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2022 SEA Symposium Abstract

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What’s in a gene? The annotated genome of the Mycobacteriophage Phegasus

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Bacteriophages, viruses that infect bacteria, have been silently waging the largest war on Earth for millions of years. Due to their bactericidal nature, bacteriophages have the potential to act as a countermeasure against antibiotic resistant bacteria. Therefore, the expansion of bacteriophage genomic libraries is critical to the advancement of bacterial treatments. As part of the HHMI-SEA-PHAGES program, a cohort of undergraduate students from Arizona State University (ASU) characterized and annotated the genome of Phegasus, which was isolated from the host Mycobacterium smegmatis mc2155. Phegasus is a member of the temperate P1 sub-cluster of the Siphoviridae morphotype. Using DNAMaster, GeneMark, and Starterator, 78 genes were annotated; one tRNA was found via Aragorn.