

# Genome Annotation Submission Cover Sheet

## Pre-QC Phage Genome Annotation Checklist

Phage Name:

Your Name:

Your Institution:

Your email:

Additional emails:  
(For correspondence)

*Please check each box indicating completion of each task. Annotation Guide section #'s indicated*

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?
2. Are all the genes "valid" when you click the "validate" button? *Section 9.3.2*
3. Have the genes been renumbered such that they go sequentially from 1 to the highest number? *Section 9.3.3*
4. Have all old BLAST hits been cleared, and all gene features reBLASTed? *Section 9.3.4*
5. Are the locus tags the phage name? *Section 9.3.3*
6. Has the Documentation been recreated to match the information in the feature table?  
*Section 1.4*
7. Have tRNA ends been adjusted with web-based Aragorn and/or tRNAscan SE? *Section 9.5.3-4*
8. For the items below, generate a genome profile, and review the following. *Section 11.3*

For the YourPhageName\_CompleteNotes.dnam5 file:

- a. Have any duplicate genes (or any with the same stop coordinate?) been removed?
- b. Does every gene have **one and only one** complete set of Notes (see fig 12.2 in the Annotation Guide)?
- c. Do the functions in the Notes match the official function list?
- d. Is the function field EMPTY for all features?
- e. Do the notes contain the initial Glimmer/GeneMark data from the autoannotation?

For the YourPhageName .dnam5 file:

- a. Have any duplicate genes (or any with the same stop coordinate?) been removed?
  - b. Is the Notes field empty for all the features with no known function?
  - c. Do the function names in the Notes match the official function list, when applicable?
  - d. Is the function field EMPTY for all features?
9. Describe any issues or specific genes that you were unable to satisfactorily resolve, and warrant further inspection in the Quality Control review.

**Cover Sheet for Mycobacteriophage Pomar16 (A2)**  
**UPRC**  
**Dr. Michael Rubin**  
**Notes and Comparisons with Mycobacteriophage D29**

1. Possible gene bp #2-#82 was eliminated (based on comparison to D29). Lacks start codon. Possible wrap around gene.
2. Pomar16 GP20 Ends different than D29 ortholog
3. Pomar16 GP24 ends different than D29 ortholog
4. Pomar16 GP28 Different Beginning than D29 ortholog
5. Pomar16 GP29 Possible Translational Frameshift. Not documented.
6. Pomar16 GP41 ends different than D29 ortholog
7. Pomar16 GP50 begins and ends different than D29 ortholog
8. Pomar16 GP61 starts upstream from D29 gp57 ortholog
9. Pomar16 GP62 starts upstream from D29 gp59 ortholog
10. Pomar16 GP69 starts upstream from D29 p65 ortholog
11. Pomar16 GP70 no ortholog in D29
12. Pomar16 GP71 = D29 p66 ortholog
13. Pomar16 GP74 Very small ~19 aa (consider deleting)
14. Pomar16 GP78 starts upstream from D29 p72 ortholog
15. Pomar16 GP79 Begin deleted region in D29 genome
16. Pomar16 GP91 Begins similar region in D29 genome
17. Pomar16 GP92 starts upstream from D29 p74 ortholog
18. Pomar16 GP97 no D29 ortholog