

grade 100%

Final Exam (Read Instructions First)

100%		
1.	Welcome to the final exam. If you haven't yet read the instructions, please exit the exam and read the Final Exam Instructions. Please run the following data set in the program(s) that you have written: dna2.fasta If you created your program(s) correctly, you will be able to answer the questions below. How many records are in the multi-FASTA file? 34 679 18 22 Correct	1/1 point
2.	What is the length of the longest sequence in the file? 4894 10457 5341 2341 Correct	1/1 point
3.	What is the length of the shortest sequence in the file? ● 115 964 78 103 ✓ Correct	1/1 point
4.	What is the length of the longest ORF appearing in reading frame 2 of any of the sequences? 1719 1644 1401 1458 ✓ Correct	1/1 point
5.	What is the starting position of the longest ORF in reading frame 3 in any of the sequences? The position should indicate the character number where the ORF begins. For instance, the following ORF: > sequence1 ATGCCCTAG starts at position 1. 6 636 153	1/1 point

	○ 758○ 832	
	✓ Correct	
6.	What is the length of the longest ORF appearing in any sequence and in any forward reading frame? 1560 2394 1719 1401	1/1 point
	✓ Correct	
7.	What is the length of the longest forward ORF that appears in the sequence with the identifier gi 142022655 gb EQ086233.1 16? 1317 1509 1281 1644	1/1 point
	✓ Correct	
8.	Find the most frequently occurring repeat of length 6 in all sequences. How many times does it occur in all? 153 219 1020 47	1/1 point
	✓ Correct	
9.	Find all repeats of length 12 in the input file. Let's use Max to specify the number of copies of the most frequent repeat of length 12. How many different 12-base sequences occur Max times? 1 10 4	1/1 point
	○ 5	
	✓ Correct	
10.	Which one of the following repeats of length 7 has a maximum number of occurrences? CATCGCC CGCGCCG GCGGCCG TGCGCCCC	1/1 point
	✓ Correct	