

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. **MooKitty**

Your Name. Amanda Freise

Your Institution. UCLA

Your email. 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.

Gene 7: We called as tail terminator, but HHpred hits are somewhat weak. Synteny adds support for this function.

Genes 10: Other AX phages call this as tail assembly chaperone, but I left as NKF. For gene 10, the only supportive HHpred hit ([PF11831.11](#)) has an e-value = 1.2, and very few pham members call a function for this pham. Synteny supports TAC call, though.

Gene 11: leaving this as NKF, though in HHpred there is a very poor (e-value = 11) hit to Phage_P2_GpE, which is described in this literature reference: Christie GE, Temple LM, Bartlett BA, Goodwin TS; , J Bacteriol 2002;184:6522-6531.: Programmed translational frameshift in the bacteriophage P2 FETUD tail gene operon. [PUBMED:12426340](#) [EPMC:12426340](#)

Gene 22 (stop at 12342): Tricky start site call. LORF (216 bp, gap 46, start@14127) is a TTG start; RBS final score -6.296. Other choice is 14148 (195 bp, gap 67) is ATG and has final score of -5.350. Chose LORF but TTG/poorer RBS might be reason to select 14148.

Gene 23 (stop 15668): Appears to be one of the variations on the HNH motif. The "HNH" is not present, but "HNN" is present over 30-40aa. [See forum post.](#)

All regions with gaps near end of genome: Looked for coding potential on GM-self and GM-host. Did not find any strong CP in ORFs in gap.

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?

Yes 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:

- X 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.:

- X PECAAN output
- DNA Master shorthand (previously used format)
- Spreadsheet
- Powerpoint
- Word document (must be easily searchable)
- Other: Describe.