Mycobacteriophage Brusacoram

The College of Saint Scholastica

Please accept our fully annotated genome of the Mycobacteriophage *Brusacoram*, annotated by students at The College of St. Scholastica. We feel confident with our gene selection and gene functions; however, we would like you to pay special attention to the following genes due to the reasons outlined below:

* Genome was validated, but 9944 – 10862 is being listed as not in frame (1 in-frame stop codon), even though it was unchanged from auto-annotate call
* Gene 12: Best blast match 15:15
* Gene 16: merged gene with gene 15 (frameshift +1) We identified that this gene is where the frameshift happened. We followed the SEA Phages manual when splitting the gene in the “Regions” tab of DNA Master.
* Gene 46 Best blast match 6:5
* Gene 53: Only blast match is 2:12 with *Kineococcus radiotolerans* (no phage blast matches)
* Gene 55: Best blast match 5:4
* Gene 56: Little coding potential present, but decided did not delete it. Glimmer and GeneMark called the gene.
* Gene 62: Best blast match 3:5
* Gene 74: There is a gap of 208 BP