Genome Annotation Submission Cover Sheet

Pre-QC Phage Genome Annotation Checklist

Phage Name: Canowicakte

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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*
- ☑ 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?

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

In this annotation, we also used comparative genomics with published annotated AK Cluster phage genome gene homologs. Most of the Canowicakte homologs are most closely related to the AK Custer Wayne homologs so most of our genes are annotated to be in a 1:1 amino acid alignment with the Wayne homologs. For homologs to AK Cluster genes previously annotated and published in GenBank, we assigned the same or similar functions unless noted in the Notes section of DNA Master.

One tRNA gene was found in the Canowicakte genome using tRNA scan. With the program tRNA scan a potential tRNA gene was found at position 40402-40313 and was included as a tRNA gene in the final annotation since the potential tRNA gene does not overlap the reverse