

Genome Annotation Submission Cover Sheet

Pre-QC Phage Genome Annotation Checklist

Phage Name: Derpp
Your Name: Sarah Ball
Your Institution: The Ohio State University
Your email: ball.1766@osu.edu
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.

Function of gp9-called it as capsid morphogenesis protein based on phamerator maps of other cluster members but that is not on approved list of function.

gp24-labeled as tail assembly chaperone based on BLAST matches but pahmerator maps of other cluster members do not show it.

Added gp66 to fill gap. Had BLAST matches

Question about function on gp73-some phamerator maps and BLASTp hits are to PLA2 protein but we did not feel like there was substantial data to support the call so we went with