Write a Python script called 'parseGFF.py' that opens and reads the
file, 'watermelon.gff'. Extract the gene name, store it in a list, then
print an alphabetized list of the genes at the end.

For the first entry, you would extract 'cox1' and print it. You can
skip all the 'similar to . . . ' entries.

We will continue to expand and update this script in the coming weeks.