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.

    Below is a list of calls we needed to discuss as a class and gaps that were investigated but remain in the genome.

|  |  |  |
| --- | --- | --- |
| **Tricky calls** | **Stop @** | **Notes: discussions, reasons for decisions made** |
| gp 19 | 14781 | gp 19 had 1 transmembrane domain found. There is not enough evidence to call it a membrane protein. |
| gp 18 | 14540 | Both GL and GM call the start @14297. There is another start @14327.Selected start @14327 because it results in a -4bp overlap with the upstream gene. |
| gp 21 | 15065 | There were different calls from GL (@15502) and GM (@15565). We decided that the start was @15565 since there was more coding potential and it had better BLAST results and more MAs. |
| gp 24 | 16774 | There was a large gap between gene 24 and the previous one. This made us believe that it could be a larger gene. We looked at the blast results and realized that it is a larger gene. So we extended the start to 16388 bp |
| tRNA | 9482 | **DNAM**: this tRNA overlaps entirely with gp 12, the tape measure protein. **ARAGORN v1.4.21** : trimmed the tRNA from 498 bp to 75 bp. c/p Output: tRNA-Leu(gag) 75 bases, %GC = 77.3 Sequence [9408,9482]. **tRNA-scanSE** - the site was down (4.7.25). We ran it again on 4.30.25 - no tRNAs found. We deleted this tRNA because of the full overlap with the tape measure protein |
|  |  |  |
| **Gap range** | **Gene added?** | **Evidence collected** |
| 2545-2672 | no | no significant start and stops that would produce a gene w/ a plausible length, and cannot extend any current gene starts. Gap also present in Teddyboy and Yubaba |
| 6998-9651 | no | No significant coding potential as there's only a slight spike of CP in the reverse frame. The gap is also present on Azizam and BurtonThePup. |
| 15876-16388 | no | Reviewed the gap and extended gp 23 (stop @16774) start to 16388. After extending the gap, there was no significant coding potential from 15876 -16388. Gap also present in TeddyBoy and Yubaba |

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):

Yes1. 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)

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.