Assign 1

Due Wednesday by 11:59pm   **Points** 15   **Submitting** a file upload

1. Write a script in Python that will translate a sequence of nucleotides into the amino acid sequences of all 6 possible reading frames.

An example of the translation into the 6 reading frames is the Expasy tool, which also finds open reading frames (ORFs) and color-codes them with a redish highlight. (An ORF is the part of a reading frame that has the potential to code for a protein or peptide. It is a continuous stretch of codons beginning with a start codon and ending with a stop codon.) You are NOT required to find the ORFs, but only to provide the 6 reading frames in which an ORF could be picked out.

Here is a link to the Expasy tool: **http://us.expasy.org/tools/dna.html.** ⤢ **(http://us.expasy.org/tools/dna.html.)**

You may assume that the gene is in proper FASTA format (ie- it contains only letters encoding nucleotides, numbers and whitespace). You may assume the letters are restricted to capital and lowercase A,C,T and G.

Your script should be able to translate the gene found here: **http://www.cs.usfca.edu/~pfrancislyon/seq.fasta.txt** ⤢ **(http://www.cs.usfca.edu/~pfrancislyon/seq.fasta.txt)**