**Actinobacteriophage Genome Annotation Submission Cover Sheet**

This Cover Sheet will accompany each genome’s annotation file(s) submission and succinctly describe the work that your students and you have done. This document ensures that the work done was as complete and thorough as it could be. Most important to the QC reviewer, denote where the trouble spots were in your annotation and how they were resolved.

Phage Name: JessellCookie

Your Name: Jaime Mayoral

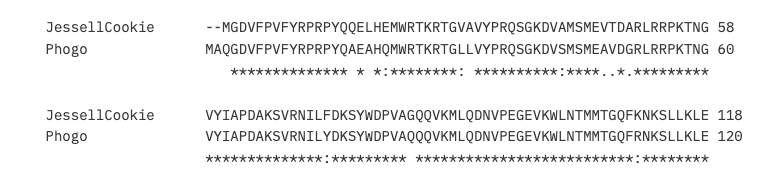
Your Institution: Florida International University

Your email: mayoralj@fiu.edu

Additional emails. (for correspondence).

Describe any issues or specific genes that you would like to highlight for the QC reviewer. This includes any genes that you had questions about or received help with or that warrant further inspection in the QC review process. Include those genes that you deliberated on and/or want to strongly advocate for. If you contacted SMART, workshop facilitator, or a buddy school for help, please document.

* We kept the orphan gene 28 (in Phamerator). See documentation for justification.
* We removed the auto annotated orphan gene 52 (in Phamerator). It overlaps another well characterized gene present in many other phages.
* Start call for gene with stop @52,772 (terminase). We made the call for 51,273 start, it is an ATG start and has 42 MAs annotation. However, the 51,267 start has the LORF, a -4 gap (seem to be in the middle of an operon), start is a GTG, but it only has 1 MA; this option gives 2 more AA to the terminase. The start option at 51,273 has an overwhelming number of MAs annotations but we think that 51,267 may be more likely to be the right start. Also, other members of the cluster EK1, don't have these 2 start options, only one, this is the case for Phogo or Townlake. An alignment of the terminase protein for Phogo (or TownLake) and JessellCookie using the start with most manual annotations falls short by 2 AA. This also may point towards 51,267 to be the right start. Again, we did not call this start due to the lack of MAs. Are we missing anything? Any insight is welcome!



Please record yes/no for each of the questions below. If further explanation is needed, please add this item to the above box.

In the submitted DNA Master file (Yes/No):

YES 1. Does the genome sequence in your submitted DNA Master file match the nucleotide fasta file posted on phagesDB (same number of bases, no N bases, etc.)?

YES 2. Are all the genes ‘Valid” when you click the [Validation button](https://seaphagesbioinformatics.helpdocsonline.com/article-84)?

YES 3. Are the genes (and matching LocusTag numbers) [sequential](https://seaphagesbioinformatics.helpdocsonline.com/article-77), starting with #1, counting by YES 4. Are the Locus Tags the “[SEA\_PHAGE NAME](https://seaphagesbioinformatics.helpdocsonline.com/article-77)” format?

YES 5. Has the [documentation been recreated](https://seaphagesbioinformatics.helpdocsonline.com/article-86) from the Feature Table to match the latest file version?

YES 6. Have tRNAs followed the [tRNA protocol](https://seaphagesbioinformatics.helpdocsonline.com/undefined), **COPYING** tRNA-AMINOACID type (DNA equivalent of the anti-codon) from Aragorn output - ﻿tRNA-Gln(ctg) - AND the ends been adjusted to match the Aragorn output?

NA 7. Has the [frameshift in the tail assembly chaperone](https://seaphagesbioinformatics.helpdocsonline.com/article-54) been annotated correctly (if applicable)?

YES 8. Have you cleared your Draft\_Blast data and have you [re-Blasted](https://seaphagesbioinformatics.helpdocsonline.com/article-57) the submitted DNA Master file?

YES 9. Has every gene been [described and supported in your Supporting Data file](https://seaphagesbioinformatics.helpdocsonline.com/article-44)?

YES 10. Did you investigate ‘[gaps](https://seaphagesbioinformatics.helpdocsonline.com/article-31)’?

YES 11. Did you [delete the genes](https://seaphagesbioinformatics.helpdocsonline.com/article-65) that you meant to delete?

Now, [make a profile of the file](https://seaphagesbioinformatics.helpdocsonline.com/article-64) you plan to send. (And you can save this file for [Review to Improve!)](https://seaphagesbioinformatics.helpdocsonline.com/untitled-18)

NA 1. Have any duplicate genes been deleted?

YES 2. Has the Notes field been cleared (using the automated buttons)?

YES 3. Do the gene numbers and locus tags match?

YES 4. Are the correct Feature\_Types correctly selected (most will be ORFs, but check that tRNAs and tmRNAs are correctly labeled)?

YES 5. Do the function names in the Product field either match the official function list or say “Hypothetical Protein”?

YES 6. Has the Function field been cleared (using the automated buttons)?

How are you documenting your gene calls in class? Choose any/all that apply:

  Spreadsheet

What is the file type (sort) submitted for QC to document your gene calls? Choose only one.:

      Spreadsheet