Phage = **Anamika**

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1. Checked. The genome lengths match.
2. Checked. All genes were validated.
3. Checked. New DNA master file uploaded with corrected numbering.
4. Checked. All gene features for which the start sites were changed were re-blasted and the old BLAST hits have been cleared.
5. Checked. Locus tags are the name of our phage.
6. Checked. Documentation recreated.
7. Checked. tRNA adjusted.
8. Checked.

For the YourPhageName\_CompleteNotes.dnam5 file:

* 1. Checked. Phage Anamika had no duplicate genes.
	2. Checked. Yes, every gene has only one complete set of notes.
	3. Checked. Yes, the functions in the notes match the official function list.
	4. Checked. Yes, the function field is empty for all features.
	5. Checked. Yes, notes contain the initial Glimmer/GeneMark data from the autoannotation.

For the YourPhageName .dnam5 file:

* + - * 1. Checked. Yes, any duplicate genes have been removed.
				2. Checked. Yes, the Notes field is empty for all the features with no known function.
				3. Checked. Yes, the function names in the Notes match the official function list, when applicable.
				4. Checked. Yes, the function field is EMPTY for all features.
1. There was not a 100% agreement with the final decisions for the following genes:
* Gene 68 originally called by Glimmer (58335-58451 Rev) but not GeneMark was deleted due to length (117bp) and lack of alignment. It does, however, have some coding potential using GeneMark (*Gordonia bronchialis*).
* Gene 73: No Known Function called. However BLASTp assigns function as hypothetical protein with an E-value of 0.0, while, HHpred suggests a function of putative membrane protein with a probability >96% and an E-value of 1.2E-3.
* Gene 81: AAA ATPase called. It was unclear which function should be assigned to this gene—BLASTp called AAA ATPase and HHPred called P-loop containing dynein motor region (probability>99%) and. E-values for both BLASTp and HHPred were below the threshold value. Phamerator indicates that there are conserved domains relating to AAA ATPase, however, since HHPred calls a different function with compelling E-value, we were undecided.

The following genes have large bp gaps. All are annotated to the longest possible ORF, with the exc eptions of 8, 68, and 90.

* RevGene 4 has a 125 bp gap
* FwdGene 8 has a 120 bp gap
* FwdGene 24 has a 112 bp gap
* RevGene 46 has a 123 bp gap
* RevGene 55 has a 217 bp gap
* RevGene 60 has a 105 bp gap
* RevGene 68 has a 439 bp gap
* RevGene 74 has a 150 bp gap
* RevGene 75 has a 122 bp gap
* RevGene 87 has a 209 bp gap
* RevGene 88 has a 207 bp gap

One tRNA and one frame shift in the tail assembly chaperone genes were found and annotated.

No integrase or immunity repressor was found.