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.

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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.

* Between gene 26 and 27 is a huge gap (423bp). This gap is the one tRNAscan indicated a potential tRNA with an inferno score of 23, which was lower than the recommended threshold. Aragorn did not return a hit for tRNA. From GeneMark pdfs, there is a weak coding potential on frame 3 in the forward direction. This gap needs to be investigated further.
* Gene 42 has a big overlap with gene 41. GeneMark pdf has a down arrow indicated at around 27150 coordinate and I am not sure what that means. We suggest that the start coordinate for gene 42 be moved from 21717 to 27399 to reduce the overlap even though it will shorten the ORF.
* Gene 60 has a weak coding potential but it marched as hypothetical protein with phages (Kuleana and Cuppelo) which are not in the same cluster. This gene needs to be investigated further or deleted.
* There is a big gap (244 bp) between gene 68 and gene 69, but there is no coding potential indicated in the Genemark pdf. This may need further evaluation.

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?

No (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?

No 7. Has the [frameshift in the tail assembly chaperone](https://seaphagesbioinformatics.helpdocsonline.com/article-54) been annotated correctly (if applicable)?

* Gene 13 and 14 are potential tail assembly chaperone. We tried to identify the slippage position in the frames but were not successful. I would like so help with this to ensure I can do it properly in futur

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)’?

NO 11. Did you [delete the genes](https://seaphagesbioinformatics.helpdocsonline.com/article-65) that you meant to delete?

* We did not delete any genes but we think that gene 60 need to be delete upon further investigation by QC

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?

* There were no duplicate genes in this phage

No 2. Has the Notes field been cleared (using the automated buttons)?

* Not sure how to do that

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”?

No 6. Has the Function field been cleared (using the automated buttons)?

* Not sure how to do that.

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

      PECAAN output

      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

      DNA Master shorthand (previously used format)

X Spreadsheet

      Powerpoint

      Word document (must be easily searchable)

      Other: Describe.