

Instructions for submission of fly sequence assignment

Your fly sequence submissions will be evaluated using a computer program, so you must follow the following guidelines; failure to do follow these guidelines **exactly** will result in incorrect grading, probably resulting in a grade of zero for the assignment.

Sequences for both of your genes must be included in a single file, saved in **plain text** format (.txt) – **not Word format** (.doc, .docx) – you can choose this option through the “Save As” option in your word processor, or you can make the process a little easier by using a text editor (e.g., Wordpad if you are using Windows; TextEdit if you are using MacOS). Some text editors (e.g., TextEdit) will often try to save the file in Rich Text Format (.rtf); do not use this format – it must be plain text instead.

Sequences must be written in FASTA format. This format has 2 parts: a definition line that begins with “>” followed by the sequence definition, followed by the sequence starting on the next line. Your definition line **must follow the following format**: your uwlax netID, and your gene name, separated by an underscore (“_”). (Note: an underscore is not the same as a dash or hyphen; be sure to use the correct symbol or your assignment will not be graded correctly). The gene name must be **exactly the same** as the one given in the **Gene name column** of the “What genes do I have?” list (<http://websites.uwlax.edu/biology/flygeneinfo.htm>). Leave one blank line between your two sequences. **Do not include any other text in your file.** Name your file with your netID_flyseq.txt . The easiest way to format your sequences is to paste the FASTA version of your sequences into a plain text file, and then just change the definition line to match the proper format.

For example, if your name is John Smith with netID smith.john, and your two genes are Lobe and forked, your file should be named **smith.john_flyseq.txt**, and your submission would look like this (the actual sequences are shortened in this example):

```
>smith.john_Lobe
ACATGGATACATTTTATGATGGGATGGGGCTCGTAGTCGATCGATTTCGATGGCTAGGGC
TGGGGGGGGGCTGATCGATGGGCTGAGGCTGATCGATGCATGCTAGCTAGCTAGCTGACT
GACTGACTCGATACGACG
```

```
>smith.john_forked
ACATGGATACATTTTATGATGGGATGGGGCTCGTAGTCGATCGATTTCGATGGCTAGGGC
TGGGGGGGGGCTGATCGATGGGCTGAGGCTGATCGATGCATGCTAGCTAGCTAGCTGACT
GACTGACTCGATACGACG
```