1. Write a loop that says hello 10 times.

2. Write a loop that prints the name of every organism, each on a separate line.

3. Write a loop that prints the genome size of every organism, next to the name of the organism.

4. Write a loop that calculates the total number of nucleotides known by BioBIKE.

5. Write a loop that calculates the probability of encountering a nucleotide sequence in a genome with $[A] = [C] = [G] = [T]$.

6. Write a loop that calculates the probability of encountering a nucleotide sequence in a genome with $[A] = 0.3$. The following template may be helpful:

   (FOR-EACH letter IN "fill-in-sequence"
    WITH fill-in
    AS A% = 0.3
    AS C% = fill-in
    AS G% = fill-in
    AS T% = fill-in
    (IF-TRUE (EQUAL letter "A")
     THEN fill-in)
    (IF-TRUE (EQUAL letter "C")
     THEN fill-in)
    . . .
    FINALLY (RETURN fill-in))

7. Write a loop that calculates the average length of a protein in SS120.

8. Write a loop that calculates and displays the name of each organism followed by the average length of a protein in that organism (this might take some 10's of seconds to execute)