Genome Sequence(s) of MyHost Phage MyPhage

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**Abstract**

Usually two to three sentences about my phage, its sequence, and any interesting or noteworthy findings. The guidelines say the abstract must be 50 or fewer words long.

The first part of a Genome Announcement often provides background information about the topic at large and the importance/relevance of said topic, such as the phage population as a whole and the depths (or lack of) to which it has been investigated. This is usually followed by general information about the phage or phage(s) themselves such as isolation location, plaque details, EM info, etc.

The second part of a Genome Announcement generally provides details on the process and results of sequencing the genome(s). This is where sequencing method, coverage, genome length, GC%, end type, and assembly software used are reported.

The third part of a Genome Announcement provides details on the process and results of annotating the genome, including software used, number of genes identified, tRNAs/tmRNAs, cluster, general genome architecture, relatedness to other genomes, presence/absence of lysogeny machinery, notable functions identified.

The last part of a Genome Announcement highlights interesting, unusual, exciting, or otherwise noteworthy findings from your genome or group of genomes. This could be unusual genes, strange genome arrangements, introns, inteins, genes gained/lost compared to relatives, new genes, GC content differences from host, genes found in phages of other hosts, short repeated sequences, genomic oddities, similarities/differences of genomes in this announcement, etc. Put anything cool here, and remember to keep everything under 500 words total!

**Nucleotide sequence accession numbers**

MyPhage is available at GenBank with Accession No. XXXXXXXX. (Will be provided after we submit the final annotation to GenBank)

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**References**

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2. **Russell DA, Hatfull GF.** 2017. PhagesDB: the actinobacteriophage database. Bioinformatics **33:**784-786.

3. **Etc.**

4. **Etc.**