**Midas\_2**

I feel rather confident on my work with the bacteriophage known as Midas\_2. I made a few changes to start codons, as well as the deletion of certain genes. This genome is of particular interest**.** This genome has the exact same number of base pairs as the bacteriophage known as COOG. It also has 100% similarities and alignments of genes. It has all the same gene calls and coding potential as COOG as well. I did the annotation on this genome and since I felt confident in my ability to annotate the genome, I made all of the same calls since I felt they were originally satisfactory.

* **Gene 4**: I changed the start codon from 2447 bp to 2354 bp which showed more coding potential with GeneMark and also made the reading frame longer, with a start codon of ATG.
* **Gene 7:** I moved the start codon from 4460 bp to 4409bp in order to make it the longest reading frame with a start codon of ATG.
* **Gene 20:** I moved the start codon to 14325 instead of the 14415, which provided a longer reading frame and when re-blasted also gave me a tail assembly chaperone function. I would like someone to look more into this one, as it does not have the best coding potential with GeneMark but it does have some coding potential.
* **Gene 30:** I changed the start codon from 25826 bp from 25772 which provided it with an ATG start codon as well as a longer reading frame.
* I deleted **gene number 31**, since there was too much overlap with the next gene, and there was no coding potential at all with genemark just glimmer, when I try to adjust the ORF it no longer has coding potential with Glimmer, so I deleted it. This was a tough call since it was a gene that originally had a length of 516bp, but did not provide any hits in blast, phamerator, or NCBI.
* **Gene numbers 47, 48, 60, 61, and 62. Where all deleted.** Genes 47 and 48 where both in the wrong direction as the rest of the genome at this part and both where very small ORF with little to no coding potential with Genemark. Genes 60, 61, and 62 all had very short ORF while still being the longest possible reading frames. All 3 genes had severe overlap with no possible combination to make them work. All 5 genes showed no blast results.
* **I also deleted Gene number 71:** It is the wrong direction and did not have coding potential with GeneMark, and it yielded no blast, or NCBI results.
* **Gene number 87: Was also deleted it, did not have agreeing coding potential.** The other possible combinations provided too much gap, and made the gene too small to even consider it being a gene.