**BLAST Lab- Part 3** Name\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Block \_\_\_\_\_ # \_\_\_\_\_

You must first complete Pre-lab, Part 1: A-Fossil Gene; Part B- GULO.

\****OMIT Part 3 from the other handout and use this sheet***.

1. You will need to watch a pre-lab tutorial before using [www.uniprot.org](http://www.uniprot.org). On youtube.com, watch: <https://www.youtube.com/watch?v=tF4bqc0Udz8>. You can also google Jason Abercrombie phylogeny tutorial. The tutorial teaches you how to search a database (UniProt) and create phylogenetic trees using select protein sequences.
2. Choose a protein (suggestions are given below) that interests you. **Check out the protein’s function before you pick 15 organisms!**  EX- for hemoglobin, you would not pick a plant! Search for that protein name at [www.uniprot.org](http://www.uniprot.org).
3. Select a total of 15 different organisms to use in the construction of your phylogeny. Copy and paste these sequences into a single document, using FASTA format. \*\***It’s crucial the sequences are in FASTA.**
4. Change all names of the 15 organisms to their *Genus species* names (google them!). Sometimes the common name works, but most often, it does not. Make sure to save this document, as it will be part of your lab grade.
5. Go to [www.NGphylogeny.fr](http://www.NGphylogeny.fr) and under “Phylogeny Analysis” select ‘one-click’ analysis to create your tree. You should give a name to your analysis. Paste all 15 sequences into the window and click submit (may have to wait for around a minute). Take a screen shot of your alignment and paste into a word doc. You should create a title above the screen shot. Also include the name of the site.
6. \*\*See if this site is up: <http://tcoffee.crg.cat/>. If it’s down, try one of the mirror sites (scroll down) or possibly try <http://phylot.biobyte.de/> (pick up the instructional handout). If coffee is up and running, paste your FASTA file of sequences into the “sequences to align” window and submit. This will generate a nice-looking alignment of the sequences. Take a screen shot and paste this into your document, as well. Make sure to give a title above the screen shot in your document. **If you used another site, BE SURE to include the name of the site you used**.

Suggested proteins to explore:

* Actin
* ATP synthase
* Catalase
* Cytochrome C
* Keratin
* Myosin
* Ubiquitin
* Pax 1
* Cytochrome c oxidase
* NADH-ubiquinone oxidoreductase
* rhodopsin
* PITX1
* MC1R **OVER 🡪**

**ANALYSIS**:

Now that you have your phylogenetic tree, you will be able to see the relationships between the species you included in your search. Note, however, that this is based on only one protein, or one protein subunit. It is possible that the results might be different if you used a different protein. Remember, too, that the tree is just information, not an “end in itself”. You must use the information to draw conclusions.

You must individually write up your results. Group members may share the sequences and tree(s), but the analysis must be each member’s own response. You can type and print out your analysis or neatly write your results. Either way, you will need to include your tree(s) and your sequences as well.

Your analysis should include the following information. DO NOT simply answer the questions (unless you want a big deduction), instead you should use the questions merely as a guide to a producing a clear, cohesive response (yes, like an FRQ). The question order does not mean your response should follow the same order!

1. Make a claim or potential answer to the ‘question’ you were investigating.
2. What does your phylogeny suggest about conserved core processes and sequence conservation among species?
3. What inferences can you make about common ancestry of the organisms you selected to analyze?
4. What did your initial search suggest about how widely distributed this gene was within and across the domains of life?
5. Was anything in your alignment ‘odd’ or ‘unexpected’? Explain
6. What other data (ex: morphological) could be added to your tree to substantiate, or extend, the tree?
7. Include explanations of other evidence provided from your tree.

What will be turned in:

* The original lab handout, with questions answered and charts completed.
* “Shared” group document containing: the protein you investigated, each species you investigated (both common names and scientific names) and the sequences and/or alignments for each, so that someone who has no access to this handout can tell what you did.
* Phylogenetic trees and/or cladograms (dendrograms). While [www.NGphylogeny.fr](http://www.NGphylogeny.fr) creates aligned “trees” and certainly must be included, I want to be wowed, so check out the other sites and paste other tree(s) on your doc.
* Your own written Analysis
* Due date: Wednesday, 11/6/2019