

Subject Code **0215**

BIOTECHNOLOGY- DSE-III

Question Booklet No.

Signature of Invigilator	To be filled in by candidate by ball-point pen only	OMR Sl. No. _____
	Roll No. _____	_____
Time of Examination	Declaration : I have read and understood the instructions given below.	Full Marks : 80/50
Date of Examination	Full Signature of Candidate	
	Name of Candidate	

Number of Questions in the Booklet } **50/40**



UU 6th Semester Examination, 2020

INSTRUCTIONS TO CANDIDATES

- Immediately after getting the booklet read instructions carefully mentioned on the front and back page of the Question Booklet. Do not open the seals unless asked by the Invigilator.
- Write your Roll No., OMR Response Sheet No., in the specified places given above and put your signature.
- Write the subject code of the booklet in your OMR Sheet.
- Make all entries in the OMR Response Sheet as per the given instructions; otherwise OMR Response Sheet will not be evaluated.
- After opening the seals, ensure that the Question Booklet contains total no. of pages as mentioned above and printing of all the **50 / 40** questions are proper. If any discrepancy is found, inform the invigilator within **15** minutes and get the correct Question Booklet.
- For each question in the Question Booklet choose the correct option from the given four alternatives and darken the same circle in the OMR Response Sheet with Black or Blue ball-point pen.
- Darken the circle of correct answer properly; otherwise answers will not be evaluated. The candidate will be fully responsible for it.
- If more than one option is darken foe a particular question, then it will be treated as wrong answer.
- After completion of the examination, only OMR Response Sheet is to be handed over to the invigilator.

THERE IS NO NEGATIVE MARKING FOR WRONG ANSWER

BIOTECHNOLOGY-DSE-III

(Answer any 40 questions)

- 1 A cladogram or phylogenetic tree
 - (A) is an hypothesis about the evolutionary relationships among a group of animal taxa
 - (B) is a diagram in which the sequence of branching illustrates the historical chronology of evolutionary event
 - (C) reflects the hierarchical classification of taxonomic groups nested within more inclusive groups.
 - (D) All of the above
- 2 A flat file format typically a
 - (A) sql file
 - (B) text file
 - (C) java file
 - (D) encrypted file
- 3 Alignment method suitable for aligning closely related sequence is
 - (A) multiple sequence alignment
 - (B) pair wise alignment
 - (C) global alignment
 - (D) local alignment
- 4 An example for protein secondary structure is _____
 - (A) alpha helix
 - (B) Cysteine
 - (C) beta sheets
 - (D) Both A and C
- 5 BLOSUM matrices are used for
 - (A) Multiple sequence alignment
 - (B) Pairwise sequence alignment
 - (C) Phylogenetic analysis
 - (D) All of the above
- 6 Chromatogram is?
 - (A) Solute concentration vs Elution time
 - (B) Solute concentration vs Elution volume
 - (C) both A and B
 - (D) None of the above
- 7 Cladogram, and dendrogram are used for what type of analysis
 - (A) Drug Design
 - (B) Database Design
 - (C) Phylogenetics Analysis
 - (D) Structure Analysis
- 8 Clastal W
 - (A) Multiple sequence alignment tool
 - (B) Protein secondary structure predicting tool
 - (C) Data retriving tool
 - (D) Nucleic acid sequence analysis tool
- 9 Data from which of the following sources are used for constructing phylogenetic trees:
 - (A) fossils
 - (B) morphological data
 - (C) molecular data
 - (D) all of the above

- 10 Data Stored in TrEMBL is
- (A) Nuclie Acid Sequence
 - (B) Nuclie Acid Structure
 - (C) Translated CDS
 - (D) Translated CDS + Submitted protein sequences
- 11 Entrez is part of
- (A) NCBI
 - (B) EMBL
 - (C) DDBJ
 - (D) SwissProt
- 12 Example for global sequence alignment algorithm?
- (A) Kadane's algorithm
 - (B) Needleman Wunsch algorithm
 - (C) Smith Waterman
 - (D) Gale-shapley algorithm
- 13 Example for local sequence alignment algorithm?
- (A) Kadane's algorithm
 - (B) Needleman Wunsch algorithm
 - (C) Smith Waterman
 - (D) Gale-shapley algorithm
- 14 FASTA Sequence starts with
- (A) Sequence name
 - (B) Accession No
 - (C) Greater-than symbol
 - (D) Less-than Symbol
- 15 Genbank is a part of
- (A) NCBI
 - (B) EMBL
 - (C) DDBJ
 - (D) SwissProt
- 16 In pairwise sequence alignment, gap score represents
- (A) Insertion/Deletion
 - (B) Insertion
 - (C) Mismatch
 - (D) Match
- 17 Nucleotide BLAST
- (A) BLASTp
 - (B) tBLASTn
 - (C) BLASTx
 - (D) BLASTn
- 18 PDB is
- (A) Primary database for macromolecules
 - (B) Can be determined by gel electrophoresis
 - (C) Composite database
 - (D) Sequence Database
- 19 Phylogenetic relationship can be shown by
- (A) Dendrogram
 - (B) Gene Bank
 - (C) Data retriving tool
 - (D) Data search tool

- 20 Protein BLAST
- (A) BLASTp
 - (B) tBLASTn
 - (C) BLASTx
 - (D) BLASTn
- 21 Protein sequence searched against translated nucleotide sequences
- (A) BLASTp
 - (B) tBLASTn
 - (C) BLASTx
 - (D) BLASTn
- 22 Proteomics refers to the study of _____.
- (A) Set of proteins in a specific region of the cell
 - (B) Biomolecules
 - (C) Set of proteins
 - (D) The entire set of expressed proteins in the cell
- 23 Ramachandran plot is used for analysis of
- (A) Protein sequence
 - (B) Nucleic Acid Sequence
 - (C) Protein Structure
 - (D) Nucleic acid Structure
- 24 Restriction enzymes are also called
- (A) molecular knives
 - (B) molecular scissors
 - (C) molecular scalpels
 - (D) all of these
- 25 Restriction enzymes capable of making internal cuts in a DNA molecule is called
- (A) restriction exonuclease
 - (B) restriction endonucleasae
 - (C) both A and B
 - (D) S1 nuclease
- 26 Reverse transcription PCR uses _____.
- (A) RNA as a template to form DNA
 - (B) mRNA as a template to form cDNA
 - (C) DNA as a template to form ssDNA
 - (D) All of the above
- 27 SAKURA was part of
- (A) NCBI
 - (B) EMBL
 - (C) DDBJ
 - (D) SwissProt
- 28 Sequence alignment helps scientists to
- (A) Trace out evolutionary relationships
 - (B) Infer the functions to newly synthesized genes
 - (C) Predict new members of gene families
 - (D) All the above
- 29 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) Molecular docking
 - (D) Molecule affinity checking

- 30 The correct order for the basic features of a mass spectrometer is
- (A) acceleration, deflection, detection, ionisation
 - (B) ionisation, acceleration, deflection, detection
 - (C) acceleration, ionisation, deflection, detection
 - (D) acceleration, deflection, ionisation, detection
- 31 The path of ions after deflection depends on
- (A) only the mass of the ion
 - (B) only the charge on the ion
 - (C) both the charge and the mass of the ion
 - (D) neither the charge nor the mass of the ion
- 32 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
- 33 The sequence recognised by the restriction enzyme to cut the DNA is called
- (A) recognition site
 - (B) restriction site
 - (C) both A and B
 - (D) cleavage sites
- 34 The stepwise method for solving problems in computer science is called _____.
- (A) Flowchart
 - (B) Algorithm
 - (C) Procedure
 - (D) Sequential design
- 35 *Thermus aquaticus* is the source of _____.
- (A) Vent polymerase
 - (B) Primase enzyme
 - (C) Taq polymerase
 - (D) Both A and C
- 36 Translated nucleotide sequence searched against protein sequences
- (A) BLASTp
 - (B) tBLASTn
 - (C) BLASTx
 - (D) BLASTn
- 37 What is EMBL?
- (A) European Molecular Biology Laboratory
 - (B) European Micro Biology Laboratory
 - (C) European Medical Biology Laboratory
 - (D) European Medical Micro Biology Laboratory
- 38 What is NCBI?
- (A) National Center for Biology Information
 - (B) National Center for Biotechnology Information
 - (C) National Center for Bioinformatics Institute
 - (D) National Center for Biological database Institute
- 39 What is plotted along the x-axis of a mass spectrum?
- (A) mass \times charge
 - (B) mass/energy
 - (C) mass/charge
 - (D) mass

- 40 What is the Analyte ?
(A) Substance for separation
(B) Substance for impurity
(C) both A and B
(D) None of the above
- 41 What sort of characters are useful in constructing phylogenetic trees?
(A) homologous traits
(B) shared derived traits
(C) both A and B
(D) None of the above
- 42 Where DDBJ is located?
(A) USA
(B) China
(C) Europe
(D) Japan
- 43 Which Clustal software was the first to have a graphical user interface.
(A) ClustalV
(B) ClustalX
(C) ClustalW
(D) Clustal©
- 44 Which compound are hold by stationary phase?
(A) Polar compound
(B) Non polar compound
(C) both A and B
(D) None of the above
- 45 Which is a high quality structure according to resolution in angstrom
(A) 1
(B) 2
(C) 3
(D) 4
- 46 Which is the optimal choice of method to get structure of a protein in short period of time for emergency use?
(A) X Ray crystallography
(B) NMR Spectroscopy
(C) Homology modeling
(D) Molecular dynamics and simulation
- 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 Which of the following is an example of Homology and similarity tool?
(A) BLAST
(B) RasMol
(C) EMBOSS
(D) PROSPECT
- 49 Which of the following is the first and the most important step in the polymerase chain reaction?
(A) Annealing
(B) Primer extension
(C) Denaturation
(D) None of the above

50 Which software is used for visualization of file downloaded from rcsb.org

- (A) BLAST
- (B) FASTA
- (C) PYMOL
- (D) CLUSTALW