

Unifying classical and molecular taxonomic classification using BLASTP-based tools

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The genome and proteome of the Klyuvera bacteriophage Kvp1 – another member of the T7-like Autographivirinae. <i>Virology Journal</i> , 2008, 5, 122.	1.4	12
2	Functional Genomic Analysis of Two <i>Staphylococcus aureus</i> Phages Isolated from the Dairy Environment. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7663-7673.	1.4	46
3	Complete Genome of the Broad-Host-Range <i>Erwinia amylovora</i> Phage Î Ea21-4 and Its Relationship to <i>Salmonella</i> Phage Felix O1. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2139-2147.	1.4	61
4	Classification of Myoviridae bacteriophages using protein sequence similarity. <i>BMC Microbiology</i> , 2009, 9, 224.	1.3	245
5	CGUG: in silico proteome and genome parsing tool for the determination of "core" and unique genes in the analysis of genomes up to ca. 1.9 Mb. <i>BMC Research Notes</i> , 2009, 2, 168.	0.6	52
6	Genomes of –phiKMV-like viruses– of <i>Pseudomonas aeruginosa</i> contain localized single-strand interruptions. <i>Virology</i> , 2009, 391, 1-4.	1.1	27
7	The adsorption of <i>Pseudomonas aeruginosa</i> bacteriophage –K1M is dependent on expression regulation of type IV pili genes. <i>FEMS Microbiology Letters</i> , 2009, 296, 210-218.	0.7	46
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13	Novel Bacteriophages in <i>Enterococcus</i> spp.. <i>Current Microbiology</i> , 2010, 60, 400-406.	1.0	29
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15	The SPO1-related bacteriophages. <i>Archives of Virology</i> , 2010, 155, 1547-1561.	0.9	91
16	Genomic analysis and relatedness of P2-like phages of the <i>Burkholderia cepacia</i> complex. <i>BMC Genomics</i> , 2010, 11, 599.	1.2	54
17	Rapid pair-wise synteny analysis of large bacterial genomes using web-based GeneOrder4.0. <i>BMC Research Notes</i> , 2010, 3, 41.	0.6	15
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33	The genome sequence of enterobacterial phage 7-11, which possesses an unusually elongated head. <i>Archives of Virology</i> , 2011, 156, 149-151.	0.9	22
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35	In silico bioinformatic tools for determining core genes from sets of genomes. <i>Drug Development Research</i> , 2011, 72, 147-152.	1.4	0
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74	Twelve previously unknown phage genera are ubiquitous in global oceans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12798-12803.	3.3	182
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104	Salmonella Phages and Prophages: Genomics, Taxonomy, and Applied Aspects. <i>Methods in Molecular Biology</i> , 2015, 1225, 237-287.	0.4	31
105	Characterization of Novel Bacteriophages for Biocontrol of Bacterial Blight in Leek Caused by <i>Pseudomonas syringae</i> pv. <i>porri</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 279.	1.5	86
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124	Comparative Omics and Trait Analyses of Marine Pseudoalteromonas Phages Advance the Phage OTU Concept. <i>Frontiers in Microbiology</i> , 2017, 8, 1241.	1.5	34
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