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Complete Genome Annotation of Actinobacteriophage StuartMinion

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Bacteriophages, viruses that infect and replicate within bacteria, play a crucial role in microbial ecology, genetic research, and biotechnology. Research discoveries in this field contribute to advancing the understanding of phages and their practical uses in addressing challenges like antibiotic resistance and microbial infections. The primary objective of studying the StuartMinion bacteriophage genome is to achieve a detailed annotation of its genetic structure and functionality through bioinformatics techniques. This involves identifying and characterizing protein-coding genes to interpret their roles. StuartMinion, a phage isolated from soil at Kunia Loa Ridge Farmlands in Kunia, Hawaiʻi, was annotated at the University of Hawaiʻi at Mānoa. Its genome annotation began with gene prediction using Glimmer and GeneMark, followed by manual verification of start sites using PECAAN and Starterator. Functional predictions for protein-coding genes were made through database searches, including NCBI Conserved Domains and BLAST against the NCBI and Actinobacteriophage Proteins databases. This process revealed 63 predicted genes, of which 38 were successfully assigned putative functions, while two were classified as orphan genes. StuartMinion belongs to the AS3 subcluster, with a genome length of 35,207 base pairs and a GC content of 66.4%. While the majority of the genes within the genome were transcribed in the forward direction, 11% were transcribed in the reverse direction. Notably, StuartMinion has the smallest genome and exhibited the lowest percentage of reverse transcription within its subcluster. Additionally, further research on StuartMinion's genome could provide valuable insights into resistance mechanisms, phage-host interactions, and biotechnological applications.