

# Genome Annotation Submission Cover Sheet

## Pre-QC Phage Genome Annotation Checklist

Phage Name: Mattes  
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(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.

SD scoring mstrix Kibler6 and Spacing weight matrix Karlin medium were used

Start choice change made for 30477-30698 that was not supported by Glimmer or Genemark, but the longer ORF that was annotated was supported by 1:1 Blast, and supported within Starterator.

Two genes were deleted from the original annotation: (1) 2631-2326 because it was in reverse direction amidst others in the forward direction and also overlapped with the next gene, which DID have a supported function, (2) 33621-33238 because it was in reverse direction amidst others in the forward direction and also overlapped with the next gene, which DID have a supported function.