\*\* Genome Sequence(s) of MyHost Phage MyPhage

\*\* Author One1, Author Two1, Author Two2,… and Corresponding Author1#.

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**Abstract**

\*\* Usually two to three sentences about MyPhage, its morphotype, its genome length, gene content and/or cluster assignment, its isolation host, and any interesting or noteworthy findings. The guidelines say the abstract must be 50 words or fewer.

\*\* The opening sentence of your manuscript should provide the rationale for isolating and studying particular bacteriophage(s). Often, this opening sentence describes the relevance of studying bacteriophage populations as a whole and/or bacteriophages for particular hosts.

\*\* The opening sentence is usually followed by general information about how the phage(s) was isolated and visible characteristics. Information you provide here should include the sample type (e.g. soil or water), sample location, the process of isolation, purification, and amplification, the temperature and media used, and the morphology of your phage, both in terms of the plaques it forms as well as the size and morphotype of individual phage particles as viewed by electron microscopy. As you provide this information, be sure to provide enough information so that another scientist might be able to replicate your process. It may be useful to include a figure of the plaques as well as electron micrograph(s) of the phage particle(s). (*Data for this section may be compiled in the “Isolation\_Characterization” tab of the MRA Data Collection template.*)

\*\* The second part of this manuscript will begin to describe the genome of the bacteriophage. This section should begin with a description of how the phage DNA was isolated and the process and results of sequencing the genome(s). You must include information on the sequencing kit, number of reads, length of reads, genome length(s), GC %, genome end type(s), cluster assignment(s), and the software and hardware used. This section is very technical, and you must provide enough information so another scientist can replicate your process. See notes for guidance. If reporting on multiple phages, it is best to present the information in a table (*Data for this section may be compiled in the “Sequencing”, “Info from Sequence Read Archive (SRA)” and “Software” tabs of the MRA Data Collection template.*)

\*\* The third part of this manuscript should begin with details on the process of annotating the genome, focusing on the software used. Like the previous section, this section is also very technical. See notes for guidance. \*\* This should then be followed with a description of what was discovered from the annotation process. Typically, this includes the number of genes that were found to encode proteins and tRNAs, putative functions for any gene products, and the arrangement of genes across the genome. (*Data for this section may be compiled in the “Software” and “Annotation” tabs of the MRA Data Collection template.*)

\*\* The last part of this manuscript highlights interesting, unusual, exciting, or otherwise noteworthy findings from your genome or group of genomes. This could be the presence of unusual genes, introns, and/or inteins, the presence or absence of notable genes compared to similar phages, 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 and Sequence Read Archive (SRA) No. XXXXXXXX. (*Data for this section may be compiled in the “Information for Dan Russell” and “GenBank Accession Numbers” tabs of the MRA Data Collection template.*)

**Acknowledgements**

\*\* This section is an opportunity to acknowledge all the individuals that provided assistance that enabled you to complete your research and/or write the manuscript. This is also a good place to acknowledge any scholarship or research funders that enable you to accomplish this work.

**\*\* References**

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