[87/A-?1]

SARDAR PATEL UNIVERSITY
M. Sc. (Integrated) Biotechnology, Fifth Semester Examination
Monday, 24th October 2016
02:00 pm to 05:00 pm
PS05CIGB04: Bioinformatics & Structural Biology

Total Marks: 70

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

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

(2) The term bioinformatics was coined by
a) J. D. Watson   b) Margaret Dayoff   c) Pauline Hogeweg   c) Frederic Sanger

(3) Hydropathy plots are usually used to predict
a) beta secondary structures   b) transmembrane domains
c) alpha secondary structures   d) tertiary structure

(4) CATH was given by?
a) A. Murzin   b) C. Orengo   c) L. Holm   d) None

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

(6) Which of the following is *not* known to be involved in the process of *assisted* folding of proteins?
a) Chaperonins   b) Disulfide interchange
c) Heat shock proteins   d) Peptide bond hydrolysis

(7) _____ is a protein structure database.
a) PDB   b) PIR   c) Gene bank   d) All of these

(8) Which amino acids do not obey Ramachandran plot?
a) Proline   b) Glycine   c) Both a and b   d) None of these

Q-2 Answer the following questions in short (**Any Seven**) [7 x 2 = 14]
i)   Write a short notes on Expasy.
ii)   Write name of at least five bioinformatics institute in India.
iii) What is ENTREZ?
iv)   Write a note on Bragg's law.
v)   Write a note on RNA structure.
vi)   Write a note on UniProt KB.
vii) Define motif and domain.
viii) Write a note on Global and Local alignment.
ix)   Write a note on application of Protein Information Resource (PIR).

Q-3 (A) Discuss NCBI database along with its application. [6]

(B) Discuss DDBJ and EMBL database in detail. [6]

OR

(B) You have been provided with an unknown nucleotide sequence (250 bp). Give a suitable explanation for its identification using various approaches. [6]

Q-4 (A) Explain Basic Local Alignment Search Tool (BLAST) and Clustal W in detail. [6]

(B) Discuss basic concept in taxonomy and Molecular phylogeny in detail. [6]

OR

(B) Explain Needleman and Wunsch global sequence alignment method for filling the scoring matrix for sequence GAATTCAGTTA (sequence #1) and GGATCGA (sequence #2). [6]

Q-5 (A) Discuss the different structure of proteins. Explain the importance of Ramachandran plot for determination of structure of proteins. [6]

(B) Write a detail note on x ray crystallography. [6]

OR

(B) Discuss protein folding and importance of Molecular chaperones in detail. [6]

Q-6 (A) Discuss CATH and SCOP in detail. [6]

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

OR

(B) Discuss protein data bank (PDB) in detail. [6]

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