Lehigh University has investigated the genome of mycobacteriophage Taptic. Since this is a new cluster (W), with no finished genomes, we would like the whole genome investigated more closely. We feel all gaps are valid. We have also called as many functions as possible.

One area to investigate more closely are gp19-20. These genes have homology to tail assembly chaperones in other phages. I have investigated the six frame translation and do not see a ‘slippery sequence’ nor anywhere a frameshift may occur. I have not called the tail assembly chaperone due to this.

Also of note, gp38 is called as the immunity repressor based on HHPred data. There is homology in HHpred from phage 434 for both repressor CI (99.61% prob, 2.9 e-15 e value) and CRO protein (99.63% prob, 2.2 e-15 evalue).

gp74 (52643-53527) has homology to Par-B dsDNA partitioning protein however no Par-A was found, this function was not called.

We have added many genes to close the large gaps. The following genes were added to close these gaps gp68 (49502-49873), gp70 (50486-50746), gp77 (54819-55070), gp89 (58811-59023).