Genome of Arthrobacter phage Muttlie – Bucknell University, Spring 2015

All genes should be annotated well.

Please check the “wrap-around” gene that goes across the ends of the genome to make sure that is annotated correctly.

We were fairly conservative with function assignments since the proposed proteins do not match many other proteins in Genbank with known or hypothetical functions. Though some functions were added after running HHpred comparisons.