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. Aoka

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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.

\*\*no tRNAs were found

Here are some notes on genes, numbered according to original (phamerator)/final

\*\*Gene 2/2(stop: 1239 ) has a homolog in Maja\_1, which in NCBI appears as transposase and in phagesdb it appears as helix-turn-helix🡪 we followed phagesdb

\*\*Gene 8/8 (stop: 7573): we had questions about the start (see documentation on 2nd tab of our notes)

\*\*Did the translational frameshift in genes 15/15 and 16/16, based off Maja’s 14 and 15. Note: MargaretKali15 and 16 need to be redone as they somehow got it to Genbank without annotating the frameshift

\*\*Gene 27/27 (stop: 23666) not sure about the function (see documentation on 2nd tab of our notes)

\*\*Gene 28/28 (stop: 24011) not sure about start (see documentation on 2nd tab of our notes)

\*\*added a gene before gene 29/30 (stop:25474) 🡪 because DNAMaster sorts by “Index” this gene appears at the end unless features are sorted by “Start”

\*Gene 31/32 (stop: 25589) changed the start

\*\*Gene 32/33 (stop:26512) not sure about start (see documentation on 2nd tab of our notes)

\*\*Gene 38/39 and 39/40 (stop: 29887 & 30518) we called it Hypothetical because Debbie said so 😊 but they look like some quenosine biosynthetic genes

\*\*deleted gene with coordinates 31889-32020 because of large overlap with other gene

\*\*The following genes had transmembrane domains called by both software and were changed from Hypothetical to Membrane Proteins:

23/23 (stop 21839); 24/24 (stop 22237); 26/26 (stop 23596); 34/35 (stop 27573); 37/38 (stop 29561); 40/41 (stop30743)

\*\* Have tried to REBLAST but it didn’t save; will try again and resubmit DNAMinimalfile within a day 🡪Third time was the charm and it worked

\*\*Genes are numbered con

\*\*Students first fill in a spreadsheet with data, and then come back later and summarize it for DNAMaster Notes

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)?

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? Have tried to REBLAST but it didn’t save; will try again and resubmit DNAMinimalfile

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

YES DNA Master shorthand (previously used format) they don’t use the shorthand, but the notes field for summary of their findings

YES 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)

YES Spreadsheet

      Powerpoint

      Word document (must be easily searchable)

      Other: Describe.