Modify and Comment each line of code to answer the following questions. **You MUST provide your working PYTHON SCRIPT at a minimum.**

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.