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. Zebo

Your Name. Marisa Pedulla and Kinsey Lechner

Your Institution. Montana Technological University

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Additional emails. (for correspondence). klechner@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.

Genes 5 and 6 were both found to encode DNA methyltransferase functions, this should be looked at closer to see if there is an atypical frameshift, or if two polypeptides are produced.

Please Examine

**Edited Starts**

Auto-annotated Zebo\_Draft\_2 (R, Start 589; Original Glimmer Call) was changed to start at 676, now ZEBO\_2

Auto-annotated Zebo\_Draft\_8 (R, Start 2477; Original Glimmer Call) was changed to start at 2666, now ZEBO\_8

Auto-annotated Zebo\_Draft\_14 (F, Start 5734; Original Glimmer Call) was changed to start at 5677, now ZEBO\_14

Auto-annotated Zebo\_Draft\_17 (F, Start 7134; Original Glimmer Call) was changed to start at 7071, now ZEBO\_17

Auto-annotated Zebo\_Draft\_26 (F, Start 12401; Original Glimmer Call) was changed to start at 11975, now ZEBO\_27

Auto-annotated Zebo\_Draft\_29 (F, Start 13077; Original Glimmer Call) was changed to start at 13080, now ZEBO\_30

Auto-annotated Zebo\_Draft\_30 (F, Start 14681; Original Glimmer Call) was changed to start at 14621, now ZEBO\_31

Auto-annotated Zebo\_Draft\_33 (F, Start 16946; Original Glimmer Call) was changed to start at 16895, now ZEBO\_34

Auto-annotated Zebo\_Draft\_43 (F, Start 22710; Original Glimmer Call) was changed to start at 22695, now ZEBO\_44

Auto-annotated Zebo\_Draft\_44 (F, Start 22966; Original Glimmer Call) was changed to start at 22999, now ZEBO\_45

Auto-annotated Zebo\_Draft\_57 (F, Start 36132; Original Glimmer Call) was changed to start at 36099, now ZEBO\_58

Auto-annotated Zebo\_Draft\_67 (F, Start 44484; Original Glimmer Call) was changed to start at 44475, now ZEBO\_68

Auto-annotated Zebo\_Draft\_77 (R, Start 49196; Original Glimmer Call) was changed to start at 49208, now ZEBO\_78

Auto-annotated Zebo\_Draft\_79 (R, Start 51014; Original Glimmer Call) was changed to start at 51164, now ZEBO\_80

Auto-annotated Zebo\_Draft\_96 (R, Start 61191; Original Glimmer Call) was changed to start at 61227, now ZEBO\_97

Auto-annotated Zebo\_Draft\_97 (R, Start 61578; Original Glimmer Call) was changed to start at 61623, now ZEBO\_98

Auto-annotated Zebo\_Draft\_107 (R, Start 65095; Original Glimmer Call) was changed to start at 65098, now ZEBO\_108

Auto-annotated Zebo\_Draft\_118 (R, Start 68161; Original Glimmer Call) was changed to start at 68251, now ZEBO\_120

Auto-annotated Zebo\_Draft\_121 (R, Start 68841; Original Glimmer Call) was changed to start at 68946, now ZEBO\_123

**Deletions**

Auto-annotated Zebo\_Draft\_21 (R, 10376-10236) Called by Glimmer and GeneMark, but replaced by final called forward genes 21 and 22

**Additions**

ZEBO\_21 (F, 10087-10281)  
 ZEBO\_22 (F, 10327-10701)

ZEBO\_31 (F, 14621-15091)

ZEBO\_65 (F, 42031-42150)

ZEBO\_88 (R, 54786-54412)

ZEBO\_114 (R, 66902-66789)

ZEBO\_117 (R, 67428-67327)

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?

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)?

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.