizability of divalent sulphur is less

30 What is the difference between conventional molecular mechanics (MM) and -Poisson Bolzmann surface area (MM-PBSA) concepts to estimate free energy of binding?

(A) Both MM and MM-PBSA methods calculate ΔG bind without solvent
(B) Solute entropy is not incorporated as a energy term to calculate MM ΔG bind
(C) Solvation free energy can be incorporated in MM method without definition of solvent
(D) Solute entropy and solvation free energy are assumed as penalty in MM methods

31 Which among the following can be considered as large-scale motions?

(A) Loop motions
(B) Helix coil transitions
(C) Domain motions (hinge bending)
(D) Subunit motions

32 In Michaelis Menten reaction, why Vm is a rarely measurable quantity?

(A) At very high [S], v does not increase with increasing [S]
(B) At low [S], v only increases linearly with [S]
(C) Since both zero and first order kinetics are involved in a single reaction
(D) Not possible to add sufficient quantities of [S] to saturate enzyme

33 Which among the following is not a KEGG main database?

(A) KEGG Network
(B) KEGG Pathway
(C) KEGG Atlas
(D) KEGG BRITE

34 Viral load is routinely tested for disease/illness except _____

(A) HIV-1
(B) Cytomegalovirus
(C) Yellow fever
(D) Hepatitis B and C viruses

35 Ethanol decreases gluconeogenesis by ___________

(A) Inhibiting glucose-6-phosphatase
(B) Inhibiting PEP carboxykinase
(C) Converting NAD+ into NADH and decreasing the availability of pyruvate
(D) Converting NAD+ into NADH and decreasing the availability of lactate

36 Cancer cells are ___________

(A) BHK
(B) Veo
(C) HL-8
(D) Hela cells

37 What type of genome map is the most ideal for understanding the nature of genes, what they code for, and their functions?

(A) Linkage maps
(B) Physical maps
(C) Sequence maps
(D) Contig maps

38 A geneticist isolates a gene for a specific trait under study. He also isolates the corresponding mRNA. Upon comparison, the mRNA is found to contain 1,000 fewer bases than the DNA sequence. Did the geneticist isolate the wrong DNA?

(A) Yes, mRNA is made from a DNA template and should be the same length as the gene sequence
(B) Yes, the mRNA should contain more bases than the DNA sequence because bases flanking the gene are also transcribed
(C) No, the final mRNA contains only exons, the introns were removed
(D) No, the mRNA was partially degraded after it was transcribed

39 The size of the human genome is about _______ times larger than that of H. influenzae.

(A) 20 million
(B) 3000
(C) 100
(D) 1500

40 Which statement is incorrect in procedure between Northern and Southern hybridizations?

(A) DMB membrane is used in Northern hybridization
(B) RNA:DNA hybrids are formed in Northern hybridization
(C) Initially fragments are separated by electrophoresis in Northen hybridization
(D) DNA denaturation is required before blotting in Southern hybridization

41 The classical pathway of complement system is activated by

(A) Antibody-antigen complexes
(B) Antigen
(C) Antigenic peptides
(D) Antigens bound to MHC

42 What will be the assembly product of two subunits 40 S and 60 S of the ribosome?

(A) 70 S
(B) 100 S
(C) 80 S
(D) 20 S

43 What does a negative value of σ signify for a substituent?

(A) It is electron donating
(B) It is electron withdrawing
(C) It is neutral
(D) It is hydrophobic

44 Which of the following statement is false when comparing 3D QSAR with conventional QSAR?

(A) Only drugs of the same structural class should be studied by 3D QSAR or QSAR
(B) 3D QSAR has a predictive quality unlike QSAR
(C) Experimental parameters are not required by 3D QSAR, but are for QSAR
(D) Results can be shown graphically in 3D QSAR, but not with QSAR

45 Some orally active drugs do not obey the rule of five. For example, some drugs with molecular weights greater than 500 are found to be orally active. Which of the following mechanisms is the most likely reason for this?

(A) Transport by transport proteins
(B) Passage through pores between the cells of the gut wall
(C) Pinocytosis
(D) Ion channels

46 Which of the following operations or calculations would generally be carried out using molecular mechanics?

(A) Molecular orbital energies
(B) Energy minimization
(C) Electrostatic potentials
(D) Transition-state geometries

47 For a spontaneous change in a system at constant temperature and pressure, which of the following statements is true?

(A) $\Delta G < 0$
(B) $\Delta G = 0$
(C) $\Delta G > 0$
(D) There is no restriction on the value of ΔG

48 What is the ultimate motive of virtual screening?

(A) Identifying the best-scoring molecules that can be tested using biochemical experiments
(B) Recognizing the scaffold which preferentially binds to the protein pocket
(C) Assessing the docking accuracy of molecular docking approach
(D) Best-scoring molecules can be directly tested in animal models without biochemical testing

49 Which among the following is not a chemical database?

(A) PubChem
(B) ChEMBL
(C) ZINC
(D) PDB

50 Which one of the following terms is not related to AutoDock Vina?

(A) Empirical scoring function
(B) Genetic algorithm
(C) Complexity
(D) Grid dimensions

51 How genetic algorithm accelerates docking calculations and provide optimal dock poses?

(A) Genetic algorithm is stochastic in nature and generates multiple solutions through randomization events such as cross-over and mutation
(B) Genetic algorithm makes systematic searches for all rotatable bonds in an incremental order to provide optimal dock poses
(C) Genetic algorithm accelerates docking calculations by pre-calculated affinity maps
(D) Genetic algorithm does not consider torsional angles while docking

52 Which one of the following statements are appropriate?

(A) T-cytotoxic cell expresses CD4, CD4 recognizes MHC Class II expressing antigen
(B) T-helper cell expresses CD4, CD4 recognizes MHC Class II expressing antigen
(C) T-helper cell expresses CD8, CD8 recognizes MHC Class I expressing antigen
(D) T-cytotoxic cell expresses CD8, CD8 recognizes MHC Class II expressing antigen

53 Which one of the following method employ molecular dynamics simulations to assess the binding ability of peptide/epitope to pMHC:T-cell receptor:CD4:pMHCI complex?

(A) Welling’s method
(B) Rothbard and Taylor method
(C) Darren Flower method
(D) Kolaskar and Tongaonkar’s method

54 What is an EST sequence?

(A) EST is a single pass, short 300-500 nucleotide sequence
(B) EST is a contig sequence obtained from various sequencing projects
(C) EST is a part of genome belonging to non-coding regions of the genome
(D) EST is a set of introns combined

55 Which of the database is used in BLASTN?

(A) WGS
(B) Swiss-Prot
(C) Refseq
(D) Nt

56 Microarray data-analysis does not include the step

(A) Quality Check
(B) Hierarchical clustering
(C) Expression Analysis
(D) Gene ontology

57 What is a CAS registry number?

(A) Unique numerical identifiers assigned by the Chemical Abstracts Service
(B) Unique numerical identifiers assigned by the NCBI
(C) Unique numerical identifiers assigned by the IUPAC committee
(D) Unique numerical identifiers assigned by the Royal Society of Chemistry

58 Which of the following is not PubChem BioAssay activity discriminator?

(A) Activity Outcome
(B) Similarity
(C) Linear Score
(D) Percentile Score

59 Grid spacing in docking and other computational approaches requires a predefined grid point spacing value? What will be criteria for choosing appropriate grid value?

(A) Roughly a quarter of the length of a carbon-carbon single bond
(B) Roughly a half of the length of a carbon-carbon single bond
(C) Equal to the length of a carbon-carbon single bond
(D) It depends upon the probe size

60 Which of the following is an example of Homology and similarity tool?

(A) 8 bp
(B) 6 bp
(C) 7 bp
(D) 5 bp

61 Which of the following is an example of Homology and similarity tool?

(A) BLAST
(B) RasMol
(C) EMBOSS
(D) PROSPECT

62 Which of the following is not a domain in GO terms?

(A) Cellular component
(B) Molecular function
(C) Biological process
(D) Mechanistic studies

63 Which among the following is a default scoring matrix in NCBI Blast program?

(A) BLOSUM45
(B) BLOSUM62
(C) PAM250
(D) PAM70

64 Levinthal paradox is a concept of ___

(A) Protein misfolding
(B) Protein aggregation
(C) Protein folding
(D) Protein mismatching

65 When [S] = KM, the velocity of an enzyme catalyzed reaction is about:

(A) 0.1x Vmax
(B) 0.2 xVmax
(C) 0.3 xVmax
(D) 0.5 xVmax

66 Succinyl co A is cleaved by-

(A) Succinate dehydrogenase
(B) Succinate thiokinase
(C) Succinate lyase
(D) Succinate thioesterase

67 Although the Ti plasmid has revolutionized plant genetic engineering, one limitation of its use is that it

(A) Cannot infect broadleaf plants.
(B) Cannot be used on fruit-bearing plants.
(C) Cannot transmit prokaryotic genes.
(D) Does not infect cereal plants such as corn and rice.

68 Which test is used for detecting susceptibility of an individual to diphtheria toxin?

(A) Schick tests
(B) Dick test
(C) V-P test
(D) Precipitin test

69 The first protein synthesized by recombinant DNA technology was

(A) Streptokinase
(B) Human growth hormone
(C) Tissue plasminogen activator
(D) Human insulin

70 Leucine zipper motif is seen in some helical proteins when leucine residues appear at every

(A) 3rd position
(B) 5th position
(C) 7th position
(D) 9th position

71 The sum total of an organism’s interaction with the biotic and abiotic resources of its environment is called its ____

(A) Logistic growth
(B) Biotic potential
(C) Ecological niche
(D) Microclimax

72 Which of the following is untrue regarding expressed sequence tags (ESTs)?

(A) One of the high throughput approaches to genome-wide profiling of gene expression is sequencing ESTs
(B) They are short sequences obtained from cDNA clones
(C) They serve as short identifiers of full-length genes
(D) They are typically in the range of 1100 to 1200 nucleotides in length

73 Small cDNA sequence that represents a unique segment of an active gene is called

(A) SNPs
(B) SnRNAs
(C) ESTs
(D) Contigs

74 In BLAST search E value becomes smaller

(A) the value K also becomes smaller
(B) The score tends to be larger
(C) the probability p tends to be larger
(D) The extreme value distribution becomes less skewed.

75 Which of the following tool is used for genome alignment?

(A) Chime
(B) clustal
(C) FASTA
(D) vista

76 In sequence alignment, Gap symbol is represented by

(A) _ or -
(B) > or <
(C) | or :
(D) $ or #

77 The retrieval and search tool of the NCBI is

(A) sakura
(B) webin
(C) entrez
(D) seqin

78 GeneBank and DDBJ are example of

(A) Primary database
(B) Secondary database
(C) Composite database
(D) Tertiary database

79 Which is the in vitro molecular biology technique which helps in identification and quantification of Protein-Protein Interactions?

(A) CRISPER
(B) Yeast-Two Hybrid System
(C) SNP Microarray Assay
(D) Oligonucleotide Microarray

80 Where does the Fluorescence in situ hybridization (FISH) probe localize to?

(A) Golgi Apparatus
(B) Cell Membrane
(C) Nucleus
(D) Cytoplasm

81 The stage in which chromosomes align on the equator of spindle fiber is

(A) Telophase
(B) Anaphase
(C) Metaphase
(D) Prophase

82 Which of the following centrifugation is used to separate certain organelles from whole cell?

(A) Rate-Zonal Centrifugation
(B) Normal Centrifugation
(C) Differential Centrifugation
(D) Isopycnic Centrifugation

83 Which of the following scientists created the first Bioinformatics database?

(A) Dayhoff
(B) Pearson
(C) Richard Durbin
(D) Michael.J.Dunn

84 Which of the following tools is used for the identification of motifs?

(A) BLAST
(B) COPIA
(C) PROSPECT
(D) Pattern hunter

85 Which of the following compounds has desirable properties to become a drug?

(A) Fit drug
(B) Lead
(C) Fit compound
(D) Receptor

86 What is the deposition of cDNA into the inert structure called?

(A) DNA probes
(B) DNA polymerase
(C) DNA microarrays
(D) DNA fingerprinting

87 The process of finding the relative location of genes on a chromosome is called __________.

(A) Gene tracking
(B) Chromosome walking
(C) Genome mapping
(D) Genome walking

88 The stepwise method for solving problems in computer science is called__________.

(A) Flowchart
(B) Algorithm
(C) Procedure
(D) Sequential design

89 Which of the following is the first completed and published gene sequence?

(A) ΦX174

(B) T4 phage

(C) M13 phage

(D) Lambda phage

90 A minimal constitutes genome, which is a _____ set of genes required for maintaining a free-living cellular organism.

(A) maximum

(B) maximal

(C) highest number of set of

(D) minimal

91 The shotgun approach _______ sequences clones from _____ of cloned DNA.

(A) randomly, one end

(B) randomly, both ends

(C) specifically, both ends

(D) specifically, one end

92 Genetic markers are ______ portions of a _______ whose inheritance patterns can be followed.

(A) unidentifiable, genes

(B) unidentifiable, chromosome

(C) identifiable, chromosome

(D) identifiable, genes

93 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

94 Motifs that can form α/β horseshoes conformation are rich with which protein residue?

(A) Proline

(B) Arginine

(C) Valine

(D) Leucine

95 Which of the following is not a member database of InterPro?

(A) Pfam

(B) PANTHER

(C) SCOP

(D) HAMAP

96 Which of the following is not a characteristic of exact matches in regular expression?

(A) There must be a strict match of sequence patterns

(B) Any variations in the query sequence from the predefined patterns are not allowed

(C) Provide more permissive matching by allowing more flexible matching of residues of similar biochemical properties

(D) Searching a motif database using this approach results in either a match or non-match

97 What is the source of protein structures in SCOP and CATH?

(A) Uniprot
(B) Protein Data Bank
(C) Ensemble
(D) InterPro

98 Which of the following statements about SUPERFAMILY database is incorrect regarding its features?

(A) Sequences can be submitted raw or FASTA format
(B) Sequences must be submitted in FASTA format only
(C) It searches the database using a superfamily, family, or species name plus a sequence, SCOP, PDB or HMM ID's
(D) It has generated GO annotations for evolutionarily closed domains and distant domains

99 Which of the following is wrong in case of substitution matrices?

(A) They determine likelihood of homology between two sequences
(B) They use system where substitutions that are more likely should get a higher score
(C) BLOSUM-X type uses logarithmic identity to find similarity
(D) They use system where substitutions that are less likely should get a lower score

100 Among the following which one is not the approach to the local alignment?

(A) Smith-Waterman algorithm
(B) K-tuple method
(C) Words method
(D) Needleman-Wunsch algorithm

101 Gibbs is a web-based program that uses the Gibbs sampling approach to look for _____ gap-free segments for either DNA or protein sequences.

(A) short, partially conserved
(B) long, partially conserved
(C) long, conserved
(D) short, not conserved

102 The softwares for dot plot analysis perform several tasks. Which one of the below is not performed by them?

(A) Gap open penalty
(B) Gap extend penalty
(C) Expectation threshold
(D) Change or mutate residues

103 The matrices PAM250 and BLOSUM62 contain _______

(A) positive and negative values
(B) positive values only
(C) negative values only
(D) neither positive nor negative values, just the percentage

104 Gaps are added to the alignment because it ______

(A) increases the matching of identical amino acids at subsequent portions in the alignment
(B) increases the matching of or dissimilar amino acids at subsequent portions in the alignment
(C) reduces the overall score
(D) enhances the area of the sequences

105 The statistical analysis of alignment scores is much better understood for ________ than for _______.

(A) global alignments, local alignments
(B) global alignments, any other alignment method
(C) local alignments, global alignments
(D) Needleman-Wunsch alignment, Smith-Waterman alignment

106 When the two sequences have substantial regions of similarity, many dots line up to form contiguous _______ lines.

(A) crossings on
(B) horizontal
(C) diagonal
(D) vertical

107 Which of the following scores are not considered while calculating the SP scores?

(A) All possible pair wise matches
(B) All possible mismatches
(C) All possible gap costs
(D) Number of gap penalties

108 Which of the following is not the objective to perform sequence comparison?

(A) To observe patterns of conservation
(B) To find the common motifs present in both sequences
(C) To study the physical properties of molecules
(D) To study evolutionary relationships

109 CLUSTALW is a more recent version of CLUSTAL with the W standing for ________

(A) Weakening
(B) Winding
(C) Weighting
(D) Wiping

110 In Genetic Algorithm, in the mutation process _______

(A) sequence is changed
(B) gaps are not inserted
(C) sequence is not changed
(D) gaps are not rearranged

111 Which of the following is not among the methods for finding localized sequence similarity?

(A) Profile Analysis
(B) Block Analysis
(C) Extraction of Blocks from a Global or Local MSA
(D) Pattern blocking

112 Profiles are found by performing the _____ MSA of a group of sequences and then removing the _______ regions in the alignment into a smaller MSA.

(A) local, more highly conserved
(B) global, low conserved
(C) global, more highly conserved
(D) local, low conserved

113 If the data set is _______ then unless the motif has __________ amino acids in each column, the column frequencies in the motif may not be highly representative of all other occurrences of the motif.

(A) small, distinct
(B) small, almost identical
(C) large, almost identical
(D) large, distinct

114 BLAST uses a _______ to find matching words, whereas FASTA identifies identical matching words using the _____

(A) substitution matrix, hashing procedure
(B) substitution matrix, blocks
(C) hashing procedure, substitution matrix
(D) ktups, substitution matrix

115 In Smith–Waterman algorithm, in initialization Step, the _________ row and ________ column are subject to gap penalty.

(A) first, first
(B) first, second
(C) second, First
(D) first, last

116 ______ the smallest amino acid, has a hydrogen atom as the R group.

(A) Valine
(B) Proline
(C) Glycine
(D) Threonine

117 A linear polymer of more than fifty amino acid residues is referred to as a ________

(A) Dipeptide
(B) Oligopeptide
(C) Peptide
(D) Polypeptide

118 Which of the following is wrong about Swiss-PDB Viewer?

(A) It is a structure viewer for multiple platforms
(B) It is a structure viewer for single platforms
(C) It is essentially a Swiss-Army knife for structure visualization and modeling
(D) It is capable of structure visualization, analysis, and homology modeling

119 The intermolecular approach is normally applied to relatively _____ structures.

(A) distinctive
(B) dissimilar
(C) similar
(D) different

120 Members within the ____ fold ______ have evolutionary relationships.

(A) same, always
(B) same, do not always
(C) one, always
(D) different, do not

121 The formation of _____ is determined by ______ interactions, whereas the formation of ____ is strongly influenced by ______ interactions.

(A) α-helices, long-range, α-helices, short-range
(B) α-helices, long-range, β-strands, short-range
(C) α-helices, short-range, β-strands, long-range
(D) β-strands, short-range, β-strands, long-range

122 The presence of ______ signal peptides can significantly compromise the prediction _______ because the programs tend to confuse hydrophobic signal peptides with membrane helices.

(A) hydrophobic, accuracy
(B) hydrophobic, error
(C) hydrophilic, accuracy
(D) hydrophilic, error

123 Which of the following is true regarding Coiled coil?

(A) They have an integral repeat of twenty residues
(B) They have an integral repeat of seven residues
(C) They have an integral repeat of thirty residues
(D) The sequence periodicity doesn't contribute in designing algorithms to predict the structural domain.

124 In Rosetta, the segments with assigned _______ structures are subsequently assembled into a ______ dimensional configuration.

(A) primary, three
(B) secondary, three
(C) secondary, two
(D) primary, two

125 Which of the following is untrue about homology modeling?

(A) Homology modeling predicts protein structures based on sequence homology with known structures
(B) It is also known as comparative modeling
(C) The principle behind it is that if two proteins share a high enough sequence similarity, they are likely to have very similar three-dimensional structures
(D) It doesn't involve the evolutionary distances anywhere

126 RNA structures can be experimentally determined using _____

(A) X-ray crystallography techniques only
(B) NMR techniques only
(C) X-ray crystallography or NMR techniques
(D) Gel electrophoresis

127 In addition to the canonical base pairing, there often exists non-canonical base pairing such as _________ and ________ base paring.

(A) G, U
(B) G, C
(C) U, C
(D) A, C

128 The ______ refers to a structure with two ends of a single-stranded region (loop) connecting a base-paired region (stem).

(A) helical junctions
(B) hairpin loop
(C) bulge loop
(D) interior loop

129 The attractive interactions lead to _________ energy.

(A) increased
(B) higher
(C) lower
(D) no change in

130 In dot matrix in ab initio methods, the diagonals _________ to the main diagonal represent regions that can self hybridize.

(A) parallel
(B) cutting in random fashion
(C) perpendicular
(D) adjacent parallel

131 In comparative approach to RNA structure prediction, in Dynalign program–by comparing _________ from each sequence, a ______ structure common to both sequences is selected that serves as the basis for sequence alignment.

(A) multiple alternative structures, lowest energy
(B) single structure, lowest energy
(C) single structure, highest energy
(D) multiple alternative structures, highest energy

132 ____ wobble pairs may be produced in these double-stranded regions.

(A) A/A
(B) A/U
(C) G/C
(D) G/U

133 Martinez (1984) made a list of possible double-stranded regions, and these regions were then given weights in proportion to their equilibrium constants, calculated by ______

(A) the Boltzmann function [exp (-ΔG/RT2)]
(B) the Boltzmann function [exp (-ΔG/RT)]
(C) the Boltzmann function [exp (-ΔG/RT -T)]
(D) the Boltzmann function [exp (ΔG/RT)]

134 ______ regions in sequences, such as those in RNA that will form secondary structures, are an example of such context-free sequences.

(A) Non-interlocking
(B) Non-Complementary
(C) Complementary
(D) Non-compatible

135 In the programs related to FOLD, the second region, the ________ region, is used to calculate the energy of the ________ structure.

(A) included, most likely
(B) included, best
(C) excluded, least likely
(D) excluded, best

136 For ______ RNA sequences, such as tRNA, some programs may be able to produce _________% accuracy.

(A) small, 70
(B) small, 40
(C) large, 90
(D) large, 75

137 The type of algorithm that _____ predefined alignment is ______ for reasonably conserved sequences.

(A) doesn't require, more successful
(B) requires, less successful
(C) doesn't require, relatively successful
(D) requires, relatively successful

138 The problem of dynamic programming to select one single structure can be complemented by adding a probability distribution function, known as the _________ which calculates a mathematical distribution of probable base pairs in thermodynamic equilibrium.

(A) partition function
(B) division function
(C) increment function
(D) fold function

139 Which of the following is a model organism database?

(A) GOLD SCOP
(B) PRO
(C) SGD GOL
(D) SGD

140 What is a biomarker?

(A) the color coding of different genes
(B) a protein that is uniquely produced in a diseased state
(C) a molecule in the genome or proteome
(D) a marker that is genetically inherited

141 You need to use a first-generation sequencing method for de novo sequencing, which template should give optimum results for this project?

(A) Genomic DNA
(B) PCR product
(C) Bacterial artificial chromosome
(D) Plasmid DNA

142 Which of the following is incorrect regarding Mass Spectrometry Protein Identification?

(A) The proteolysis doesn’t generate a pattern according to molecular weight
(B) Proteins can be identified and characterized using MS
(C) The proteins from a two dimensional gel system are first digested in situ with a protease
(D) Protein spots of interest are excised from the two-dimensional gel

143 Which of the following is not true for Differential In-Gel Electrophoresis?

(A) Proteins from experimental and control samples are labeled with differently colored fluorescent dyes
(B) Differentially expressed proteins in both conditions can’t be visualized in the same gel
(C) Proteins are mixed together before electrophoresis on a two-dimensional gel
(D) In this, Differences in protein expression patterns can be detected in a similar way as in fluorescent-labeled DNA microarrays

144 In a statistical learning process called support vector machine (SVM), a hyperplane is _____.

(A) a linear or nonlinear mathematical function
(B) nonlinear mathematical function
(C) linear mathematical function
(D) exponential mathematical function

145 A disulfide bridge is a unique type of _____ modification in which _____ bonds are formed between cysteine residues.

(A) posttranslational, covalent
(B) translational, covalent
(C) translational, ionic
(D) posttranslational, ionic

146 The signal sequences have a _________ consensus but contain some specific features. They all have a ______ core region preceded by one or more positively charged residues.

(A) strong, hydrophilic
(B) weak, hydrophilic
(C) weak, hydrophobic
(D) strong, hydrophobic

147 The justification behind Rosetta stone method is that when two domains are fused in a single protein, they have to be in _______ proximity to perform a common function.

(A) distant
(B) close
(C) extremely distant
(D) extremely close

148 Which of the following is untrue regarding the classic yeast two-hybrid method?

(A) It is used for the detection of Protein interactions
(B) Method that relies on the interaction of “bait” and “prey” proteins in molecular constructs in yeast
(C) DNA-binding domain and a trans-activation domain don’t necessarily interact
(D) In this strategy, a two-domain transcriptional activator is employed as a helper for determining protein–protein interactions

149 Which of the following is improper about a microarray?

(A) It is the most commonly used global gene expression profiling method
(B) Each oligomer is spotted on the slide and serves as a probe for binding to a unique complementary cDNA
(C) Array of immobilized DNA oligomers cannot be cDNAs
(D) It is a slide attached with a high-density array of immobilized DNA oligomers representing the entire genome of the species under study

150 Which of the following is not among the methods for finding localized sequence similarity?

(A) Pattern blocking
(B) Extraction of Blocks from a Global or Local MSA
(C) Block Analysis
(D) Profile Analysis

151 The descriptions of morphological traits are often _____ which are due to _____

(A) clear, multiple genetic factors
(B) ambiguous, multiple genetic factors
(C) lucid, more than one genetic factors
(D) ambiguous, one or two genetic factors

152 To use molecular data to reconstruct evolutionary history requires making a number of reasonable assumptions. Which of the following is incorrect about it?

(A) The molecular sequences used in phylogenetic construction are homologous
(B) The molecular sequences used in phylogenetic construction share a common origin
(C) Phylogenetic divergence cannot be bifurcating
(D) Parent branch splits into two daughter branches at any given point

153 It is often desirable to define the root of a tree. There are two ways to define the root of a tree. One is to use an outgroup, which ______

(A) is a sequence that is homologous to the sequences under consideration
(B) is separated from those sequences at an early evolutionary time
(C) is generally determined from independent sources of information
(D) is generally determined from similar or related sources of information

154 For sequences that have ________ a phylogenetic analysis is __________

(A) diverged considerably, more challenging
(B) not diverged, more challenging
(C) diverged considerably, less challenging
(D) diverged considerably, a less work to do

155 Which of the following is wrong statement about the maximum likelihood approach?

(A) This method doesn’t always involve probability calculations
(B) It finds a tree that best accounts for the variation in a set of sequences
(C) The method is similar to the maximum parsimony method
(D) The analysis is performed on each column of a multiple sequence alignment

156 Which of the following is untrue regarding the distance methods?

(A) The distance method was pioneered by Feng and Doolittle
(B) A collection of programs by authors Feng and Doolittle will produce both an alignment and tree of a set of protein sequences
(C) The program CLUSTALW uses the neighbor-joining distance method as a guide to multiple sequence alignments
(D) Among the Programs of the PHYLIP package, DNADIST is not one of them

157 Which of the following is a wrong statement?

(A) Prokaryotes include bacteria and Archaea
(B) Prokaryotes have relatively large genomes
(C) Prokaryotes have relatively small genomes
(D) In Prokaryotes, The gene density in the genomes is high, with more than 90% of a genome sequence containing coding sequence

158 The presence of the codons at The beginning of the frame _____ give a clear indication of the translation initiation site.

(A) always
(B) does not necessarily
(C) does not
(D) never

159 Most vertebrate genes use __________ as the translation start codon and have a uniquely conserved flanking sequence call a Kozak sequence (CCGCCATGG).

(A) AAG
(B) ATG
(C) AUG
(D) AGG

160 In case of Protein-ligand docking, ______ ligands are often _____ in adapting their shape to fit the receptor binding pocket.

(A) small molecule, highly flexible
(B) large molecule, highly flexible
(C) large molecule, more flexible
(D) small molecule, less flexible

161 An understanding of the importance of different factors in a particular interaction is important if confidence in the results is required. Which of the following are not those factors?

(A) pH
(B) Electrostatics
(C) Hydrophobicity
(D) Shape

162 Interactions between proteins can be predicted computationally by looking for sets of genes that occur as a _______

(A) single gene in at least one genome
(B) multiple genes in at least one genome
(C) multiple genes in various genomes
(D) single gene in various genomes

163 Which of the following information Sequence comparisons do not provide?

(A) Gene relationships
(B) Function history
(C) Evolutionary history
(D) Gene locations

164 In protein/domain analysis, each protein in the predicted proteome is again used as a query of a curated protein sequence database such as ____ in order to locate similar domains and sequences. To find orthologs, very low E value scores (E<10<20) for the

(A) PubChem
(B) MeSH
(C) Genbank
(D) SwissProt

165 _______ of the Drosophila sequence is composed of TEs and _____ is heterochromatic regions that do not include genes.

(A) one-sixth, one-third
(B) one-fifth, one-fourth
(C) one-fourth, one-third
(D) one-sixth, one-eighth

166 According to standard amino acid code letters which of the given pair is not right?

(A) Q- glutamine
(B) R- serine
(C) K- lysine
(D) Y- tyrosine

167 Screening the predicted protein sequences against ______ library confirms the prediction and expression of the gene.

(A) expressed sequence tag (EST)
(B) tags
(C) palindromes
(D) proteomes

168 Which of the following information is not directly obtained by microarray analysis?

(A) Which genes are expressed at a particular stage of the cell cycle
(B) Which genes are depleted at what time
(C) Which genes are expressed at a particular stage of developmental cycle of an organism
(D) Genes that respond to a given environmental signal to the same extent

169 The human genome contains about _________ of class II of elements that probably predate human evolution (Smit 1996).

(A) 2,000 copies
(B) 2,00,00,000 copies
(C) 20,00,000 copies
(D) 200,000 copies

170 Which of the given is wrongly matched?

(A) Escherichia coli – Bacteria
(B) Methanococcus jannaschii – Archaea
(C) Synechocystis sp. – Archaea
(D) Aquifex aeolicus – Bacteria

171 Which of the following is incorrect about ENTREZ?

(A) One straightforward way to access the sequence databases is through ENTREZ
(B) It is a resource prepared only by the staff of the National Center for Biotechnology Information
(C) It provides a series of forms that can be filled out to retrieve a Medline reference related to the molecular biology sequence databases
(D) It provides a series of forms that can be filled out to retrieve a DNA or protein sequence

172 Knowing ________ should be enough to find the required entry quickly.

(A) publication date, protein name, journal name
(B) accession number, protein name, or name of gene
(C) publication date, protein name, or volume
(D) properties, protein name, or title word

173 Which of the following is untrue about Shotgun Sequencing?

(A) When DNA fragments derived from different chromosomal regions have repeats of the same sequence, they will appear to scrutinize
(B) In a new whole shotgun approach, Celera Genomics is sequencing both ends of DNA fragments of short (2 kb), medium (10 kb), and long (BAC or >100 kb) lengths
(C) A large number of reads are then assembled by computer
(D) When DNA fragments derived from different chromosomal regions have repeats of the same sequence, they will appear to overlap

174 Emotif uses which databases for alignment of sequences?

(A) BLOCKS and PRINTS databases
(B) PROSITE
(C) BLOCKS
(D) PRINTS

175 Which of the following is not a software for dot plot analysis?

(A) SIMMI
(B) DOTLET
(C) DOTMATCHER
(D) LALIGN

176 What is used to generate parameters for the extreme distribution?

(A) The pool of alignment scores from the shuffled sequences
(B) A single score of a shuffled sequence
(C) The pool of alignment scores from the unshuffled sequences
(D) The basic optimal score computed at the beginning of the test

177 Which of the following is incorrect regarding sequence homology?

(A) Two sequences can have homologous relationship even if have do not have common origin
(B) It is an important concept in sequence analysis
(C) When two sequences are descended from a common evolutionary origin, they are said to have a homologous relationship
(D) When two sequences are descended from a common evolutionary origin, they are said to share homology

178 Which of the following is not correct about the α-Helices?

(A) An α-helix has a main chain backbone conformation that resembles a corkscrew
(B) Nearly all known α-helices are right handed, exhibiting a leftward spiral form
(C) Nearly all known α-helices are right handed, exhibiting a rightward spiral form
(D) In right handed helix, there are 3.6 amino acids per helical turn

179 The type of algorithm that requires predefined alignment, requires the user to provide ______ alignment as input.

(A) not necessarily an alignment
(B) multiple only
(C) pairwise or multiple
(D) pair wise only

180 Information obtained by microscopic analysis of stained chromosomes is used in:

(A) cytogenetic mapping
(B) radiation hybrid mapping
(C) sequence mapping
(D) RFLP mapping

181 Which of the following is inappropriate about Bootstrapping?

(A) It is a statistical technique that tests the sampling errors of a phylogenetic tree
(B) It does the tests by repeatedly sampling trees through slightly perturbed datasets
(C) A newly constructed tree is not biased at all
(D) The robustness of the original tree can be assessed here

182 In the final steps of the bootstrap method, the _______ the decay value, the ________ significant the original branches.

(A) greater, less
(B) greater, more
(C) lesser, more
(D) more, less

183 The main disadvantage of maximum likelihood methods is that they are _____

(A) computationally lucid
(B) mathematically less complex
(C) computationally intense
(D) mathematically less folded

184 WU-BLAST produces P scores and BLAST (NCBI) produces E scores where _________

(A) E = ln (1 + P2)
(B) E = ln (1 – P2)
(C) E = ln (1 + P)
(D) E = ln (1 – P)

185 The sequences of satellite DNA fall into different types, each with a different repeat unit of length _____

(A) 5–400 Mbp
(B) 3–300 kbp
(C) 6–900 Mbp
(D) 5–200 bp

186 Which is the main characteristic of all fatty acid components in the lipid?

(A) They all contain an unbranched carbon chain.
(B) They all contain unconjugated cis double bonds.
(C) They all are joined to glycerol through an ester bond.
(D) They all are hydrophilic because they contain oxygen.

187 Most of the carbon dioxide produced in the tissues is transported to the lungs as

(A) carbonates
(B) bicarbonates
(C) dissolved in the blood
(D) attached to hemoglobin

188 Which one of the following is not included in defence barriers of innate immunity

(A) Phagocytic Barriers
(B) Antibodies
(C) Blood Proteins
(D) Cytokines

189 Which is the METHOD used to produce a snapshot of the messenger RNA population?

(A) OMIM
(B) SNP
(C) SIFT
(D) SAGE

190 Beta-oxidation is the process by which fatty acid molecules are broken down in the mitochondria to generate _____

(A) Citric acid
(B) Pyruvate dehydrogenase
(C) Acetyl-coA
(D) Phosphatidylinositol phosphates

191 Which one of the following terms is not best suited to describe epitope and paratope?

(A) Epitopes are antigenic determinants
(B) Paratopes are parts of antibody where epitope interactions occur
(C) Epitope-paratope interaction is necessary for antigen-antibody reactions
(D) Epitopes are very rigid in nature whereas paratope is very flexible for binding

192 Conformational epitopes are recognized by?

(A) T-helper cells
(B) T-cytotoxic cells
(C) B lymphocytes
(D) Both T-helper cells and B lymphocytes

193 A clade is a monophyletic tree with ___ ancestor and all its descendants.

(A) Only 1
(B) 2
(C) No
(D) No specific number of

194 In Ramachandran's plot the value of Phi is the rotation angle around:

(A) N-Cα bond
(B) Cα-C bond
(C) C-N bond
(D) N-H bond

195 Conserved non-coding sequences often harbor

(A) Cis-regulatory elements
(B) Trans-regulatory elements
(C) Transposons
(D) Feromones

196 Semiconservative DNA or chromosome replication using 14N was demonstrated by

(A) Messelson
(B) Tylor
(C) Messelson and Stahl
(D) Hershey and Chase

197 Evolution of a particular sequence _______ correlate with the evolutionary path of the species.

(A) does not
(B) always
(C) does not necessarily
(D) invariably

198 Which of the following is not correct about FASTA?

(A) Its stands for FAST ALL
(B) It was in fact the first database similarity search tool developed, preceding the development of BLAST
(C) FASTA uses a 'hashing' strategy to find matches for a short stretch of identical residues with a length of k
(D) The string of residues is known as blocks

199 Which of the following is not true regarding TMHMM?

(A) It is a web-based program based on an HMM algorithm
(B) It is trained to recognize transmembrane helical patterns
(C) It is not trained to recognize transmembrane helical patterns
(D) When a query sequence is scanned, the probability of having an α-helical domain is given

200 Ab initio approach makes structural predictions based on ______

(A) a single RNA sequence
(B) comparing RNA sequences
(C) evolutionary basis
(D) pure phylogenetics

Computational Biotechnology
Provisional Answer Key

Q.No	Option	Q.No	Option	Q.No	Option	Q.No	Option
1	A	51	A	101	A	151	B
2	D	52	B	102	D	152	C
3	B	53	C	103	A	153	D
4	A	54	A	104	A	154	D
5	C	55	D	105	C	155	A
6	A	56	D	106	C	156	D
7	C	57	A	107	D	157	B
8	A	58	B	108	C	158	B
9	C	59	A	109	C	159	B
10	B	60	C	110	C	160	A
11	C	61	A	111	D	161	A
12	B	62	D	112	C	162	A
13	C	63	B	113	B	163	D
14	C	64	C	114	A	164	D
15	B	65	D	115	A	165	A
16	B	66	B	116	C	166	B
17	C	67	D	117	D	167	A
18	C	68	A	118	B	168	B
19	B	69	D	119	C	169	D
20	D	70	C	120	B	170	C
21	C	71	C	121	C	171	B
22	B	72	D	122	A	172	B
23	A	73	C	123	B	173	A
24	A	74	B	124	B	174	A
25	B	75	D	125	D	175	A
26	C	76	A	126	C	176	A
27	C	77	C	127	A	177	A
28	A	78	A	128	B	178	B
29	C	79	B	129	C	179	C
30	B	80	C	130	C	180	A
31	B	81	C	131	A	181	C
32	D	82	C	132	D	182	B
33	A	83	A	133	B	183	C
34	C	84	B	134	C	184	D
35	C	85	B	135	D	185	D
36	D	86	C	136	A	186	A
37	C	87	C	137	D	187	B
38	C	88	B	138	A	188	B
39	D	89	A	139	D	189	D
40	C	90	D	140	B	190	C
41	A	91	B	141	C	191	D
42	C	92	C	142	A	192	D
43	A	93	C	143	B	193	A
44	A	94	D	144	A	194	A
45	C	95	C	145	A	195	A
46	B	96	C	146	C	196	C
47	A	97	B	147	D	197	C
48	A	98	B	148	C	198	D
49	D	99	C	149	C	199	C
50	C	100	D	150	A	200	A