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. **Rowlf**

Your Name. **Michael** **Thomas**

Your Institution.      **Idaho State University**

Your email.      **mthomas@isu.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 see PECAAN for data support and notes reflecting our discussions about these**

* **We annotated gp26 as Purple Acid Phosphatase, which is unusual for cluster EG phages (see pham 155044). We think the annotation is correct, but wanted to flag it.**
* **Some confusion about gp48. Pham 163681 has many “DNA recombinase” calls, but that is no longer a valid function; others have “RecA-like DNA recombinase” but all appear to come up short w/ respect to required conserved domains in Spud (which is in a different pham).**
* **For gp21 (major capsid hexamer prot) – we used synteny; there were no good blast or hhpred hits.**
* **For gp16 (terminase) – HHPred suggests that this is a large subunit; however, there isn’t a good candidate for small subunit (except maybe gp12?), so we just called this Terminase; most EGs in pham agree. For gp12, some members of our team thought this should be terminase, small subunit, but supporting evidence really wasn’t there.**
* **For gp19 (major capsid and protease fusion protein) – seems to be also evidence for capsid maturation protease, but on discussion we like the evidence (esp from hhpred) of a fused protein**

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):

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? **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? **YES (no tRNAs annotated)**

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?

9. Has every gene been [described and supported in your Supporting Data file](https://seaphagesbioinformatics.helpdocsonline.com/article-44)? **YES, but please see PECAAN for updated search results and other supporting notes**

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? **YES**

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)

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)? **YES**

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

      PECAAN output **YES – our primary tool for sharing info; please see PECAAN for blast/hhpred and other supporting data. The primary prof re-checked each gene call before submission and inserted notes regarding annotation decisions.**

      DNA Master shorthand (previously used format)

      Spreadsheet **YES – we used an assignment sheet**

      Powerpoint **YES – we used google slides, which have been added below**

      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)

      Spreadsheet

      Powerpoint **YES – but please see notes in PECAAN (with blast/hhpred results, etc)**

      Word document (must be easily searchable)

      Other: Describe.