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2025 SEA Symposium Abstract

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An Annotation Journey in the EA1 Cluster: Mapping the Genes of JeriBeth

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Bacteriophages (Phages) are a crucial part of scientific exploration and discovery. Despite therapeutic properties, much of phage biology remains unknown. Genetic sequencing and annotation of these phages can further benefit medical and scientific research. Following isolation from an enriched soil sample, phage JeriBeth was sequenced and annotated using bioinformatic tools such as PECAAN, Phamerator, Starterator, BLAST, HHPRED, and TMHMM. JeriBeth was determined to be part of the EA1 cluster, a large family of phage. During annotation, JeriBeth was found to have 63 genes with 27 forward genes and 36 reverse genes. Additional work to characterize the function of these genes, and the genomes of similar phages, will contribute to our understanding of other phages in the EA1 cluster.