# Genome Annotation Submission Cover Sheet

**Pre-QC Phage Genome Annotation Checklist**

| | |
|---|---|
| Phage Name: | C3PO |
| Your Name: | Denise Monti |
| Your Institution: | University of Alabama at Birmingham |
| Your email: | dmonti@uab.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.

This was the first Corynebacterium annotated although this is being submitted for QC after Phage Darwin (also a Corynebacterium). We have checked the gaps between genes 86 and 87, 91-21, and 97-end for putative genes and we do not believe there are any calls in these regions that warrant being added to the genome. tRNA calls were made with Aragorn. Functional assignment was conservative. There were 2 potential functions (genes 37 and 38) but we left these as NKF because the e-value via BLAST or HHPred was not terribly convincing (e-30 or so) and the alignments were not of good quality.