[This question paper contains 6 printed pages.]

Your Roll No............

Sr. No. of Question Paper : 1256

Unique Paper Code : 32167608

Name of the Paper : DSE Bioinformatics

Name of the Course : **B.Sc. (Hons.) Botany**

Semester : VI

Duration : 3.5 Hours Maximum Marks : 75

Instructions for Candidates

1. Write your Roll No. on the top immediately on receipt of this question paper.
2. Attempt **five** questions in all.
3. Question No. **1** is compulsory.
4. All parts of the questions must be answered together.

1. (a) Give the full form **(any five)** : (1×5=5)

   (i) MIAME

   (ii) QSAR

   (iii) PDB

   (iv) PIR

P.T.O.

(v) MSA

(vi) NIH

(vii) ORF

(b) Match the following **(any five)** : (1×5=5)

Column 'A'	**Column 'B'**
(i) MegaBLAST	Unique identifier of a given protein or DNA sequence
(ii) TrEMBL	A web based sequence submission tool of NCBI
(iii) GCG	A PDB database which provides annotation and three-dimensional structure of protein sequences
(iv) Barcode	A computer-annotated protein sequence database supplementing the Swiss-Prot
(v) Accession number	Program for aligning long sequences
(vi) NRL_3D	Practical Extraction and Report Languages
(vii) PEARL	Genetic Computer Group

(c) Define the following **(any Five)** : (1×5=5)

(i) SRS

(ii) Rooted and Unrooted Tree

(iii) Python

(iv) MEGA

(v) Conserved sequence

(vi) Rasmol

(vii) GeneScan

2. Write short notes **(any three)** : (5×3=15)

(a) NGS and WGS

(b) Sequence File formats

(c) Gene prediction methods

(d) Molecular docking

P.T.O.

(e) Transcriptomics

3. Differentiate the following **(any three)** : (3×5=15)

(a) Cladogram and Phylogram

(b) PAM and BLOSUM

(c) BLAST and FASTA

(d) Genbank and Genpept

(e) CATH and SCOP

4. (a) Discuss metabolic pathways database and describe any two small molecule databases. (3+4=7)

(b) Discuss one protein sequence database and one protein structural databases? (4+4=8)

5. (a) What is sequence alignment? Explain pairwise and multiple sequence alignment with their significance. (2+6=8)

(b) Discuss different level of protein structures and describe computational method of protein structure prediction. (3.5+3.5=7)

6. (a) What do you understand by Computer-aided drug designing and also mention various phases of clinical trials? (5+2=7)

(b) What is Molecular phylogeny and compare Neighbour Joining, Maximum Parsimony and Maximum Likelihood methods of phylogeny reconstruction. (2+6=8)

7. (a) Give a comparative account on the various data submission and retrieval tools of NCBI and EMBL. (3.5+3.5=7)

(b) What do you understand by bioinformatics? Discuss its applications, scopes and limitations. (2+6=8)

8. (a) What do you understand by biological databases? Discuss about Primary, Secondary and Composite database. (2+6=8)

(b) What do understand by sequence homology and explain local and global alignment with diagram? (2+5=7)