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2021 SEA Symposium Abstract

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All Hail Bacteriophages! The Genomic Annotation of the Mycobacteriophage Hail

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In collaboration with the HHMI SEA-PHAGES program, students at the University of Massachusetts Amherst successfully annotated the genome of the bacteriophage Hail. Discovered by the University of Pittsburgh, Hail has a temperate life cycle, siphoviridae morphotype, and belongs to Cluster Q. Hail's isolation host is Mycobacterium smegmatis, therefore Hail is a mycobacteriophage. The phage's genome is 53,746 base pairs long, with a GC content of 67.5%. Through the utilization of several bioinformatic tools such as BLAST, Genemark, Glimmer, HHPred and Phamerator, 87 genes were discovered, with 34 of them found to have an identified function. As the annotation was analyzed, it became evident that the last gene in the annotation, Gene 87, should be eliminated from the genome.