# Genome Annotation Submission Cover Sheet

**Preliminary Annotation Review Checklist 5-15-2018**


Phage Name: NadineRae

Your Name: Daniel Westholm

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Additional emails:
(For correspondence)


*Please check each box indicating completion of each task. If you are not sure how to do something, please see the Online Bioinformatics manual page "How to Pass Preliminary Review".*

- [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?
- [x] 3. Have the genes been renumbered such that they go sequentially from 1 to the highest number?
- [x] 4. Have all old BLAST hits been cleared, and all gene features reBLASTed?
- [x] 5. Are the locus tags the"SEA_ PHAGENAME"?
- [x] 6. Has the Documentation been recreated to match the information in the feature table?
- [x] 7. Have tRNA ends been adjusted with web-based Aragorn and/or tRNAscan SE?
- [x] 8. Has the frameshift in the tail assembly chaperone been annotated (where applicable?)

9. For the items below, generate a genome profile, and review the following. 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
- [x] c. Do the functions in the Notes match the official function list?
- [x] d. Are all three lines of functional evidence described for EVERY gene?
- [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 (including hidden marks?)
- [x] c. Do the function names in the Product field either match the official function list or say "Hypothetical Protein"?
- [x] d. Is the Function field empty (including hidden marks?)

- [ ] 10. Did you use PECAAN to annotate your phage?

If, so please describe how in the text field after question 11.

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

Please accept this annotation of cluster CR4 Gordonia terrae phage Nadine Rae. Overall, we have confidence in our annotation but the following areas of the genome warrant closer inspection. Genes 15 and 44 were added, while three genes in total were deleted. When gene 44 was added, it produced a 214 base pair overlap with the preceding gene and it caused us to shorten gene 45, which resulted in a 1:128 blast match with Bipauneto. Although there is precedent for this addition in other phages, the length of the overlap is highly unusual. The deleted genes had either extensive overlapping of coding potential with other genes, or were transcribed in the opposite direction in the middle of an operon. Three genes in particular had unusual blast matches that cannot be rectified. Gene 62 had a 17:39 blast match, gene 90 had a 13:13 blast match, and gene 91 had a 48:4 blast match. In addition, gene 71 had an