Saint Joseph's University

Spirit | Intellect | Purpose

Department of Biology

May 21, 2015

Dear Colleagues,

Thank you for your review of Arthrobacter phage Wilde. I did not format the second "minimalistic" Final dnam5 file since the collection of Arthrobacter phages is not quite as vast as those for Mycobacteriophages and the functions of many gene features are still unknown.

The 68203 bp genome of Wilde contained 589 bp overlap at the 5' and 3' ends. One gene feature at the ends that was partially duplicated was deleted. Gene feature that starts at 10185 showed a possible frame shift with the following feature, but the slippery sequences were GGAAA (rather than GGAAAA).

Best,
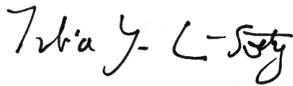
Julia Y. Lee-Soety, PhD
Associate Professor of Biology
610-660-3439
jlee04@sju.edu