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2025 SEA Symposium Abstract

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Bioinformatic Annotation of Mycobacteriophage Glubnar

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A bacteriophage is a virus that infects and replicates inside bacteria. Phages are highly diverse and can be found in nearly every environment that harbor bacteria. Throughout the spring semester as part of the SEAPHAGES program, we have used various bioinformatic tools and techniques to verify the auto annotation of the 68,397 base pair genome of Mycobacteriophage Glubnar. We first verify that the predicted open reading frame (ORF) has coding potential and meets all requirements to be called a gene. Next, we use multiple programs to determine the start location for the gene using HHMI’s guiding principles. Afterwords to determine function, we use Phamerator, Blast, and HHPred. These programs help us identify homology in amino acid sequences and protein structure. By following these steps, we have compiled evidence to call a start location and proposed function for each gene in Glubnar.