# Genome Annotation Submission Cover Sheet

## Pre-QC Phage Genome Annotation Checklist

Phage Name:

Your Name:

Your Institution:

Your email:

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*

NA
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?    Some differences in P. acnes
   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.

Gene 44: This gene was added in, due to the DNAMaster genome comparison tool with other P. acnes phages. The start site was estimated by using other P. acnes phage genes' start sites. Several potential start sites for this gene from DNA Master were BLASTed to find some sort of alignment to other gene proteins from other P. acnes phages. The top hit had 1:1 alignment while the alignnments for the other hits were significantly different. However, we are also skeptical since there was no report for coding potential. Gene 45:This gene was also added in, after using the DNAMaster genome comparison tool with other P. acnes phages. Starterator was used to estimate the start position of the gene using other reported P. acnes phage. However, this gene had a reported coding potential. It had a successful alignment with other phages  and was reported as a putative endonuclease. But, we wish that it be confirmed that it exists as an actual gene.