# Genome Annotation Submission Cover Sheet

**Pre-QC Phage Genome Annotation Checklist**


| | |
|---|---|
| Phage Name: | Noodletree |
| Your Name: | Bridgette Kirkpatrick |
| Your Institution: | Collin College |
| Your email: | bkirkpatrick@collin.edu |
| Additional emails: (For correspondence) | ctwichell@collin.edu, jlawson@collin.edu |


*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?

Y 9. Did you use PECAAN to annotate your phage?

a. If, so please describe how in the text field after question 10.

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

We used PECAAN when we reviewed the annotation that was done by the students the long way.

Genes 21 and 257 have no blast results with DNAM; I can't reconcile that--maybe that they are small, but have coding potential. n PECAAN, 257 aligns with a Gizmo phage, and 21 aligns poorly with a Rhodococcus protein.