Genome Annotation Submission Cover Sheet

Pre-QC Phage Genome Annotation Checklist

Phage Name:	Iridoclysis
Your Name:	Marie Fogarty
Your Institution:	Durham Technical Community College
Your email:	fogartym@durhamtech.edu
Additional emails: (For correspondence)	leadons@durhamtech.edu

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*
- [ ] 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.

This genome was relatively straightforward (compared to out cluster C phage).
Iridoclysis is a cluster B phage with 68597 bp and 101 features.
There were no translational frameshifts and no tRNAs. Some gene deletions and additions were carried out, mostly using evidence from phamerator examination of closely related phages.
One gene that was deleted 54796 - 54939 (rev), we did struggle with. The gene was not present in closely related phage (phamerator) and the starterator results seemed to only include draft genomes. The GenemarkS file did show coding potential for this gene which is why we were in two minds about whether to delete.
Also, gene 29 15847 - 16623 has evidence as a Queuine tRNA-ribosyltransferase. This was