If possible once completed, please send QC annotation notes to [ConboyA@chc.edu](mailto:ConboyA@chc.edu). We would like to review the feedback! Thanks a lot!

**Dewayne 3** - Start site changed from 690 to 591 to yield better blast results, the longest ORF, to agree with starterator, and to shorten the gap. However, it gives a worse SD score, and goes against Glimmer and GeneMark.

**Dewayne 9** - Start site changed from 5661 to 5652 to increase ORF, decrease gap, to agree with GeneMark and Starterator, and give better blast alignments. However, this gives a worse SD score. Arthrobacter Phage Courtney3 calls this ORF a 'Major Tail Protein' via phagesdb blast. After downloading Courtney3 DNAM file, this function was not called in the original annotation. This ORF aligns 1-to-1 with Courtney3\_9 - but other phage homolog calls an Unknown Function here.

**Dewayne 14** - Called this protein a 'minor tail' function, but could not find other evidence other than phage homologs. HHPred does not give any results, nor does NCBI have any putative or conserved domains. In phagesdb blast, about half of the phage homologs call this gene NKF while half call it minor tail.

**Dewayne 18** - Called this protein a ‘holin’ function. HHPred gives a relatively poor hit to a holin with about 72% probability and 15 e-value. However, many other phage homologs call this protein a homolog, as seen from phagesdb blast.

**Dewayne** **19** - Start site changed from 12875 to 12887 to decrease the large overlap, to align 1:1 with other phage homologs, to give the best SD score, to match with Starterator and to better blast results. However, we go against both glimmer and Genemark. HHPred gives good hit to hemolysin, but function is not appropriate for phages. A lysin would make sense in this part of the genome, however, because it was preceded by a putative holin, an endolysin, and an amidase.

**Dewayne 21** - Start site changed from 13746 to 13653 to yield longest ORF, shorten gap, better SD score, and to match 1-to-1 to only blast hit. This gene is not called in many other phage homologs, and is not called by GeneMark. However, this goes Glimmer's and Starterator's suggested start site.

**Dewayne 24** (14128 - 14424) - Gene was deleted because it was a reverse gene that completely overlapped a forward gene with a known function. This ORF also was not in other annotated phage homologs, was not called by Glimmer, and did not have significant blast or HHPred results.

**Dewayne 27** (15288 - 46) - Wraparound gene with a very high overlap (48 bp) of previous gene.