Genome Annotation Submission Cover Sheet

Preliminary Annotation Review Checklist 4-4-2018

Phage Name:	DrFeelGood
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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?
- [ ] b. Is the Notes field empty for all the features with no known function (including hidden marks?
- [x] c. Do the function names in the Notes match the official function list?
- [x] d. Is the function field EMPTY for all features?

- [ ] 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.

Gene 47** function call different depending on going off of Blast vs HHPred 50/50 split in pham.
Gene 49** Function call difficult- most in pham call as metallophosphoeterase, but BLAST calls it RDF.
Gene 52 and Gene 53** DNA Primase, please check as split into two overlapping reading frames re: the cluster specific forum
Gene 70** Function call difficult. Atypical coding potential, but no normal coding potential, HHPred not helpful, but BLAST calls it the immunity repressor,which we did not identify