

## 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. PumpkinSpice  
Your Name. Amanda Freise  
Your Institution. UCLA  
Your email. [afreise@ucla.edu](mailto:afreise@ucla.edu)  
Additional emails. (for correspondence).

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.

**This was the first time I ever had to annotate tRNAs, and there were a LOT! I believe I've trimmed them all correctly and haven't missed any, but a closer look in the middle of the genome where all these tRNAs are located would be very helpful. Thank you!**

**PumpkinSpice\_190 is a tmRNA – I hope I've annotated that correctly. I also noticed in the DNAM minimal file that for tRNAs, I am getting an extra invisible hard return in the notes section after the tRNA description. I tried removing these manually but they came back after I recreated documentation. I'm not sure what's up.**

**Stop @ 57458:** Went with DNA primase based on other members of pham, but there are also HHpred hits for both polymerase AND helicase.

**Stop @ 69199:** Some limited evidence to call DNA binding protein, but not very strong - your thoughts?

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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?

**Yes** 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)?

**No** 8. Have you [cleared your Draft\\_Blast](#) data and have you [re-Blasted](#) the submitted DNA Master file?

**I was unable to re-BLAST within DNA master and have yet to figure out what the issue is. Debbie said it would be fine for now to note this here and submit.**

**Yes** 9. Has every gene been [described and supported in your Supporting Data file](#)?

**Yes** 10. Did you investigate '[gaps](#)'?

**Yes** 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

DNA Master shorthand (previously used format)

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)

Spreadsheet

Powerpoint

Word document (must be easily searchable)

Other: Describe.