



4. CCA → amino acid: \_\_\_\_\_ abbreviation: \_\_\_\_\_
5. UGA → amino acid: **stop** \_\_\_\_\_ abbreviation: \_\_\_\_\_
6. AAG → amino acid: \_\_\_\_\_ abbreviation: \_\_\_\_\_
7. UAA → amino acid: \_\_\_\_\_ abbreviation: \_\_\_\_\_

Your challenge is to write a Python program that acts like a ribosome: given a sequence of RNA codons, your program should translate it into the amino acids that print out the corresponding protein. When your program sees one of the three stop codons (“UAA”, “UAG”, or “UGA”), it should stop, print out the protein, and quit. For example, if your program is given this sequence of RNA codons:

**AUGGCCGGUAGAGAAACUUGA**

It should correctly translate it into the following protein:

**MAGRET**

As you work on this problem, think about how best to write the code that translates RNA codons into amino acids. There are 64 possible RNA codons: you could write 64 *if* statements in your code, but that would take you a long time to type and is unnecessarily complex. Looking at the table, we see that there are only 20 amino acids; see if you can use this to your advantage.