

# Genome Annotation Submission Cover Sheet

## Pre-QC Phage Genome Annotation Checklist

Phage Name: Aggie  
Your Name: Roy Coomans  
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Your email: coomansr@ncat.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.

- 3 Listed ribonucleotide as function. Strong support from HHpred.
- 25 Uncertain of start selection.
- 27 Start agrees with neither, but comfortable with it.
- 31 Start site selection; see Logic in Notes.
- 43/44 See Notes to 43; possible programmed frameshift.
- 56 See Notes. Could delete preceding gene and move start to reduce gap with 54; went with ST and GM and agreement with BLASTp results.
- 57 Start selection uncertainty.
- 67 Looked at shortening 67 and adding a gene in the +1 reading frame to fill the gap. Not much support for adding the gene in terms of BLASTp hits. so didn't do so.