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2021 SEA Symposium Abstract

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Annotating Akhila’s genome, a first encounter with Bioinformatics.

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SUNY Old Westbury is a part of the 10th Cohort of the HHMI Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science (SEA-PHAGES). The phage Akhila was isolated in Fall 2019 as part of the phage discovery component that was integrated into the honors section of general biology I laboratory (BS2401). As this section was switched to a remote format in Fall 2020, students in this course instead annotated Akhila’s genome as a part of the SEA-PHAGES Bioinformatics project. Herein the results of Akhila’s annotation are reported. Akhila has a Siphoviridae morphotype with a temperate life cycle. It was sequenced at the University of Pittsburgh Bacteriophage Institute using Illumina sequencing with a shotgun coverage of 1484. It has 56,251 base pairs and 62.1% GC content. It belongs to the F1 cluster of Mycobacterium smegmatis mc2155 phages. Following this annotation, Akhila was noted to contain 101 genes.