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Complete Genome Annotation of Gordonia bacteriophage Halo3

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Gordonia phage Halo3 was discovered by Haley Chavey of Kansas State University in Wamego, KS during 2021. The virus was isolated from chicken coop detritus using host Gordonia terrae CAG3. Halo3 was adopted and annotated at Franklin Pierce University

Its genome is 59,182 base pairs long with a GC content of 67.9%. The genome contains 93 open reading frames. Its closest relative by nucleotide identity is Evamon (87% coverage 98.62% identity). Its closest relatives by amino acid alignment are Twister6, Wizard, and Yungmoney.

Halo3 belongs to the cluster DC, which includes 30 other members. The average length of the members within the cluster are 58,871 base pairs long with an average GC content of 67.7%. Most of the genes (76 of 93) show strong synteny with Salvador and Evamon: mostly forward genes and few orphams. No tRNAs were detected. But, a DNA methytransferase was identified and a putative DNAJ-like chaperone.