Assignment 5 Due Monday 25 Jan
BLAST -- please provide all answers as hard copy.

5.1 Go to
https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome
(blastn, blast a nucleotide sequence against a nucleotide database)

Use query NM_033360.4 (a KRAS transcript; KRAS is a famous oncogene)

Under "Choose Search Set" select "Reference RNA sequences (refseq_rna) and "Organism" human (taxid 9606); under "Program Selection" select radio button "Somewhat similar sequences (blastn). Check "show results in new window" (at the very bottom of the page). Run the query and wait for the result in the other window.

5.1.1 What is the identifier for the first alignment to KRAS that was not the query, and what is the value for the "Query cover" for this alignment?

5.1.2 What is the first non-KRAS transcript with an alignment? Copy out all alignments between the query and this transcript and put it in a document to print out.

5.2 Go to
https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome

Use query NP_203524.1

Leave the database alone ("Non-redundant protein sequences (nr)")

Don't enter an organism.

Leave the Program Selection / Algorithm as "blastp (protein-protein BLAST)

Check "Show results in new window"

Look at resulting alignments and find the one for "Latimeria chalumnae"

5.2.1 Why do you think the Latimeria chalumnae protein sequence is flagged as "predicted"?

5.2.2 Get a picture of a Latimeria chalumnae (the animal, not the alignment) and put it the response document.

5.2.3 What is the difference between the protein sequence for humans and L. chalumnae? Why is it counted as a "positive" even though the amino acids are different?

5.2.3 Extra credit: approximately when did the last common ancestor of L. chalumnae and you live?