**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. GoldenAsh

Your Name. Andrea Panagakis

Your Institution. Salish Kootenai College

Your email. andrea\_panagakis@skc.edu

Additional emails (for correspondence). N/A

**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. All genes were annotated and validated in PECAAN. GoldenAsh\_1-15 were also annotated the long way (i.e. using all of the programs and databases separately) using an annotation template in MW Word before segueing to PECAAN. The CDS full annotation file from PECAAN was then imported into DNAMaster. The frameshift (GoldenAsh\_14,15) was entered manually into DNA Master.

B. GoldenAsh\_14,15: -1 frameshift mutation, tail assembly chaperone protein. Used Remy19\_14,15 (G1) as model.

C. GoldenAsh\_30, Stop 27,110: Evidence for start at 26,790: Starterator NI; gap of 4 bp; LORF; contains all GM coding potential; better BLASTP and HHPred alignment to other phages-hypothetical protein.

D. GoldenAsh\_36, Stop 30,749: Evidence for start at 30,147: gap of -4 bp; Starterator NI; LORF; contains all GM coding potential; better BLASTP and HHPred alignment to other phages-hypothetical protein.

E. GoldenAsh\_60, Stop 40,620, Start 41,441: Deleted. Reverse gene,-1 frame, overlaps with forward genes 59+61 in forward direction. Small amount of typical and atypical GM coding potential. Poor alignment with phagesdb, NCBI, HHPred. Not present in similar manually-annotated phages, G1 subcluster.

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:

Yes PECAAN output

Yes 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

Yes DNA Master shorthand (previously used format)

      Spreadsheet

      Powerpoint

      Word document (must be easily searchable)

      Other: Describe.