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. MUWow

Your Name. Brian Burnes

Your Institution. Mississippi University for Women

Your email. bsburnes@muw.edu

Additional emails. (for correspondence). none

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.

This is our first annotation, so I expect a few mistakes. We left features that should be deleted in the final draft (genes 45, 47, 57, 94, and 97) because we want SMART feedback on them before doing anything. We think genes 15 and 16 are overlapping because we looked for a possible programmed translational frameshift from gene 15 to gene 16. Near end of gene 15 at 10229, there is CCCTTTTT, a slippery sequence that can allow a +2 frameshift, which puts the ribosome in frame with gene 16 that starts at 10424. We answered a set of questions to call genes in the classroom…these questions and answers are in the notes. Be kind to us; this is our first time!

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. No, they are multiples of ten…can’t find how to change to integers.

4. Are the Locus Tags the “[SEA\_PHAGE NAME](https://seaphagesbioinformatics.helpdocsonline.com/article-77)” format? Yes, example SEA\_MUWOW\_10.

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? No tRNAs are included. But, we looked for them…there is one. In tRNA 1 of MUWow, 6 of the 7 hydrogen bonds are bonded and the acceptor arm contains CCA. The cove score is 16.41 which is less than the 20 cut off. tRNA: 1 does not overlap with any other genes.

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

8. Have you cleared your Draft\_Blast data and have you [re-Blasted](https://seaphagesbioinformatics.helpdocsonline.com/article-57) the submitted DNA Master file? No, recent instructions said not to.

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, for possible coding potential.

11. Did you [delete the genes](https://seaphagesbioinformatics.helpdocsonline.com/article-65) that you meant to delete? No, we are scared to delete anything until someone looks at it and gives feedback.

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? No

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:

x PECAAN output

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.:

x PECAAN output

DNA Master shorthand (previously used format)

Spreadsheet

Powerpoint

Word document (must be easily searchable)

Other: Describe.