Genome Annotation Submission Cover Sheet

Pre-QC Phage Genome Annotation Checklist

Phage Name:	Krueger
Your Name:	Aaron Best
Your Institution:	Hope College
Your email:	best@hope.edu
Additional emails: (For correspondence)	

Please check each box indicating completion of each task. Annotation Guide section #'s indicated

- [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? *Section 9.3.2*
- [x] 3. Have the genes been renumbered such that they go sequentially from 1 to the highest number? *Section 9.3.3*
- [x] 4. Have all old BLAST hits been cleared, and all gene features reBLASTed? *Section 9.3.4*
- [x] 5. Are the locus tags the phage name? *Section 9.3.3*
- [x] 6. Has the Documentation been recreated to match the information in the feature table? *Section 1.4*
- [x] 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:

- [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 (see fig 12.2 in the Annotation Guide)?
- [x] c. Do the functions in the Notes match the official function list?
- [x] d. Is the function field EMPTY for all features?
- [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 for all the features with no known function?
- [x] c. Do the function names in the Notes match the official function list, when applicable?
- [x] 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.

See cover letter.

Hope COLLEGE

May 10, 2016

Dear SMART member,

Please find attached the Hope College Fall 2015/Spring 2016 Mycobacteriophage Krueger annotation files and author list. Krueger is a Subcluster K6 phage with high identity to other newly sequenced K6 phages. Below is a series of notes highlighting things we believe you should be aware of regarding the annotation.

Many large gaps throughout genome: Krueger appears to contain a large number of gaps greater than 100 bases, some ranging to several hundred bases. We have looked through each of these regions and minimized them where possible by extending ORFs to their longest starts or adding a limited number of genes. We believe that the gaps as they stand in the annotated version do not contain legitimate ORFs.

Additions: We added three ORFs – gp68, gp74, gp98.

Of Special Note:

gp18 and gp19 – gp19 is called to reflect a programmed translational frameshift and annotated (along with gp18) as a tail assembly chaperone immediately upstream of the tape measure protein.

gp21-gp28 – Each of these has been annotated as a minor tail protein. Please verify that this is warranted in each case.

Thank you for your efforts on the QC process. Please let me know if you have any questions or concerns.

Sincerely,

Aaron A. Best, Ph.D.

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