(2) SARDAR PATEL UNIVERSITY
M. Sc. Integrated Biotechnology, Fifth Semester Examination
Day and Date: Monday, 30-04-2018
Time: 10:00 Pm to 1:00 pm
Paper Code and Subject: PS05CIGB04; Bioinformatics & Structural Biology

Total Marks: 70

Q-1   Multiple choice questions (**All are compulsory**).   [8 x 1 = 8]

(i)   An algorithm used to perform local alignment
       a) Needleman Wunsch algorithm   b) Smith Watermann algorithm
       c) Dot matrix   d) PHYLIP

(ii)   Which area is considered to be the well-conserved regions in multiple sequence alignments?
       a) Reflect areas of structural importance   b) Reflect areas of functional importance
       c) Reflect areas of both functional and structural importance
       d) Reflect areas likely to be of functional and/or structural importance

(iii) HTGS is a division maintained by _____.
       a) NCBI   b) PDB   c) SCOP   d) OWL

(iv)   Which one of the following is a life science search engine?
       a) PubMed   b) Entrez   c) Mozilla   d) None

(v)   The _____ tool compares translated nucleotide query sequence against protein databases
       a) blastp   b) tblastn   c) blastx   d) tblastx

(vi)   Expand UPGMA.
       a) Unweighted Pair Group Method with Arithmetic Mean
       b) Unweighted Pair Group Method with All Mean
       c) Upregulated Gene Method with Arithmetic Mean
       d) None

(vii) Which one is the protein classification database?
       a) CATH   b) SCOP   c) NCBI   d) RCSB

(viii) Which of the following is a multiple sequence alignment tool?
       a) Clustal W   b) Chime   c) Dismol   d) PDB

Q-2   Answer the following questions in short (**Any Seven**)   [7 x 2 = 14]
      i)   Write a short note on EMBL.
      ii)   What is DDBJ?
      iii)   Define sequence retrieval system (SRS).
      iv)   What is alignment?
      v)   Write a note on Expasy.
      vi)   Write notes on helix turn helix (HTH) and Zinc finger motifs (ZFM).
      vii)   Write a note on UPGMA.
      viii)   Write a note on Clustal W.
      ix)   Define gap penalties.

PTO

(1)

Q-3 (A) Discuss NCBI database and tools in detail. [6]

(B) Discuss the method for submission the sequence you have sequenced in different database? [6]

OR

(B) Explain Protein information resources (PIR) and its application in detail. [6]

Q-4 (A) Discuss the concepts of alignment in detail? [6]

(B) Explain molecular phylogeny in detail. [6]

OR

(B) Discuss BLAST technique with a suitable example. [6]

Q-5 (A) Discuss the primary, secondary and tertiary structure of proteins. [6]

(B) What is the principle of x-ray crystallography? Discuss its application in determination of protein structure. [6]

OR

(B) Explain protein folding in detail. [6]

Q-6 (A) Discuss protein data bank (PDB) and Nucleotide data bank (NDB). [6]

(B) Discuss CATH and SCOP in detail. [6]

OR

(B) Explain homology modeling in detail. [6]

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