

CORRECTION

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Correction to: Complete genome of a novel virulent phage ST0 lysing *Escherichia coli* H8

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Correction

Table 1 of this original publication contained an error. The updated Table 1 is published in this correction article [1].

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Reference

1. Liu et al. Complete genome of a novel virulent phage ST0 lysing *Escherichia coli* H8. *Stand Genomic Sci.* 2017;12:85. <https://doi.org/10.1186/s40793-017-0304-9>.

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Table 1 Classification and general features of *Genusspecies* strain designation^T [19]

MIGS ID	Property	Term	Evidence code ^a
	Classification	Domain: Viruses, dsDNA viruses Phylum: unassigned Class: unassigned Order: <i>Caudovirales</i> Family: <i>Myoviridae</i> Genus: unassigned Species: unassigned (Type) strain: unassigned	TAS [21] TAS [21] TAS [21]
	Gram stain	N/A	
	Cell shape	N/A	
	Motility	N/A	
	Sporulation	N/A	
	Temperature range	N/A	
	Optimum temperature	N/A	
	pH range; Optimum	N/A	
	Carbon source	N/A	
MIGS-6	Habitat	Water	IDA
MIGS-6.3	Salinity	N/A	
MIGS-22	Oxygen requirement	N/A	
MIGS-15	Biotic relationship	Intracellular parasite of <i>Escherichia coli</i> H8	IDA
MIGS-14	Pathogenicity	Lytic phage of <i>Escherichia coli</i> H8	IDA
MIGS-4	Geographic location	China	IDA
MIGS-5	Sample collection	April, 2017	IDA
MIGS-4.1	Latitude	40°N	IDA
MIGS-4.2	Longitude	116°E	IDA
MIGS-4.4	Altitude	Unknown	

^aEvidence codes - *IDA* inferred from direct assay, *TAS* traceable author statement (i.e., a direct report exists in the literature). These evidence codes are from the Gene Ontology project [20]