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. SilentWarrior

Your Name. Sveinn V. Einarsson

Your Institution. Queens University of Charlotte

Your email. einarssons@queens.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.

* Membrane proteins: As I understand the newest docs and forum discussions, we can call it a membrane protein with 1 or more transmembrane proteins. Based on the documentation, I don’t think we had a signal protein. However, I would appreciate feedback on this if there is a signal protein in this genome, and not a membrane protein (GP59 for example). One membrane protein didn’t have supporting Blast information but DeepTmHMM showed transmembrane proteins.
* Gp43: The Blast results are variable and support exonuclease, Cas4 family, for example but not Rec-B like exonuclease/helicase but our HHpred results showed helicase and nuclease domain.
* Gp46: I believe it doesn’t have N Terminus or Mg++ binding tail, and using the forum powerpoint slides on RecA recominases, we called this a ASCE ATPase
* Gp47: I don’t think there is evidence for primase but the consensus from the phage cluster is DNA primase/helicase. I’m just not sure about this one. We went with the cluster consensus and called this a DNA primase/helicase.
* Gp 54, 71, 74: Please review the Starterator reports here. We went with our best guess, but the reports had a lot of variability in the calls for this gene. It gets difficult to figure out which start to go with when there are -1, -4 overlaps with ATG, GTG codons, respectively. Usually the GTG -4 start has a better RBS but the -1 ATG cluster overlap is the consensus choice. Based on the reading ATG is much more common and wetlab supported but any input on this or feedback on these annotations would be very welcome!

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?

NA 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 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)?

      10. Did you investigate ‘[gaps](https://seaphagesbioinformatics.helpdocsonline.com/article-31)’?

NA 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)

No 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)?

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

 PECAAN output

X 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.:

      PECAAN output

X DNA Master shorthand (previously used format)

      Spreadsheet

      Powerpoint

      Word document (must be easily searchable)

      Other: Describe.