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. Anedea

Your Name. Marisa Pedulla and Casey McConnell

Your Institution. Montana Technological University

Your email. mpedulla@mtech.edu

Additional emails. (for correspondence). cmcconnell@mtech.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.

I included Andrea Martinez and Eden Neka as authors, but do not have contact information to verify permission.

Please examine

 Edited Starts

 Auto-annotated Anedea\_Draft\_43 (F, Start 21646; Original Glimmer Call) was changed to start at 21646, now ANEDEA\_42

 Auto-annotated Anedea\_Draft\_45 (F, Start 23928; Original Glimmer Call) was changed to 23913, now ANEDEA\_44.

 Auto-annotated Anedea\_Draft\_58 (F, Start 33331; Original Glimmer Call) was changed to 33307, now ANEDEA\_57

 Auto-annotated Anedea\_Draft\_59 (F, Start 39645; Original Glimmer Call) was changed to 39639, now ANEDEA\_58.

 Auto-annotated Anedea\_Draft\_65 (F, Start 50749; Original Glimmer Call) was changed to 50725, now ANEDEA\_64.

 Auto-annotation Anedea\_Draft\_71 (F, Start 53195; Original Glimmer Call) was changed to 53108, now ANEDEA\_70.

 Auto-annotation Anedea\_Draft\_162 (F, Start 90805; Original Glimmer Call) was changed to 90802, now ANEDEA\_164.

 Auto-annotation Anedea\_Draft\_201 (F, Start 102507; Original Glimmer Call) was changed to 102588, now ANEDEA\_204.

 Auto-annotation Anedea\_Draft\_219 (F, Start 107489; Original Glimmer Call) was changed to 107432, now ANEDEA\_221.

 Auto-Annotation Aneadea\_Draft\_221 (F, Start 107832; Original Glimmer Call) was changed to 107754, now ANEDEA\_223.

 Auto-annotation Aneadea\_Draft\_222 (F, Start 108103; Original Glimmer Call) was changed to 108049, now ANEDEA\_224

 Auto-annotation Anedea\_Draft\_223 (F, Start 108236; Original Glimmer Call) was changed to 108221, now ANEDEA\_225.

 Auto-Annotation Anedea\_Draft\_226 (F, Start 109044; Original Glimmer Call) was changed to 108996, now ANEDEA\_228.

 Auto-annotation Anedea\_Draft\_229 (F, Start 109741; Original Glimmer Call) was changed to 109729, now ANEDEA\_231.

 Auto-annotation Anedea\_Draft\_245 (F, Start 117261; Original Glimmer Call) was changed to 117258, now ANEDEA\_247.

 Auto-annotation Anedea\_Draft\_254 (F, Start 119895; Original Glimmer Call) was changed to 119874, now ANEDEA\_256.

 Auto-annotation Anedea\_Draft\_260 (F, Start 122108; Original Glimmer Call) was changed to 122063, now ANEDEA\_264.

 Deletions

 Auto-annotated Anedea­­\_Draft\_1 (R, Start 1; not called by Genemark)

 Auto-annotated Anedea\_Draft\_205 (R, 104246-104031)

 Auto-annotated Anedea\_Draft\_263 (R, 122962-122813)

 Additions

 ANEDEA\_75 (F, 55753-56049)

 ANEDEA\_81 (F, 61820-62020)

 ANEDEA\_117 (F, 77302-77514)

 ANEDEA\_203 (F, 102404-102595)

 ANEDEA\_257 (F, 120010-120138)

 ANEDEA\_258 (F, 120110-120259)

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?

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?

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? *\*the program stalls during blast, ~140 gene products’ blast results were completed. We are currently reblasting and will upload a new file when all gene products’ results are complete* The blasts completed over two days. We are replacing this coversheet and DNAM 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:

      PECAAN output

      DNA Master shorthand (previously used format)

      Spreadsheet

      Powerpoint

Yes 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)

      Spreadsheet

      Powerpoint

Yes\* Word document (must be easily searchable)

      Other: Describe.

\*Word document contains “Header” listing of each gene to assist in navigation of the document.