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. Kinny

Your Name. Allie C Smith

Your Institution. Texas Tech University

Your email. allie.c.smith@ttu.edu

Additional emails. (for correspondence). lisa.bono@ttu.edu

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.

* Auto-annotated Features in DNA Master largely do not match the gene numbers in PECAAN; please cross reference by bp position
* Feature 3 on PECAAN and Phamerator starts @bp1095 and ends @1511 and does not appear on DNA Master. The Feature 3 listed here and on DNA Master is listed as Feature 4 on PECAAN and Phamerator.
* Feature 10 (5770-6861bp): high probability in HHPred and one hit in BLASTp for amidase
* Feature 16 (10398-12560bp): Possible Major Capsid Protein, according to hhPred
* Feature 27 (20136-20441bp): HHpred gives 98.3% that it is a tail fiber chaperone protein. DNAmaster calls 26, while PECAAN calls it 27
* Feature 33 (27835-28137bp): HHpred gives 95% that it is a cytokine receptor (for a house mouse). DNAmaster calls it 32, while PECAAN calls it 33
* Feature 35 (28593-28856bp): HHpred gives 95% for a phage shock protein with good coverage. DNAmaster calls it 34, while PECAAN calls it 35
* Feature 36 (28866-29252bp): Possible holin according to hhPred match
* Feature 42 (31143-31352bp): Manual Annotation for ORF that does not align with RBS Scores
* Feature 53 (35140-35388bp): Maybe nuclease function on Phamerator
* Feature 57 (36253-36567bp): May be HNH endonuclease on Phamerator
* Feature 64 (39405-43256bp): Potentially DNA primase/polymerase but top hits do not have enough gene coverage
* Feature 70 (44269-44853bp): Some coverage of top hits, high consistency of single-stranded DNA binding protein. 99.61% match to single-stranded DNA binding protein. One phamerator gene match.
* Feature 74 (45775-46215bp): Some coverage of top hits, high consistency of Ryanodine receptor. 99.72% match to Ryanodine receptor function.
* Features after #85 do not match on Phamerator
* Feature 91 likely needs to be split in to two 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?

      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)?

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

X PECAAN output

X DNA Master shorthand (previously used format)

X 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.