Python Unit 3 programming problem

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Algorithm 1 Pseudocode for Unit3 programming problem

```
initialize empty string Seq
open Human_HRAS.fasta file
  for each line in file
    if line doesn't contain ">"
      add line to Seq
close file

initialize empty dictionary GenCode
open GeneticCode_standard.csv file
  for each line in file
    split line into components
    add line elements to GenCode using codon as key and aminoacid as value
close file

initialize empty string rcSeq
initialize empty dictionary Complement containing pairs of complementary bases
for each base in Seq
  add rcSeq to the complement of current base

open output file:
  for Strand in [Seq,rcSeq]:
    for Frame in [1,2,3]:
      initialize empty string Protein
      for each Position in current Strand from Frame to end step 3
        define CurrentCodon as a slice of Strand from Position to Position+2
        add CurrentCodon to Protein
      write to file Protein
```