

Genome Annotation Submission Cover Sheet

Preliminary Annotation Review Checklist 5-15-2018

Phage Name: Rasovi
Your Name: Parks Collins
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(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".

- 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?
- 3. Have the genes been renumbered such that they go sequentially from 1 to the highest number?
- 4. Have all old BLAST hits been cleared, and all gene features reBLASTed?
- 5. Are the locus tags the "SEA_PHAGENAME"?
- 6. Has the Documentation been recreated to match the information in the feature table?
- 7. Have tRNA ends been adjusted with web-based Aragorn and/or tRNAscan SE?
- 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:

- 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
- c. Do the functions in the Notes match the official function list?
- d. Are all three lines of functional evidence described for EVERY gene?
- 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 (including hidden marks?)
- c. Do the function names in the Product field either match the official function list or say "Hypothetical Protein"?
- 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.

We deleted a gene (13320, 13508) and fixed the programmed translational frameshift. TO do this we added a gene that matched pham #114135 from Goodman and Johann. We decided to keep the orpham @ gene 35556-35819 because of synteny with another orpham for Sucha. GeneMark also shows strong coding potential here.

We used both DNA Master and PECAAN to annotate Rasovi. We used Starterator, Host-Trained GeneMark, and the Gene Candidates section to determine the start points for each gene. We used the data listed on PECAAN from Phagesdb BLAST, HHPRED, and NCBI BLAST to determine the functions for each gene. When we needed, we used the individual programs to compare data.

Auto-Annotation called a tRNA sequence with a low infernal score. We decided to keep it because of a cluster specific forum post by Dr. Pope.