**Genome Annotation Submission Cover Sheet**

**Pre-QC Phage Genome Annotation Checklist**

Phage Name: Kingsolomon

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(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?

xx

x

x

1. Are all the genes “valid” when you click the “validate” button? *Section 9.3.2*
2. Have the genes been renumbered such that they go sequentially from 1 to the highest number? *Section 9.3.3*

|  |
| --- |
| x |
| x |
| x |
| x |

1. Have all old BLAST hits been cleared, and all gene features reBLASTed? *Section 9.3.4*
2. Are the locus tags the phage name? *Section 9.3.3*
3. Has the Documentation been recreated to match the information in the feature table?

*Section 1.4*

1. Have tRNA ends been adjusted with web-based Aragorn and/or tRNAscan SE? *Section 9.5.3-4*
2. For the items below, generate a genome profile, and review the following. *Section 11.3*

For the YourPhageName\_CompleteNotes.dnam5 file:

* 1. Have any duplicate genes (or any with the same stop coordinate?) been removed?

x

* 1. Does every gene have **one and only one** complete set of Notes (see fig 12.2 in the Annotation Guide)?

x

* 1. Do the functions in the Notes match the official function list?

x

* 1. Is the function field EMPTY for all features?

|  |
| --- |
| x |
| x |

* 1. Do the notes contain the initial Glimmer/GeneMark data from the autoannotation?

For the YourPhageName .dnam5 file:

1. Have any duplicate genes (or any with the same stop coordinate?) been removed?

|  |
| --- |
| x |
| x |
| x |
| x |

1. Is the Notes field empty for all the features with no known function?
2. Do the function names in the Notes match the official function list, when applicable?
3. Is the function field EMPTY for all features?
4. Describe any issues or specific genes that you were unable to satisfactorily resolve, and warrant further inspection in the Quality Control review.
* Gene 69 is a 207 bp long gene not called by GeneMark, it has 49 bp overlapping with the upstream gene. The evidence for calling this gene deserves further examination.
* Gene 99 [62477-62734] calling does not agree with Glimmer or GeneMark, it does give better Blast match. It deserves further examination.
* Gene 104 [63397-63570] calling does not agree with Glimmer or GeneMark, it does leaves no overlap with the upstream tRNA gene, and give good Blast match. It deserves further examination.
* Gene 116 [REV 65966-66592] does not agree with GM or Glimmer but this start position gives better blast match than the original calling by Glimmer. It deserves further examination.