# Genome Annotation Submission Cover Sheet

**Preliminary Annotation Review Checklist 5-15-2018**


| | |
|---|---|
| Phage Name: | Eradicator |
| Your Name: | Abbie George |
| Your Institution: | Montana Technological University |
| Your email: | ageorge@mtech.edu |
| Additional emails: (For correspondence) | mpedulla@mtech.edu |


*Please check each box indicating completion of each task. If you are not sure how to do something, please see the Online Bioinformatics manual page "How to Pass Preliminary Review".*

- [x] 1. Does the genome sequence in your final contain the same number of bases and is it the same as the posted sequence on phagesdb.org?
- [x] 2. Are all the genes "valid" when you click the "validate" button?
- [x] 3. Have the genes been renumbered such that they go sequentially from 1 to the highest number?
- [ ] 4. Have all old BLAST hits been cleared, and all gene features reBLASTed?
- [x] 5. Are the locus tags the"SEA_ PHAGENAME"?
- [x] 6. Has the Documentation been recreated to match the information in the feature table?
- [x] 7. Have tRNA ends been adjusted with web-based Aragorn and/or tRNAscan SE?
- [x] 8. Has the frameshift in the tail assembly chaperone been annotated (where applicable?)

9. For the items below, generate a genome profile, and review the following. For the

YourPhageName_CompleteNotes.dnam5 file:

- [x] a. Have any duplicate genes (or any with the same stop coordinate?) been removed?
- [x] b. Does every gene have **one and only one** complete set of Notes
- [x] c. Do the functions in the Notes match the official function list?
- [x] d. Are all three lines of functional evidence described for EVERY gene?
- [x] e. Do the notes contain the initial Glimmer/GeneMark data from the autoannotation?

For the YourPhageName .dnam5 file:

- [x] a. Have any duplicate genes (or any with the same stop coordinate?) been removed?
- [x] b. Is the Notes field empty (including hidden marks?)
- [x] c. Do the function names in the Product field either match the official function list or say "Hypothetical Protein"?
- [x] d. Is the Function field empty (including hidden marks?)

- [ ] 10. Did you use PECAAN to annotate your phage?

If, so please describe how in the text field after question 11.

11. Describe any issues or specific genes that you were unable to satisfactorily resolve, and warrant further inspection in the Quality Control review.

The annotated genome BLAST failed multiple times and was therefore unable to be reBLASTed. Interestingly, there was a transposase gene where similar phages predicted an integrase gene. The final gene count was determined to be 95 compared to the 96 genes that were originally called. Genes 32, 38, 39, and 66 from the prediction were deleted and genes 94, 95, and 96 were determined to be forward genes rather than the original call of reverse genes in that location. Several genes were also added such as a reverse gene 37, as well as forward genes 40 and 75 in the newly renumbered genome