

10. Which of the following is not a secondary structure is due to tertiary interactions of RNA strand?
[] bulge loop [] kissing hairpin
[] pseudoknot [] hairpin bulge contact

II. Calculate the values. [5Q. × 1 = 5 marks]

11. The sequence similarity for Seq#1 ATCGATCGATCG and ATCCACCGATTC is _____.
12. The E-value for a database search is _____ if the size of the search space is 10^{10} and the bit score is 30.
13. The number of total possible rooted trees produced for 10 taxa is _____.
14. Sequences A and B that differ by 40%. If 30% of changes are a result of transitions and 10% of changes are a result of transversions, the evolutionary distance will be _____.
15. Out of 100 DNA regions predicted, 40 were correctly predicted as a gene, 5 were incorrectly predicted as a gene, 10 actual genes were not predicted successfully and 45 non coding regions were correctly predicted to be not a gene. The sensitivity of the test will be _____.

III. Fill in the blanks. [5Q. × 1 = 5 marks]

16. _____ is a structured database containing information about metabolic pathways in many organisms.
17. Local alignments uses _____ algorithm
18. In a coding region: 3rd position of a codon has more preferences towards _____ bases than _____ bases.
19. Aspartic acid, asparagine, and _____ are more likely to be found in turn because they have short side chains that can form hydrogen bonds with the own backbone.
20. Draw a phylogenetic tree from the Newick's format: (((a,c),b),((d,e),(f,g)))