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2021 SEA Symposium Abstract

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Complete genome sequence of Microbacterium bacteriophage Erla

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We characterized the complete genome sequence of *Siphoviridae* bacteriophage Erla, an obligatory lytic subcluster EA1 bacteriophage infecting *Microbacterium foliorum* NRRL B-24224, with a capsid width of 65 nm and a tail length of 112 nm. The 41.5-kb genome, encompassing 62 predicted protein-coding genes, is highly similar (99.52% identity) to that of bacteriophage Calix.