

## 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. Sourignavong  
Your Name. Megan Porter  
Your Institution. University of Hawai'i at Mānoa  
Your email. mlporter@hawaii.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.

- I am submitting PECAAN files for my notes and minimal files. I have answered the questions below based on those files but did not do some of the steps that are unique to DNAMaster; for those questions I have indicated N/A.
- There are no tRNAs or tmRNAs, so those questions are also N/A
- There were no tail assembly chaperones in this phage, so the frameshift question is also N/A
- There were no large gaps to investigate after initial annotation based on GeneMark
- Gene 25 in the original GeneMark annotation has been deleted (reverse, start: 14493, stop: 14197) because it is an orpham, in the reverse direction, and completely overlapping with gene 24
- Glimmer called an extra gene after gene 26 that had no coding potential and was deleted (forward, start:15297, stop: 46)

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.)?
- N/A 2. Are all the genes "Valid" when you click the [Validation button](#)?
- YES 3. Are the genes (and matching LocusTag numbers) [sequential](#), starting with #1, counting by 1s.
- YES 4. Are the Locus Tags the "[SEA PHAGE NAME](#)" format?
- YES 5. Has the [documentation been recreated](#) from the Feature Table to match the latest file version?
- N/A 6. Have tRNAs followed the [tRNA protocol](#), **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?
- N/A 7. Has the [frameshift in the tail assembly chaperone](#) been annotated correctly (if applicable)?
- N/A 8. Have you [cleared your Draft\\_Blast](#) data and have you [re-Blasted](#) the submitted DNA Master file?
- YES 9. Has every gene been [described and supported in your Supporting Data file](#)?
- YES 10. Did you investigate [gaps](#)'?
- YES 11. Did you [delete the genes](#) that you meant to delete?

Now, [make a profile of the file](#) you plan to send. (And you can save this file for [Review to Improve!](#))

- YES 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"?
- N/A 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:

- PECAAN output  
DNA Master shorthand (previously used format)  
Spreadsheet  
Powerpoint
- Word document (must be easily searchable)
- Other: Describe. Google Doc

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

- PECAAN output  
DNA Master shorthand (previously used format)  
Spreadsheet  
Powerpoint  
Word document (must be easily searchable)  
Other: Describe.