Actinobacteriophage Genome Annotation Submission Cover Sheet

This Cover Sheet will accompany each genome’s annotation file submission and will 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: GMonster

Your Name: Jenna Greene

Your Institution: Providence College

Your email: jgreene5@friars.providence.edu

Additional emails (for correspondence): kcornely@providence.edu

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, a workshop facilitator, or a buddy school for help, please document.

|  |  |
| --- | --- |
| **Gene number** | **Problem to be addressed** |
| Start 12761 Stop 13210 | Does not have hits to SPP1 for PDB |
| Start 35332 Stop 35192 | Tiny protein but all BLAST data says RDF; didn’t assign as RDF; instead, assigned that function to the following gene |
| Start 36099 Stop 35332 | In same pham as RedRock\_58 but only 62% similar protein sequence; assigned function as a recombination directionality factor, but unsure if maybe it was a metallophosphoesterase, since many BLAST hits were to metallophosphoesterases |
| Start 20476 Stop 22278 | Start call does not agree with Glimmer, GeneMark, or Starterator; we went with the most annotated start because we got better BLAST hits |
| Start 46192 Stop 45722 | Immunity repressor in a different pham than other A1 phages, so we didn’t have much information to guide us.We went with the GeneMark call to improve alignment and decrease gap |
| Start 49747 Stop 48830 | We assigned the function as a PAPS reductase-like domain but were not sure if it might be a ribonucleotide reductase. |

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 Locus Tag numbers) [sequential](https://seaphagesbioinformatics.helpdocsonline.com/article-77), starting with #1, counting by ones?

YES 4. Are the Locus Tags the “[SEA\_PHAGE NAME](https://seaphagesbioinformatics.helpdocsonline.com/article-77)” format?

YES5. Has the [documentation been recreated](https://seaphagesbioinformatics.helpdocsonline.com/article-86) from the Feature Table to match the latest file version?

NA 6. Have tRNAs been documented following 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)’?

No 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)

NA 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: DNA Master shorthand (previously used format)

YES: Spreadsheet

What is the file type (sort) submitted for QC to document your gene calls? Choose only one:

YES, DNA Master shorthand (previously used format)