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. Pherobrine

Your Name. Marie Fogarty

Your Institution. Durham Tech

Your email. fogartym@durhamtech.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.

**Please Take a look at the following functions (Not start sites)**

**Gene 13: RNA ligase.** There is some evidence for calling this an RNA ligase we have called it for now, but appreciate a look by QC. Five other DJ phages did call the function and there is a HHPRED hit (but only with 25 % coverage).

**Gene 27:** Some amount of supporting evidence for minor tail protein, but we did not feel confident in that call – 2 DJ phages did call this as a minor tail protein. There is no HHPRED hit and in the other cluster where mostly called (CZ1), the minor tail protein is downstream of tape measure as is more usual for minor tail proteins.

**Gene 69:** Some functional evidence for ssDNA, **we called the function for now**. Only one other DJ phage has called a function. Phagesdb BLAST: Figliar, ssDNA binding protein

Blast NCBI function match with E value should be 10-7 or less: ssDNA binding protein, phage Figliar, E-value: 8.54674e-114

HHPRED Match with > 90% probability: 1JE5\_A, DNA binding protein, 75 % coverage

**Gene 70:** Could be called as PnuC-like Nicotinamide riboside transporter or alternatively a more cautious **membrane protein**. We called it as the transporter in Pherobrine but as membrane protein in our other DJ phage, Burley. On the fence about this function. The HHPRED hit seems strong, but many DJ phages have not called it. Many PnuC-like nicotinamide riboside transporter function calls in cluster C1, but only 1 in cluster DJ. which Pherobrine and Burley are in. SOSUI and TMHMM called this as a membrane protein.

All gaps were explored, and some genes were added. There is an area of the genome ( ~gp37 – gp 55) that shows some repeated patterns among DJ phages but variability in gene order. In this area, interestingly there are ~ 11 membrane proteins in close proximity. **There are some gaps between genes in this variable region** but those gaps seem to be consistent across phages and we did not see good evidence for adding genes.

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 1s.

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?

N/A 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?

N/A 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)

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 FeatureTypes 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”?

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

Yes

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

Yes - PECAAN output

      DNA Master shorthand (previously used format)

Yes - 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

      DNA Master shorthand (previously used format)

SS. Spreadsheet

      Powerpoint

      Word document (must be easily searchable)

      Other: Describe.