# 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. Coletti
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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.

Coletti_8

There is best start @4438 that makes gene fit portal protein like in many their phages. All program do not call for this start. We think, it should be changed to start @4438 ATG, with the best Z and Final scores and smaller gap of 29 bps.

Coletti_43

GenMark indicate better start @39029 with the logical 4 bps overlap and better scores. This start called as most. Annotated for majority of similar phages which makes longer (97 AA) protein than 84 AA , although still with unknown function

Coletti_46

GenMark indicate start @40326 with better Z and Final scores. Although majority of annotations called for this start, it makes shorter ORF.

Coletti_52

Gene starts @47469 was not found by DNA Master. However, it looks like promising sequence, and we included it to the gene list. Many members of the phame have gene like that.

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?
yes 3. Are the genes (and matching LocusTag numbers) sequential, starting with #1, counting by 1s.
yes 4. Are the Locus Tags the "SEA_PHAGE NAME" format?
yes 5. Has the documentation been recreated from the Feature Table to match the latest file version?
n/a 6. Have tRNAs followed the tRNA protocol, **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 been annotated correctly (if applicable)?
yes 8. Have you cleared your Draft_Blast data and have you re-Blasted the submitted DNA Master file?
yes 9. Has every gene been described and supported in your Supporting Data file?
yes 10. Did you investigate 'gaps'?
n/a 11. Did you delete the genes that you meant to delete?

Now, make a profile of the file you plan to send. (And you can save this file for Review to Improve!)

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)
Spreadsheet
yes 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)
Spreadsheet
yes Powerpoint
Word document (must be easily searchable)
Other: Describe.