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. Thimann

Your Name. Matt Mastropaolo

Your Institution. Neumann University

Your email. mastropm@neumann.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.

-A reverse gene at 445 – 2 bp was deleted. This gene completely overlapped a forward gene, gp1, at 47 – 517 bp.

-Please examine gene 49, 34778-35143 bp, this gene is being included since it has coding potential in GeneMark and has some possible hits from HHPred, but with lower probability. It also has similarities to another gene found in the phage EnalisNailo. The gene that is replacing was called by Glimmer at 34839-35048 bp lacks coding potential in GeneMark and has no credible hits in HHPred or NCBI.

-Gene 54, 37092-37303 bp is being added to the genome. This gene is called in other CZ4 phage such as Oregano and there is evidence of strong coding potential in the GeneMarkS report. The pham for this gene is 79365.

-Please examine gp57, 38439-39587 bp, the Official function list says that this gene should be a RecT-like ssDNA pairing protein if it is downstream of a RecE-like exonuclease. It then says on the line below the function name is RecT-like DNA pairing protein. The function RecT-like ssDNA pairing protein is not listed in PECAAN, but the RecT-like DNA pairing protein function is listed.

-Gene 81, 47892-47599 bp, is an orpham that is a reverse gene and over gene 80, 47611 – 47919 bp which is a forward gene. However, it has transmembrane domains and is being called a membrane protein. This needs to be further investigated, please recheck for us.

-Blast searches will not save to our DNAMaster and it also does not allow us to clear blast searches. All annotations were done in PECAAN and re-blasted the day we quality controlled them before submission.

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?

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

See above 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?

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:

X PECAAN output

X DNA Master shorthand (previously used format)

X Spreadsheet

      Powerpoint

X 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.