Spring 2019 Day 3 of class/Group project day 2 Name:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Find the gene related to your protein sequence from last class in FlyBase ([www.flybase.org)](http://www.flybase.org))

Record the results to the following questions in Benching

1. What is your gene of interest’s FlyBase ID? This number will be useful for importing your sequence into Benchling.
2. What is its annotation symbol (CG number)?
3. What chromosome is it on? What is its sequence location? What do the numbers mean? What about the [+] or [-]? (Ask if you are unclear!)
4. How long is the gene in base pairs?
5. What genes are on either side of it?
6. What are some other types of information you can find out about a gene using FlyBase? Pick out at least four examples.
7. Compare using UniProt and FlyBase. Identify a few similarities and differences and discuss why there is a use for both!

[See back of page, too!]

1. Make sure someone in your group imports the gene sequence into Benchling (use the FlyBase ID) and that each of you link to the sequence in your notes. You could upload multiple copies with slightly different names if you all want your own sequence to play around with.
2. Investigate the chromatin state found for your gene in a commonly used *Drosophila* cell line called “S2”

This is based on the discussion in <http://modencode.sciencemag.org/chromatin/fly> but I found the images in the linked file to not be entirely accurate. I recommend following my directions below:

1. Click on GBrowse
2. Scroll down to the “Select tracks” button at the bottom (middle of page) and click on it
3. Scroll down to the section called “Noncoding features” and click on the box “Chromatin Domains (9-state model, S2 cells)”
4. Click the “Back to Browser” button at the bottom of the page
5. Look at the track that just appeared and note the color(s) along the length of your gene of interest
6. Take a screen shot of the track
7. Record your results and an interpretation in Benchling