

You have a long nucleotide sequence. You want to translate that sequence into amino acids. And, you want your script to work for any nucleotide sequence you give it in the future. I, being the benevolent teacher, will give you the code for the nucleotide and amino acids. However, you must make the dictionary!

You can use this as your practice sequence which you will give as a system argument once you are finished, while building your script write this sequence into the script saved as a variable so that you can make sure your code works: atcggacttcat

Your answer should be: IGLH

#Code to get you started

```
bases = ['t', 'c', 'a', 'g']
codons = [a+b+c for a in bases for b in bases for c in bases]
amino_acids =
'FFLLSSSSYY*CC*WLLLLPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG'
```

this means stop codon

1. Create a dictionary from the important lists given in the code provided. I have not taught you how to do that. You must figure out which lists from the previous code are important for your dictionary and how to convert these two lists into a dictionary.

Hint: Google “create dictionary from two lists python” – usually stack overflow will give the most understandable answers to google questions.

Hint2: It’s probably easier if your nucleotide list comprises your dictionary keys and the amino acid list will be values for your keys.

2. Create a for loop that iterates by position so that it iterates in steps or intervals of 3 (you are using this to break your DNA string into codons)

3. Within your for loop assign each group of 3 nucleotides to a variable (remember how we indexed using range method?)

4. Use the variable that you created in step 3 to index your dictionary within your for loop

5. You can save the results of your for loop as a list

6. Use the join method to join your list into a string and print this as output

7. Delete your example sequence variable from your script and give to your script as a system argument