**Perl Program (35 points total)**

A Navy Seals unit retrieved a mysterious sample from a suspected Al Qaeda hideout, and to support the president’s war on terror, you are asked to prove that it’s related to biological weapon research. So far, a crack team of lab techs at the CDC extracted RNA from the sample, which turned out to be low quality. They made what cDNA they could out of it, and then amplified it using non-specific PCR. The DNA was run out on a gel, and a large band was found that turned out to be a 188 base pair fragment with the following sequence:

CATTACGATGCATTGATTTTTCAAAGGAATGTACTATCGAAATCACAAGTCGTGGACTACGGTTTGCAGTGGAGGAATCGCAGTCTTTGCAGGCTCACGCCTTTCTTGATAAGTCGTTGTTTCAAACGTTTAATTTTCAGGGTGATTCAGATGGGGATACATATATGTTCCAGACGATGATTTCACCT

The initial results didn’t support the right conclusion, so now its up to you. The only problem is that you have no idea about the correct reading frame or direction for this sequence. Write a perl program that can translate this sequence in all six reading frames, and use the results to infer the most likely amino acid sequence that this fragment encodes. You can use the skeleton code (see ps1\_skeleton.pl file) as a guideline. Your code should print the following to output:

1. Transcribed sequence (i.e., converted to RNA) (5 points)

2. Translated sequence in the first three reading frames (10 points)

3. The reverse-complement RNA sequence (10 points)

4. Translation of the reverse-complement RNA sequence (5 points) Submit this output, as well as your source code, with your problem set.

What does the translate\_codon subroutine do and how? Annotate each line and submit the annotated version with your problem set (5 points)

Credits: MIT