**BLAST Homework**

**Learning Goals**

• Become familiar with BLAST and be able to use it for homology searches

• Be able to interpret BLAST results

* Go to the NCBI website at [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)
* Use the dropdown menu to select “nucleotide”
* Enter accession number NM\_001026785.1

1. What information is available at this entry page? What gene is this?

* Run BLAST search for this sequence (see menu on right hand side)
* Choose the right database: Human, Mouse, or Other
* Choose megabast or blastn

2. What are the best hits for megablast?

3. What does the color code on the graphical interface represent? (Paste a screen shot of the graphical interface)

4. What are the best hits for blastn?

5. How are these results different? (Paste a screen shot of the graphical interface)

6. List the major taxonomic groups with homologs (be sure that the E-value is significant).

7. Were there any homologs in any plant species? Support your answer with E-values.

8. How would you identify a closely related species to your query sequence?

9. What other information can you find from here?

## Teaching Notes

### By *Erin Morris, Baker University*

*emorris@bakeru.edu*

**Course Information**

Department: **Biology & Chemistry**

Level: Lower/Upper Undergraduate (select one) **Upper undergraduate**

Course type: Lab/Lecture/Both (other, please describe) (select one) **Lab**

Students: Majors/Non-majors (select one) **Biology and Biochemistry majors**

Number of Students: **10**

**Module Information**

Original Module Name: **Lesson I - Introduction to Genome Solver**

Link to Original: <https://qubeshub.org/qubesresources/publications/808/1>

[Adapted Module Name: (if applicable). Introduction to Genome Annotation

Link to Adapted Module]

Modified Module Name: **BLAST Homework**

Files associated: (ie. Class Worksheet, Summative Quiz, Lecture Powerpoint, etc)

**Class worksheet; Genome solver slide deck used in class: “Basic Local Alignment Search Tool (BLAST)”**

Modification Learning Goals:

**• Become familiar with BLAST and be able to use it for homology searches**

**• Be able to interpret BLAST results**

**Teaching Notes**

*(Think about what you would like to read about this activity if you came back to it in 2 years)*

Suggestions for this section (not all required, and extras always welcome):

1. What did you change and why?

**I focused on one part of the GS activity, Part B that investigates the SOD sequence. This was going to be a one-day unit, so I wanted them to be able to complete the activity in a timely manner.**

2. How did the activity go?

**Students were engaged, included screen shots, and were able to interpret results outside of class.**

3. What went well and why?

**We had used NCBI to find sequences previously, but not BLAST. This is a warm up before we use BLAST to analyze results from a cloning experiment, this exercise is more straight forward.**

4. What went wrong and why?

**The slides were a little slow, hard to look at software through screen shots if you have not used it before.**

5. What was the prep like?

**As with any worksheet involving websites, one must check that each link is live and that the website did not change in appearance. The NCBI website is notorious about changing.**

6. How much time went into prep?

**Not much prep, just have to think through the entire assignment (and do the assignment) so you know all of the directions are up to date.**

7. Did you have to do any prep (i.e. grow cultures, grow seeds, order supplies) ahead of implementation?

**No prep for this one.**

8. Would you do this activity again?

**I will definitely do this again, maybe even find a way to do it with freshmen in Geneitcs.**

9. What would you change in the future?

**Not sure yet. Now that I have done it once, the second time through I can really assess how the students engage and if there are any questions/directions to add.**

10. What do you wish you’d known before you ran the activity?

11. Is there anything else you would like to make note of?

**Run through it every year! NCBI makes changes constantly.**

12. How does this activity fit in your overall course curriculum?

**It follows PCR, RE digest, cloning. We use it analyze our results. We did use NCBI to find sequences prior to this, but this was our first BLAST. It was good prep for more complicated sequence comparison/identification in our cloning project.**

13. In what ways, if any, did you modify your teaching practice with this activity?