Seat No. _____

HB-003-2016043

B. Sc. (Sem. VI) Examination

April - 2023

Biotechnology - BT 603

(Advance Molecular Biology and Bioinformatics)

Faculty Code : 003
Subject Code : 2016043

Time : $2\frac{1}{2}$ / Total Marks : **70**

1 **(a)** Answer the questions : (One mark each)   **4**

    (1) Real time PCR is used to _____ DNA.

    (2) Pyrosequencing relies on _____ detection for sequencing.

    (3) Western blotting is used for the detection of _____.

    (4) Emulsion PCR refers to amplification of DNA in _____.

(b) Answer the question : (any one out of two)   **2**

    (1) What are the types of hybridization technique ?

    (2) What is bridge and emulsion PCR ?

(c) Answer the question : (any one out of two)   **3**

    (1) Application of PCR techniques.

    (2) Explain the mechanism of pyrosequencing.

(d) Answer the question : (any one out of two)   **5**

    (1) Explain Illumina and Solid sequencing method in detail.

    (2) Explain the mechanism of artificial synthesis of DNA.

2 **(a)** Answer the questions : (One mark each)   **4**

    (1) RAPD is a _____ based method.

    (2) ADA deficiency is caused due to _____ of the gene for adenosine deaminase.

    (3) DNA foot printing is used to study DNA _____ interaction.

    (4) Chromosome walking is _____ technique.

(b) Answer the question : (any one out of two)　　　**2**
　(1) What is restriction mapping ?
　(2) What is mini satellite and micro satellite ?

(c) Answer the question : (any one out of two)　　　**3**
　(1) Explain the mechanism of DNA foot printing technique.
　(2) Write the ideal characteristics of molecular markers.

(d) Answer the question : (any one out of two)　　　**5**
　(1) What is gene therapy? Explain types of gene therapy.
　(2) Explain the methods of chromosome jumping and walking.

3 (a) Answer the questions : (One mark each)　　　**4**
　(1) Genbank database is maintained by _____.
　(2) The identification of drugs through the genomic study is called _____.
　(3) MAtDB is a model organism database for _____.
　(4) The computational methodology that tries to identify the best matching between two molecules, a ligand and receptor are known as _____.

(b) Answer the question : (any one out of two)　　　**2**
　(1) Define bioinformatics.
　(2) What is biological database ?

(c) Answer the question : (any one out of two)　　　**3**
　(1) What are the objectives of human genome project ?
　(2) Importance of biological database.

(d) Answer the question : (any one out of two)　　　**5**
　(1) Enlist and explain any two major bioinformatics resources.
　(2) Enlist the branches of bioinformatics and its role in biotechnology.

4 (a) Answer the questions : (One mark each)　　　**4**
　(1) BankIt and Sequin are sequence submission tools at _____.
　(2) _____ is a metabolic database.
　(3) PDB is database of protein.
　(4) The signatures from InterPro come from ____member database.

(b) Answer the question : (any one out of two) 2
    (1) Which are the primary and secondary database ?
    (2) What is CATH ?
(c) Answer the question : (any one out of two) 3
    (1) Explain the levels of SCOP.
    (2) What are the importance of PubMed ?
(d) Answer the question : (any one out of two) 5
    (1) Write a note on UniProt.
    (2) Write a note on InterPro.

5 (a) Answer the questions : (One mark each) 4
    (1) The stepwise method for solving problems in computer science is called _____.
    (2) FASTA is derived from logic of the dot plot (True/False)
    (3) Full form of BLOSUM
    (4) QSAR method involves _____ properties.
(b) Answer the question : (any one out of two) 2
    (1) What is functional genomics ?
    (2) What is global and local alignment ?
(c) Answer the question : (any one out of two) 3
    (1) What is primer designing ?
    (2) What are the types of BLAST ?
(d) Answer the question : (any one out of two) 5
    (1) Write a note on computer aided drug discovery.
    (2) What is the mechanism of microarray and write its application.

_____