R2785	Sub. Code
	502201

M.Sc. DEGREE EXAMINATION, APRIL – 2025

Second Semester

Bioinformatics

PHYLOGENY AND PHYLOGENOMICS

(CBCS – 2022 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 1 = 10)

Answer **all** the following objective questions by choosing the correct option.

1. What is the primary goal of phylogenetic analysis in molecular evolution? (CO1, K2)

   (a) To study protein folding

   (b) To reconstruct evolutionary relationships

   (c) To identify mutations

   (d) To calculate mutation rates

2. Gene duplication events play a significant role in molecular evolution by (CO1, K2)

   (a) Removing redundant genes

   (b) Creating opportunities for functional innovation

   (c) Accelerating mutation rates

   (d) Maintaining genetic stability

3. Which of the following is the primary goal of sequence alignment? (CO2, K4)

   (a) To determine the function of proteins

   (b) To identify evolutionary relationships between sequences

   (c) To construct phylogenetic trees

   (d) To calculate molecular weights of sequences

4. What is the key feature of the Needleman-Wunsch algorithm? (CO2, K4)

   (a) It performs local sequence alignment

   (b) It uses dynamic programming for global sequence alignment

   (c) It is a heuristic algorithm for sequence alignment

   (d) It calculates the percentage similarity between sequences

5. In protein sequence analysis, a conserved motif typically indicates: (CO3, K1)

   (a) A non-functional region

   (b) A region under positive selection pressure

   (c) A region critical for the protein's function or structure

   (d) A sequence prone to mutation

6. What is the primary purpose of discovering sequence motifs in DNA? (CO3, K1)

   (a) To identify protein tertiary structures

   (b) To understand regulatory elements like promoters or enhancers

   (c) To measure GC content

   (d) To calculate the molecular weight of DNA

7. Which method is commonly used to construct phylogenetic trees? (CO4, K2)

(a) BLAST

(b) Maximum Parsimony

(c) K-means clustering

(d) PCR amplification

8. What is the principle of Maximum Parsimony in phylogenetics? (CO4, K2)

(a) Choosing the tree with the highest likelihood value

(b) Using the simplest tree with the least evolutionary changes

(c) Generating a tree with the maximum number of species

(d) Finding the tree with the most genetic diversity

9. Which of the following is a software commonly used for phylogenetic tree construction? (CO5, K4)

(a) BLAST (b) MEGA

(c) PyMOL (d) Genome Browser

10. Which of the following tools is designed for visualizing and editing phylogenetic trees? (CO5, K4)

(a) PhyML (b) TreeView

(c) ClustalW (d) MEGA

Part B (5 × 5 = 25)

Answer **all** the questions not more than 500 words each.

11. (a) Outline the importance of molecular clocks in evolutionary timelines. (CO1, K2)

Or

(b) Explain how does gene duplication contribute to molecular innovation. (CO1, K2)

12. (a) Briefly describe the role of scoring matrices (e.g., PAM or BLOSUM) in sequence alignment algorithms. (CO2, K4)

Or

(b) List two real-world applications of sequence alignment and briefly explain their importance. (CO2, K4)

13. (a) List and briefly describe two algorithms commonly used for motif discovery in DNA sequences. (CO3, K1)

Or

(b) What are conserved patterns in protein sequences and what do they reveal about protein structure and function? (CO3, K1)

14. (a) Briefly describe two methods used to construct phylogenetic trees, such as Maximum Parsimony and Neighbor-Joining. (CO4, K2)

Or

(b) List two applications of phylogenetic analysis in biological research. (CO4, K2)

15. (a) Describe the PHYLIP software package and discuss its capabilities for phylogenetic analysis, including the algorithms it supports. (CO5, K4)

Or

(b) How is ClustalW used in conjunction with phylogenetic analysis? Discuss its role in multiple sequence alignment and tree construction. (CO5, K4)

Part C ($5 \times 8 = 40$)

Answer **all** the questions not more than 1000 words each.

16. (a) Compare and Contrast the different types of speciation with examples. (CO1, K2)

Or

(b) Describe the neutral theory of molecular evolution and its implications for genetic variation. (CO1, K2)

17. (a) Compare the Needleman-Wunsch and Smith-Waterman algorithms in terms of methodology, applications, and computational complexity. (CO2, K4)

Or

(b) Explain the role of dynamic programming in sequence alignment algorithms. Provide a step-by-step description of the Needleman-Wunsch algorithm. (CO2, K4)

18. (a) Describe the role of Hidden Markov Models (HMMs) in discovering and characterizing sequence motifs. How do they represent conserved regions in sequences? (CO3, K1)

Or

(b) Discuss two bioinformatics tools or databases used for pattern discovery and characterization. Explain their features and applications. (CO3, K1)

19. (a) Describe the Maximum Likelihood method for phylogenetic tree construction. Discuss its advantages and limitations compared to other methods. (CO4, K2)

Or

(b) Discuss the concept of bootstrapping and how it is used to assess the reliability of phylogenetic trees, and describe the general procedure involved. (CO4, K2)

20. (a) Explain the role of tree visualization softwares in presenting phylogenetic trees. How do these tools enhance the interpretability of phylogenetic results for researchers? (CO5, K4)

Or

(b) Discuss the different types of dendrograms and their applications in biological studies. (CO5, K4)

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R2786

Sub. Code
502202

M.Sc. DEGREE EXAMINATION, APRIL – 2025

Second Semester

Bioinformatics

MOLECULAR MODELING AND DRUG DESIGN

(CBCS – 2022 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 1 = 10)

Answer **all** the following objective questions by choosing the correct option.

1. Which force field is widely used in molecular dynamics simulations of biomolecules? (CO2, K2)

   (a) AMBER

   (b) Hartree-Fock

   (c) Density Functional theory

   (d) B3LYP

2. Which of the following is NOT a component of a typical molecular force field? (CO1, K2)

   (a) Bond stretching

   (b) Van der Waals interactions

   (c) Proton transfer

   (d) Angle bending

3. The molecular modeling method involves solving the Schrödinger equation for electronic structure calculations is? (CO2, K2)

(a) Quantum Mechanics

(b) Molecular Dynamics

(c) Monte Carlo Simulation

(d) Energy Minimization

4. What is the primary purpose of molecular docking in molecular modelling? (CO1, K5)

(a) To predict the electronic structure of molecules

(b) To predict the binding orientation of two molecules

(c) To simulate molecular vibrations

(d) To minimize molecular energy

5. Match the following. (CO1, K2)

Field	Statement
1. Quantum Mechanics (QM)	A. Simulates large systems like proteins and membranes using simplified models.
2. Coarse-grained Modeling	B. Used to predict electron density and chemical Reactions.
3. Root-mean-square Deviation (RMSD)	C. Measures the deviation between two structures in molecular dynamics.
4. GROMACS	D. A popular software used for molecular dynamics simulations.
5. Hybrid QM/MM	E. Combines quantum and molecular mechanics for systems involving reactions.

(a) 1-D, 2-A, 3-E, 4-B, 5-C

(b) 1-E, 2-D, 3-C, 4-A, 5-B

(c) 1-C, 2-B, 3-E, 4-A, 5-D

(d) 1-B, 2-A, 3-C, 4-D, 5-E

6. Which of the following factors affects drug absorption? (CO3, K2)

(a) Solubility of the drug

(b) Gastrointestinal motility

(c) Blood flow to the absorption site

(d) All of the above

7. Which of the following proteins function as a catalyst? (CO4, K3)

(a) Hemoglobin (b) Insulin

(c) Enzyme (d) Collagen

8. Which amino acid contains sulfur? (CO2, K3)

(a) Glycine (b) Cysteine

(c) Phenylalanine (d) Lysine

9. What is the primary purpose of Lipinski's Rule of Five? (CO2, K5)

(a) To predict a drug's toxicity

(b) To evaluate a compound's solubility

(c) To assess a compound's drug-likeness based on its absorption and permeability

(d) To determine a drug's potency

10. What is the primary advantage of virtual screening in pharmacoinformatic? (CO1, K2)

(a) It eliminates the need for clinical trials

(b) It speeds up the drug discovery process by screening compounds computationally

(c) It ensures the safety of all tested drugs

(d) It predicts the cost of drug development

Part B (5 × 5 = 25)

Answer **all** the questions not more than 500 words each.

11. (a) Define Molecular modeling and pharmacoinformatic in Drug design (CO2, K2)

Or

(b) Write the advantages and disadvantages of finding a new drug target. (CO4, K2)

12. (a) Describe in detail about Molecular graphics surfaces and the applications of Molecular Graphics. (CO2, K2)

Or

(b) What are the general features of Molecular Mechanics Force Field, write down its applications? (CO1, K2)

13. (a) Give a detailed note on any three tools for predicting protein structure. (CO3, K2)

Or

(b) Write briefly about Ramachandran plot with diagram and other structure validation tools. (CO3, K3)

14. (a) Explain pharmacophore identification and mapping in drug design. (CO3, K5)

Or

(b) Differentiate Virtual screening and High throughput virtual screening and write down the applications. (CO1, K5)

15. (a) Describe and Differentiate Pharmacodynamics and Pharmacokinetics. (CO2, K2)

Or

(b) Explain the Theories of Enzyme inhibition and inactivation. (CO3, K2)

Part C (5 × 8 = 40)

Answer **all** the questions not more than 1000 words each.

16. (a) Write a brief note about Pharmacophore Modelling in drug Discovery and its applications. (CO1, K2)

Or

(b) Describe briefly about Phases of drug discovery, target identification, validation, lead identification and optimization. (CO3, K2)

17. (a) Calculate thermodynamic property using force field and write down the applications. (CO1, K2)

Or

(b) Explain briefly about Energy concept and its importance in drug action, write the applications of energy minimization. (CO3, K2)

18. (a) Briefly describe about Geometry optimization procedure using Density Functional theory. (CO4, K3)

Or

(b) Describe in detail about protein structure classifications and *abinitio* modeling. (CO1, K2)

19. (a) Discuss Ligand based and structure-based drug design with Fragment based approaches. (CO1, K5)

Or

(b) Elaborate QSAR, molecular docking and De-novo ligand design. (CO2, K5)

20. (a) Discuss in detail about Chemistry of drug metabolism and chemistry of ADME and Toxicity properties of drugs. (CO1, K2)

Or

(b) Write a brief note on Drug receptor interactions, receptor theories and drug action and its applications in different fields. (CO3, K2)

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R2787

Sub. Code
502203

M.Sc. DEGREE EXAMINATION, APRIL – 2025

Second Semester

Bioinformatics

COMPUTATIONAL BIOLOGY

(CBCS – 2022 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 1 = 10)

Answer **all** the following objective questions by choosing the correct option.

1. The molecular complexity of biosimilars arises due to _____ linked to the process, conversion, and formulation. (CO1, K2)

   (a) Modifications (b) Stability

   (c) Concentration (d) Molecular weight

2. _____ and _____ matrices are commonly used substitution matrices in computational biology. (CO2, K2)

   (a) FFT, BLOSUM (b) PSSM, PWM

   (c) PAM, BLOSUM (d) CID, BLOSUM

3. _____ is a graphical method for visualizing similarities between sequences. (CO3, K3)

   (a) Heat map (b) Dot plot

   (c) Phylogenetic tree (d) Global Alignment

4. Match the Following : (CO4, K4)

A		B	
A.	Double design problem	i.	Comparative sequence analysis
B.	Border block graph	ii.	Synthetic DNA construction
C.	Multiple sequence alignment	iii.	Resolving sequence ambiguities
D.	Plasmid design	iv.	Represents restriction maps

(a) A-i, B-ii, C-iii, D-iv

(b) A-ii, B-iv, C-i, D-iii

(c) A-iv, B-ii, C-i, D-iii

(d) A-iii, B-iv, C-i, D-ii

5. In synthetic biology, codon optimization improves _____ in a host organism. (CO5, K5)

(a) Protein stability (b) Gene expression

(c) Gene replication (d) Codon diversity

6. The concept of an expression cassette is _____ to the production of biosimilars. (CO1, K2)

(a) Crucial (b) Irrelevant

(c) Optional (d) Insignificant

7. Global alignment aims to align sequences over their entire length. (CO2, K3)

(a) True (b) False

8. The Progressive method in sequence alignment : (CO3, K3)

(a) Uses dynamic programming to align sequences

(b) Builds alignments step-by-step

(c) Aligns sequences globally

(d) Uses probabilistic models for alignment

9. Statement : Cassette transformation is used for simplifying restriction maps. (CO4, K4)

Reason : Cassette transformation groups overlapping fragments for better visualization.

(a) Both statement and reason are true, and the reason is correct

(b) Both statement and reason are true, but the reason is incorrect

(c) The statement is true, but the reason is false

(d) Both statement and reason are false

10. Hückel Theory is primarily associated with which of the following concepts in molecular orbital theory? (CO5, K5)

(a) Predicting the electron distribution in covalent bonds

(b) Analyzing π-electron systems using a semi-empirical approach

(c) Calculating the bond angles in organic molecules

(d) Describing the interaction of atomic orbitals in ionic compounds

Part B (5 × 5 = 25)

Answer **all** the questions not more than 500 words each.

11. (a) Define biosimilars with examples. (CO1, K2)

Or

(b) Explain the concept of expression cassette and vector. (CO1, K2)

12. (a) Define computational biology and explain its scope. (CO2, K3)

Or

(b) What is a substitution matrix? Compare PAM and BLOSUM matrices. (CO2, K2)

13. (a) Briefly explain the dynamic programming method in sequence alignment. (CO3, K3)

Or

(b) What are hidden Markov models, and where are they applied in sequence analysis? (CO3, K3)

14. (a) What is a restriction map, and how is it constructed? (CO4, K4)

Or

(b) What is vector and plasmid design in computational biology? (CO4, K4)

15. (a) What is synthetic biology, and what are its ethical concerns? (CO5, K5)

Or

(b) What is the Huckel Theory? (CO5, K5)

Part C (5 × 8 = 40)

Answer **all** the questions not more than 1000 words each.

16. (a) Describe the challenges in the production of biosimilars and modifications linked to their process and formulation. (CO1, K2)

Or

(b) Discuss the non-clinical and clinical aspects of biosimilars in detail. (CO1, K2)

17. (a) Describe the biological interpretation of the alignment problem with examples. (CO2, K2)

Or

(b) Discuss similarity and distance measures sequence alignment. (CO2, K2)

18. (a) Compare and contrast the Bayesian and progressive methods of sequence alignment. (CO3, K3)

Or

(b) Explain the Markov chain model and its significance in bioinformatics. (CO3, K3)

19. (a) Describe the process of multiple sequence alignment and its significance in bioinformatics. (CO4, K4)

Or

(b) Discuss the double design problem and its application in computational sequence analysis. (CO4, K4)

20. (a) Describe the concept of AND gate and OR gate biology with examples. (CO5, K5)

Or

(b) Explain molecular orbitals and Hartree-Fock equations in computational quantum mechanics. (CO5, K5)

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R2788	Sub. Code
	502204

M.Sc. DEGREE EXAMINATION, APRIL – 2025

Second Semester

Bioinformatics

PROGRAMMING IN SCRIPTING LANGUAGES (PYTHON, PERL AND R)

(CBCS – 2022 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 1 = 10)

Answer **all** the following objective questions by choosing the correct option.

1. What is the result of variable interpolation in Perl when you print a scalar variable inside double quotes? (CO1, K1)

   (a) The value of the variable is printed

   (b) The variable name is printed

   (c) An error occurs

   (d) Nothing is printed

2. In Perl, how do you declare a hash? (CO1, K1)

   (a) %hash = (“key 1 “, “value 1”, “key 2” => “value 2”);

   (b) hash = (“key 1”, “value 1”, “key 2”, “value 2”);

   (c) hash = {key 1 => value 1, key 2 => value 2};

   (d) @hash = (“key 1”, “value1”, “key2”, value2”) ;

3. Which of the following is the correct way to define a function in Python? (CO2, K2)

(a) Funcion my func ( ):

(b) def my_fune:

(c) def my_func ( ):

(d) function def my_func ( ) :

4. Which operator has the highest precedence in Python? (CO2, K2)

(a) + (b) *

(c) * * (d) –

5. Which function is used to substitute a pattern in a string using regular expressions in python? (CO3, K1)

(a) re.match (b) re.split ( )

(c) re.plae ( ) (d) re. sub ( )

6. Which of the following is not a valid regular expression metaharacter in python? (CO3, K2)

(a) ^ (b) $

(c) + (d) –

7. Which of the following is true about Python tuples? (CO4, K2)

(a) Tuples are mutable and can be modified after creation

(b) Tuples can be changed after creation by adding or removing elements

(c) Tuples are immutable and cannot be modified after creation

(d) Tuples are only used to store single values

8. Which of the following is true about a balanced search tree? (CO4, K1)

(a) It ensures that the tree's height remains balanced for optimal search operations

(b) It guarantees the fastest search time in any scenario

(c) It is designed to store only numerical values

(d) It allows for only sequential search operations

9. Which of the following functions in R allows you to apply a function to a vector without explicitly using a loop? (CO5, K2)

(a) apply( ) (b) lapply( )

(c) sapply( ) (d) vapply( )

10. What type of analysis would you use for predicting a continuous outcome variable in R? (CO5, K2)

(a) Classification

(b) Regression

(c) Clustering

(d) Principal component analysis

Part B ($5 \times 5 = 25$)

Answer **all** questions not more than 500 words each.

11. (a) What is array in Perl? How do you define and access elements in an array? (CO1, K2)

Or

(b) What is an if statement in Perl? Explain its basic syntax with an example. (CO1, K2)

12. (a) Explain the difference between expressions and statements in python. Provide examples for each. (CO2, K2)

Or

(b) Discuss python's string handling capabilities. Explain the immutability of string. (CO2, K2)

13. (a) Discuss the usage of the split() and join() functions in Python. Provide examples of how they are used for string manipulation. (CO3, K4)

Or

(b) Explain the use of quantifiers and meta-characters in regular expressions. Examples to define patterns for matching strings. (CO3, K4)

14. (a) Describe the concept of aliasing and cloning in Python with respect to lists. (CO4, K4)

Or

(b) Describe the concept of a balanced search tree explain how it is implemented in Python. (CO4, K4)

15. (a) Explain data visualization in R using base plotting functions and ggplot2 with an example. (CO5, K6)

Or

(b) Discuss data manipulation in R using functions. (CO5, K6)

Part C (5 × 8 = 40)

Answer **all** questions not more than 1000 words each.

16. (a) What is variable interpolation in Perl? How does it work with strings and scalars? Provide examples. (CO1, K2)

Or

(b) Discuss the control flow in Perl using if, else, elsif, and unless with example programs for each. (CO1, K2)

17. (a) Write a Python function to find the largest number in a list and discuss function composition and scope. (CO2, K2)

Or

(b) Explain Python's data types, operators, its precedence, and how expressions are evaluated. (CO2, K2)

18. (a) What are regular expressions in Python? (CO3, K4)

Or

(b) Discuss Python's special variables for file handling and explain local vs global variable scope with examples. (CO3, K4)

19. (a) Explain the mergesort algorithm with an example implementation in Python. Describe its time complexity and how it works. (CO4, K4)

Or

(b) Describe the concept of queues in Python. How can a queue be implemented using lists and the collections.deque module? Provide a code example. (CO4, K4)

20. (a) Describe the process of clustering ‘n R using the kmeans() function and how to visualize the results. (CO5, K6)

Or

(b) Explain the concept of recursive functions in R with an example of a simple factorial function using recursion. (CO5, K6)

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R2789

Sub. Code
502401

M.Sc. DEGREE EXAMINATION, APRIL – 2025

Fourth Semester

Bioinformatics

MACHINE LEARNING AND ARTIFICIAL INTELLIGENCE

(CBCS – 2022 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 1 = 10)

Answer **all** the objective type question by choosing the correct answer.

1. What does Θ notation represent in algorithm analysis? (CO1, K1)

   (a) The worst-case time complexity

   (b) The average-case time complexity

   (c) Both the worst-case and best-case time complexities

   (d) The best-case time complexity

2. _____ technique is used for solving puzzles like the 8-puzzle or 15-puzzle. (CO1, K1)

   (a) DFS

   (b) BFS

   (c) Both DFS and BFS

   (d) Neither DFS nor BFS

3. _____ is NOT a commonly used knowledge representation technique in game playing. (CO2, K1)

(a) State space representation

(b) Rule-based systems

(c) Neural networks

(d) Decision trees

4. In predicate logic, what does the symbol '∀' stand for? (CO2, K2)

(a) There exists (b) Not

(c) For all (d) And

5. The primary goal of decision tree learning is _____. (CO3, K2)

(a) To minimize computational complexity

(b) To maximize model interpretability

(c) To maximize predictive accuracy

(d) To minimize feature selection

6. Which heuristic search algorithm prioritizes nodes based solely on the heuristic evaluation of their cost to reach the goal? (CO3, K1)

(a) Breadth-First Search (BFS)

(b) Depth-First Search (DFS)

(c) Greedy Best-First Search

(d) Uniform Cost Search

7. _____ clustering algorithm can identify outliers as noise points. (CO4, K1)

(a) K-means

(b) DBSCAN

(c) Agglomerative clustering

(d) Spectral clustering

8. Support Vector Machine (SVM) is primarily used for (CO4, K1)

(a) Classification (b) Regression

(c) Clustering (d) Dimensionality reduction

9. Analytical Learning primarily focused on _____. (CO5, K2)

(a) Identifying patterns and relationships in data

(b) Generating rules from data

(c) Explaining the reasoning behind decisions

(d) Evaluating the performance of machine learning models

10. In Q-Learning, what is the function $Q(s, a)$ used to represent? (CO5, K3)

(a) State-action pairs

(b) Rewards

(c) State values

(d) Policy probabilities

Part B (5 × 5 = 25)

Answer **all** the questions not more than 500 words each.

11. (a) Discuss various types of control strategy to be followed to formulating an AI problem with an use-case. (CO1, K2)

Or

(b) Explain graph methods to represent problem states. (CO1, K4)

12. (a) Explain the Quantifiers used to represent predicate Logic. (CO2, K2)

Or

(b) Discuss the knowledge representation frames and slots with an use-case. (CO2, K2)

13. (a) Elaborate on concept learning and list the challenges. (CO3, K3)

Or

(b) Discuss the components of Decision Tree Learning representation. (CO3, K2)

14. (a) Explain K-Nearest neighbour Algorithm. (CO4, K2)

Or

(b) Compare the clustering approaches of Distance, Hierarchy, Density based methods. (CO4, K3)

15. (a) Elaborate on first order rules. (CO5, K3)

Or

(b) Brief on perfect domain theories. (CO5, K6)

Part C (5 × 8 = 40)

Answer **all** the questions not more than 1000 words each.

16. (a) Elaborate on the considerations to be practised for representing problem states in AI with an example. (CO1, K6)

Or

(b) Explain DFS technique to represent problem state with an example. (CO1, K4)

17. (a) Explain knowledge representation using predicate logic. (CO2, K3)

Or

(b) Describe frames and slot to represent knowledge with an example. (CO2, K4)

18. (a) Discuss the Machine Learning approach version space. (CO3, K3)

Or

(b) Describe Decision Tree learning components and approaches. (CO3, K3)

19. (a) Discuss the various kernel methods and compare the difference between kernel and regressor linear models. (CO4, K5)

Or

(b) Explain DBSCAN algorithm and state its advantages and limitations. (CO4, K3)

20. (a) Explain the various induction techniques to formulate rules. (CO5, K2)

Or

(b) Explain reinforcement learning with an real time usecase. (CO5, K3)

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R2790

Sub. Code
502402

M.Sc. DEGREE EXAMINATION, APRIL – 2025

Fourth Semester

Bioinformatics

SYSTEMS BIOLOGY

(CBCS – 2022 onwards)

Time : 3 Hours Maximum : 75 Marks

Part A (10 × 1 = 10)

Answer **all** the following objective questions by choosing the correct option.

1. Which of the following provides higher resolution in MALDI-TOF? (CO1, K1)

   (a) Blocker (b) Channel

   (c) Transmitter (d) Reflector

2. There exist three types of interactions between domains. Which of the following is not one of them? (CO1, K2)

   (a) Stable complex

   (b) Transient interaction

   (c) Multi-domain protein

   (d) Unstable interaction

3. Which of the following is untrue regarding the classic yeast two-hybrid method? (CO2, K2)

(a) Protein-protein interaction networks of yeast and a small number of other species have been subsequently determined using this method

(b) This technique is a high throughput approach

(c) Each bait and prey construct has to be prepared individually to map interactions between all proteins

(d) It has been systematically applied to study interactions at the whole proteome level

4. Mass spectrometry is used in _____. (CO2, K1)

(a) Transcriptome analysis

(b) Protein separation

(c) Proteome analysis

(d) All of the above

5. Which of these conclusions might be drawn from the results of a 2D gel electrophoresis experiment? (CO5, K2)

(a) Levels of mRNA expression for two different genes are lower under one set of conditions than another

(b) In a mutant cell, the lack of protein expression is due to production of unstable mRNA, which is rapidly degraded

(c) A mutation prevents proper posttranslational modification of a protein

(d) None of these are reasonable conclusions

6. Protein-protein interactions can be identified by _____. (CO3, K1)

(a) Microarrays

(b) Hierarchical clustering

(c) Mass spectrometry

(d) Immunoprecipitation

7. Polypeptides _____. (CO3, K1)

(a) Can fold into a double helix

(b) Can have a tertiary structure

(c) Can contain phosphate

(d) Consist of nucleotides

8. Microarrays _____. (CO4, K1)

(a) Are used for analysis of transcriptomes

(b) Are made of glass

(c) Contain RNA sequences

(d) Are smaller than DNA chips

9. Omics research field that measures the rates of all intracellular fluxes in the central metabolism of biological systems. (CO4, K1)

(a) Lipidomics (b) Fluxomics

(c) Biomics (d) All of the above

10. The Successful design and development of the first working version of the _____ system of software modeling by Koichi Takahashi. (CO5, K1)

(a) E-CELL (b) V-CELL

(c) GROMOS (d) None of these

Part B (5 × 5 = 25)

Answer **all** the questions not more than 500 words each.

11. (a) Write notes on Protein microarrays. (CO1, K2)

Or

(b) Explain the Blood disease profiles. (CO1, K3)

12. (a) Describe in detailed account on the databases such as Inter Pro. (CO2, K3)

Or

(b) Write down based tools for analysis of proteomic data in Bioinformatics. (CO2, K4)

13. (a) Comment on protein interaction networks. (CO3, K4)

Or

(b) Explain about Regulatory networks. (CO3, K3)

14. (a) Discuss the Glycoproteins and Metaglycomes. (CO4, K4)

Or

(b) Write in detailed notes on the Glycan Recognition Molecules. (CO4, K3)

15. (a) Explain the Gene 5 regulatory networks. (CO5, K3)

Or

(b) Describe the V-CELL and GROMOS. (CO5, K3)

Part C (5 × 8 = 40)

Answer **all** the questions not more than 1000 words each.

16. (a) Write in detail about MALDI-TOF MS, QTrap MS/MS and 2D Gel Electrophoresis. (CO1, K4)

Or

(b) Discuss in detailed account on ITC. (CO1, K3)

17. (a) Give an elaborate account on the databases such as STRINGS and DIP. (CO2, K3)

Or

(b) Explain the basic principles and Computational methods for identification of polypeptides. (CO2, K4)

18. (a) Describe in detailed account on Structures of Regulatory networks and Neural Network models. (CO3, K4)

Or

(b) Write in detail about Protein network analysis in Cytoscape and Python. (CO3, K3)

19. (a) Describe the Challenge and promise of Glycomics. (CO4, K5)

Or

(b) Explain the Transcriptomics and Metabolomics and its applications. (CO4, K4)

20. (a) Discuss the metabolic pathways databases such as KEGG and AraCyc. (CO5, K4)

Or

(b) Write in detail about Random and Scale free networks. (CO5, K3)

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