Assignment 3

The due date for submitting this assignment has passed. As per our course rules, you have not submitted this assignment.

1) Which of the following statements is incorrect?  
   - Closely related sequences  
   - Distinctly related sequences  
   - Both closely and distinctly related sequences  
   - None of the above
   
   Accepted Answers:  
   [ ] Closely related sequences
   [x] Distinctly related sequences
   [ ] Both closely and distinctly related sequences
   [ ] None of the above

2) In which of the multiple choice questions, which statement is the most acceptable one?  
   - Go to Asia  
   - Go to Asia  
   - Go to Asia  
   - Go to Asia
   
   Accepted Answers:  
   [x] Go to Asia

3) Which statement is the expansion for the basic local alignment search tool?  
   - Basic local alignment similarity tool  
   - Library local alignment search tool  
   - Basic local alignment search tool  
   - Basic local alignment search tool
   
   Accepted Answers:  
   [x] Basic local alignment search tool

4) Which of the following statements is used for global alignment?  
   - Smith Waterman  
   - Needleman-Wunsch  
   - Needleman-Wunsch  
   - Needleman-Wunsch
   
   Accepted Answers:  
   [x] Needleman-Wunsch

5) The scores obtained in local alignment is  
   - 0  
   - Positive  
   - Negative  
   - Negative and positive
   
   Accepted Answers:  
   [x] Positive

6) Local alignment is used for identifying  
   - Similar sub-sequences  
   - General alignment efficiency  
   - Number of gaps  
   - Number of resistant enzymes
   
   Accepted Answers:  
   [x] Similar sub-sequences

7) The quality and time for database search depend on  
   - Size of the query sequence  
   - Number of sequences in the database  
   - Sort A and B  
   - None of the above
   
   Accepted Answers:  
   [x] Size of the query sequence

8) How are the human and chicken hemoglobin β chains similar?  
   - 63%  
   - 62%  
   - 61%  
   - 67%
   
   Accepted Answers:  
   [x] 67%

9) In a multiple sequence alignment, if a particular position is occupied with the same amino acid residue, the conservation score obtained by reverse based measure is  
   - 1  
   - 0  
   - 0.5  
   - 0.7
   
   Accepted Answers:  
   [x] 0.5

10) Which of the following software is used for calculating the conservation score?  
    - CHASE  
    - MSA  
    - ALCO  
    - BLAST
    
    Accepted Answers:  
    [x] ALCO

Due on 2020-02-15, 23:58 IST.