Modify and Comment each line of code to answer the following questions.

1. How many results do you get when you search for all 28 rRNA genes that are over 700 bp from a a) nematode, b) a green algae species, and c) an ascomycete fungus? (Give a different number for a, b, and c).

Please use Python to answer this – **Hint:** print(records[‘Count’])

2. Save all 28 rRNA genes that are over 700 bp from all green algae species to a file named “long\_28rrna\_greenalgae.fa”

**Hint:** Modify in\_class\_solution.py to do a loop after the search instead of taking the top record

3. Save all the **Protein IDs** of ATPase genes from the first Galdieria sulphuraria *whole genome* scaffold that you find. Save them into a file called G\_sulphuraria\_atpase\_ids.

**Hint:** You are going to have to modify my “retrieve\_nucleotide\_genbank\_example.py” to search for *feature types* of CDS then look for *feature qualifiers* of products that contain ATPase (**Hint**: if ‘ATPase’ in feature.qualifiers['product'][0]). Note that instead of extracting the DNA sequence, you will need to write the feature qualifier named ‘protein\_id’ out to a file.