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Assessment: Biostrings

The eco sequence shown here is a short excerpt from the *E. coli* K12 strain genome. We will detect and analyze the peptide encoded by this genome fragment.

eco <- DNAString("GGTTTCACCGCCGGTAATGAAAAAGGCGAACTGGTGGTGCTTGGACGCAACGGTTCCGACTACTCTGCTGCGGTGCTGGCTC
eco

✓

Q1: Number of bases in DNAString

1/1 point (graded)
How many bases are in eco?

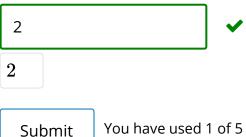


Q2: Counting occurrences of a pattern

1/1 point (graded)

In DNA, the start codon is encoded by the trinucleotide ATG.

How many potential start codons are in the eco sequence?



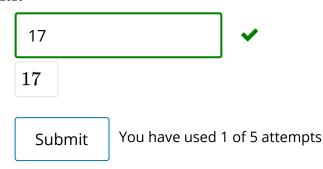
You have used 1 of 5 attempts

Q3: Location of a pattern

1/1 point (graded)

Find the locations of these ATG trinucleotides.

What is the start location of the first ATG?



Q4: Subsetting and translation

1/1 point (graded)

Take the substring of eco that starts at the location found in the previous question. Translate this sequence into amino acids.

How long is the resulting AAString?



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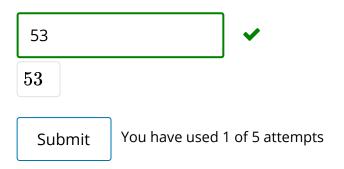
You have used 1 of 5 attempts

Q5: Location of stop codon in AAString

1/1 point (graded)

In AAStrings, the * character represents a stop codon.

What is the location of the stop codon in the AAString?



Q6: Sequence of AAString

2/2 points (graded)

Subset the *AAString* to end just before the stop codon; that is, do not include the stop codon or anything following it in the *AAString*.

How many amino acids are in the resulting AAString?



What is the resulting amino acid sequence?



Q7: Amino acid frequencies and net charge

3.0/3.0 points (graded)

At pH 7, two amino acids are negatively charged (D, E) and three amino acids are positively charged (H, K, R). Assume this peptide is at pH 7. The net charge of a peptide is the number of positively charged amino acids minus the number of negatively charged amino acids.

How many positively charged amino acids are in the sequence?



How many negatively charged amino acids are in the sequence?



What is the net charge of this peptide at pH 7?



You have used 3 of 5 attempts

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