Genome Annotation Submission Cover Sheet

Pre-QC Phage Genome Annotation Checklist

Phage Name: Glexan

Your Name: Steven Leadon

Your Institution: Durham Technical Community College

Your email: leadons@durhamtech.edu

Additional emails:
(For correspondence)

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

- [x] 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?
- [x] 2. Are all the genes "valid" when you click the "validate" button? *Section 9.3.2*
- [x] 3. Have the genes been renumbered such that they go sequentially from 1 to the highest number? *Section 9.3.3*
- [x] 4. Have all old BLAST hits been cleared, and all gene features reBLASTed? *Section 9.3.4*
- [x] 5. Are the locus tags the phage name? *Section 9.3.3*
- [x] 6. Has the Documentation been recreated to match the information in the feature table? *Section 1.4*
- [x] 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:

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

For the YourPhageName .dnam5 file:

- [x] a. Have any duplicate genes (or any with the same stop coordinate?) been removed?
- [x] b. Is the Notes field empty for all the features with no known function?
- [x] c. Do the function names in the Notes match the official function list, when applicable?
- [x] 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 score for all genes used Kibler6/Karlin Medium settings
Genes added
Gene 44 - SSC:35936-36505 (REV): Original gene call by autoannotation was a forward gene that was not present in related phages according to Phamerator. Gene was added using the largest ORF, however, the BLASTp results do not show any 1:1 alignments.
Gene 96 - SSC: 59099-59662: Original autoannotation left a large gap that was not conserved in related phages according to Phamerator. Newly added gene shows some alignment in BLASTp. Function was designated as NKF since BLASTp, HHPred, and Phamerator gave conflicting results for function.
Gene 120 - SSC: 67543-67755 and Gene 121 - SSC: 67736-67990: Original autoannotation