Genome Annotation Submission Cover Sheet

Pre-SM*ART QC Phage Genome Annotation Checklist

Phage Name:	CGermain
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Please check each box indicating completion of each task.

- ☑ 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 for all the features with no known function (including hidden marks?
- ☑ c. Do the function names in the Notes match the official function list?
- ☑ d. Is the function field EMPTY for all features?

9. Did you use PECAAN to annotate your phage?
   a. If, so please describe how in the text field after question 10.

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

Start sites for genes #3, #9, #19, #21 were changed. More information can be found in their notes sections. Gene #24 was deleted because it was a reverse gene that completely overlapped a forward gene with a known function. It was neither called a gene by other phage homologs, nor by Glimmer and did not have blast or HHPred results. Gene 27 (15288 - 46) is a wraparound gene with large overlap. We called gene #18 a 'holin' citing a few phage homologs as well as a modest HHPred result. Lastly, gene #17 was called an amidase because N-acetylmuramoyl-L-alanine amidase xlyA was not in the official function list. Thank you!