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. MiniMommy

Your Name. Sarah Swerdlow

Your Institution. University of Pittsburgh, Greensburg

Your email. Sjs308@pitt.edu

Additional emails. (for correspondence). [jal326@pitt.edu](mailto:jal326@pitt.edu) – Jennifer Labbe-Kinney (Student that worked on the project)

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.

**The students went through this genome and I reviewed it. We deleted some genes and they really looked at everything. They included a lot of notes. This was a question from the student: “My only questions were on the couple of genes where Genemark and glimmer had called a different start.  In some cases the searches revealed a function for those genes if we used the Genemark call rather than the Glimmer call.  For example, 17409-17750, 18507-18773, 20683-21231, 21467-22306, 22618-23001, 23734-24084, 33178-33990, 37687-37971, and 40492-40875.  All of these had different GeneMark calls, some of which would have made for shorter gaps between genes.” They left them as called because it matched with startorator.**

**In the notes it mentions JasmineDragon as a draft because JasmineDragon was finalized a few days ago because last week – it was still a draft. We did review it and everything still looks good and MiniMommy seems to be closest to JasmineDragon.**

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):

X 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.)?

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

X 3. Are the genes (and matching LocusTag numbers) [sequential](https://seaphagesbioinformatics.helpdocsonline.com/article-77), starting with #1, counting by 1s.

X 4. Are the Locus Tags the “[SEA\_PHAGE NAME](https://seaphagesbioinformatics.helpdocsonline.com/article-77)” format?

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

X 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?

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

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

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

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

X 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)

X 1. Have any duplicate genes been deleted?

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

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

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

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

X 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:

X PECAAN output

X DNA Master shorthand (previously used format)

      Spreadsheet

      Powerpoint

      Word document (must be easily searchable)

      Other: Describe.

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

      PECAAN output

X DNA Master shorthand (previously used format)

      Spreadsheet

      Powerpoint

      Word document (must be easily searchable)

      Other: Describe.