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SARDAR PATEL UNIVERSITY

M.Sc. Integrated Biotechnology Examination, Fifth Semester

5ᵗʰ December, 2012 Wednesday

Time: - 10:30 a.m. to 1:30 p.m.

Subject: - PS05CIGB04 –Bioinformatics And Structural Biology

Total Marks: - 70

Q 1   Choose the most appropriate option from the following: -   [08]

1.   Pubmed is used for accessing

      a) abstracts   b) fill length articles   c) both a & b   d) none of these

2.   _____ is a nucleotide sequence database.

      a) PIR   b) PDB   c) Genbank   d) SCOP

3.   File format for performing BLAST is_____.

      a) PDF   b) PDB   c) FASTA   d) GIF

4.   Which of the following is a phylogenetic analysis algorithm?

      a) UPGMA   b) Maximum Parsimony
      c) both a & b   d) none of these

5.   Ramchandran plot shows the values of _____ angles for amino acids.

      a) Omega   b) Peptide   c) Torsion   d) all of these

6.   _____ is a RNA secondary structure

      a) Hairpin   b) Bulge   c) Interior Junction   d) all of these

7.   _____ is a structural database.

      a) SCOP   b) PDB   c) PIR   d) DDBJ

8.   Which of the following is a protein structure prediction method?

      a) Ab initio   b) Homology modelling
      c) both a and b   d) None of these

P.T.O.

1

Q 2   Answer the following (any seven):-   [14]

1. What is Entrez?
2. Give full form of EBI, EST, STS, NIH.
3. What do you mean by phylogenetic tree?
4. Define alignment and write its types.
5. What is domain and motifs?
6. List out the secondary and tertiary structure of RNA.
7. Name the levels of CATH & SCOP.
8. What is homology modelling?
9. Give a labelled diagram of Ramchandran plot.

Q 3
A.   Write a brief note on nucleotide sequence database.   [06]

B   Discuss in detail about NCBI.   [06]

OR

B.   " Bioinformatics is a multidisciplinary subject" Justify.   [06]

Q 4
A.   Write a short note on BLAST.   [06]

B.   Calculate the Needleman and Wunsch algorithm for the sequences given below.
     Sequence 1: GAATTCAGTTA
     Sequence 2: GGATCGA   [06]

OR

B.   Discuss in detail multiple sequence alignment.   [06]

Q 5
A.   Explain the secondary and tertiary structures of protein.   [06]

B.   Explain the principle and instrumentation of X – ray crystallography.   [06]

OR

B.   Write a short note on validation tools for protein structure.   [06]

Q 6
A.   Give a detail note on the protein classification databases.   [06]

B.   Explain in brief the RNA secondary structure methods.   [06]

OR

B.   Discuss in detail Ab initio method for protein structure prediction.   [06]

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