

Andrew M Kropinski

List of Publications by Year in descending order

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27035

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204
docs citations

204
times ranked

11689
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete Genome Sequence of a Jumbo Bacteriophage, Escherichia Phage vB_EcoM_EC001. Microbiology Resource Announcements, 2022, 11, e0001722.	0.3	1
2	ICTV Virus Taxonomy Profile: Chaseviridae 2022. Journal of General Virology, 2022, 103, .	1.3	2
3	A Roadmap for Genome-Based Phage Taxonomy. Viruses, 2021, 13, 506.	1.5	268
4	Bacterial Viruses Subcommittee and Archaeal Viruses Subcommittee of the ICTV: update of taxonomy changes in 2021. Archives of Virology, 2021, 166, 3239-3244.	0.9	24
5	Characterization of the first Pseudomonas grimontii bacteriophage, PMBT3. Archives of Virology, 2021, 166, 2887-2894.	0.9	0
6	Phage Annotation Guide: Guidelines for Assembly and High-Quality Annotation. Phage, 2021, 2, 170-182.	0.8	24
7	Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. Systematic Biology, 2020, 69, 110-123.	2.7	89
8	Binomial nomenclature for virus species: a consultation. Archives of Virology, 2020, 165, 519-525.	0.9	51
9	From Orphan Phage to a Proposed New Family—The Diversity of N4-Like Viruses. Antibiotics, 2020, 9, 663.	1.5	39
10	VIRIDIC—A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses, 2020, 12, 1268.	1.5	274
11	Changes to virus taxonomy and the Statutes ratified by the International Committee on Taxonomy of Viruses (2020). Archives of Virology, 2020, 165, 2737-2748.	0.9	202
12	Characteristic of a Distant Relative of Teseptimavirus Genus Phages That Acquired the Ability to Lysozenize Its Host. Proceedings (mdpi), 2020, 50, .	0.2	0
13	Taxonomy of prokaryotic viruses: 2018-2019 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. Archives of Virology, 2020, 165, 1253-1260.	0.9	144
14	ICTV Virus Taxonomy Profile: Herelleviridae. Journal of General Virology, 2020, 101, 362-363.	1.3	37
15	Additional changes to taxonomy ratified in a special vote by the International Committee on Taxonomy of Viruses (October 2018). Archives of Virology, 2019, 164, 943-946.	0.9	102
16	Changes to virus taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2019). Archives of Virology, 2019, 164, 2417-2429.	0.9	257
17	Still Something to Discover: Novel Insights into Escherichia coli Phage Diversity and Taxonomy. Viruses, 2019, 11, 454.	1.5	77
18	Complete genome sequence analysis of temperate Erwinia bacteriophages 49 and 59. Journal of Basic Microbiology, 2019, 59, 754-764.	1.8	7

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19	Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. <i>Nature Biotechnology</i> , 2019, 37, 632-639.	9.4	569
20	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
21	Strengthening the Interaction of the Virology Community with the International Committee on Taxonomy of Viruses (ICTV) by Linking Virus Names and Their Abbreviations to Virus Species. <i>Systematic Biology</i> , 2019, 68, 828-839.	2.7	11
22	Investigation of putative invasion determinants of <i>Actinobacillus</i> species using comparative genomics. <i>Genomics</i> , 2019, 111, 59-66.	1.3	4
23	Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2018, 163, 1125-1129.	0.9	172
24	Genomic analysis and immune response in a murine mastitis model of vB_EcoM-U1FV13, a potential biocontrol agent for use in dairy cows. <i>Scientific Reports</i> , 2018, 8, 6845.	1.6	26
25	A T4virus prevents biofilm formation by <i>Trueperella pyogenes</i> . <i>Veterinary Microbiology</i> , 2018, 218, 45-51.	0.8	10
26	Bacteriophage Taxonomy: An Evolving Discipline. <i>Methods in Molecular Biology</i> , 2018, 1693, 57-71.	0.4	34
27	Essential Steps in Characterizing Bacteriophages: Biology, Taxonomy, and Genome Analysis. <i>Methods in Molecular Biology</i> , 2018, 1681, 197-215.	0.4	20
28	Practical Advice on the One-Step Growth Curve. <i>Methods in Molecular Biology</i> , 2018, 1681, 41-47.	0.4	106
29	Evaluation of the genomic diversity of viruses infecting bacteria, archaea and eukaryotes using a common bioinformatic platform: steps towards a unified taxonomy. <i>Journal of General Virology</i> , 2018, 99, 1331-1343.	1.3	72
30	Two novel temperate bacteriophages infecting <i>Streptococcus pyogenes</i> : Their genomes, morphology and stability. <i>PLoS ONE</i> , 2018, 13, e0205995.	1.1	15
31	Bacteriophage research – What we have learnt and what still needs to be addressed. <i>Research in Microbiology</i> , 2018, 169, 481-487.	1.0	22
32	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2018). <i>Archives of Virology</i> , 2018, 163, 2601-2631.	0.9	567
33	Sequence, genome organization, annotation and proteomics of the thermophilic, 47.7-kb <i>Geobacillus stearothermophilus</i> bacteriophage TP-84 and its classification in the new Tp84virus genus. <i>PLoS ONE</i> , 2018, 13, e0195449.	1.1	14
34	Comparative Analysis of 37 <i>Acinetobacter</i> Bacteriophages. <i>Viruses</i> , 2018, 10, 5.	1.5	37
35	The Sequence of Two Bacteriophages with Hypermodified Bases Reveals Novel Phage-Host Interactions. <i>Viruses</i> , 2018, 10, 217.	1.5	5
36	Characterization and genomic analyses of two newly isolated <i>Morganella</i> phages define distant members among <i>Tevenvirinae</i> and <i>Autographivirinae</i> subfamilies. <i>Scientific Reports</i> , 2017, 7, 46157.	1.6	23

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37	50 years of the International Committee on Taxonomy of Viruses: progress and prospects. <i>Archives of Virology</i> , 2017, 162, 1441-1446.	0.9	72
38	Changes to taxonomy and the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2017). <i>Archives of Virology</i> , 2017, 162, 2505-2538.	0.9	506
39	A Lytic <i>Providencia rettgeri</i> Virus of Potential Therapeutic Value Is a Deep-Branching Member of the <i>T5virus</i> Genus. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	13
40	Taxonomy of prokaryotic viruses: 2016 update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2017, 162, 1153-1157.	0.9	57
41	<i>Klebsiella</i> phages representing a novel clade of viruses with an unknown DNA modification and biotechnologically interesting enzymes. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 673-684.	1.7	49
42	Thermal-Stability and Reconstitution Ability of <i>Listeria</i> Phages P100 and A511. <i>Frontiers in Microbiology</i> , 2017, 8, 2375.	1.5	34
43	Development of a Phage Cocktail to Control <i>Proteus mirabilis</i> Catheter-associated Urinary Tract Infections. <i>Frontiers in Microbiology</i> , 2016, 7, 1024.	1.5	100
44	Plasmid Characterization and Chromosome Analysis of Two netF+ <i>Clostridium perfringens</i> Isolates Associated with Foal and Canine Necrotizing Enteritis. <i>PLoS ONE</i> , 2016, 11, e0148344.	1.1	32
45	<i>Yersinia enterocolitica</i> -Specific Infection by Bacteriophages TG1 and R1-RT Is Dependent on Temperature-Regulated Expression of the Phage Host Receptor OmpF. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5340-5353.	1.4	44
46	Complete Genome Sequence of vB_EcoM-UFV13, a New Bacteriophage Able To Disrupt <i>Trueperella pyogenes</i> Biofilm. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
47	Evaluation of Molecular Methods for Identification of <i>Salmonella</i> Serovars. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1992-1998.	1.8	30
48	Ratification vote on taxonomic proposals to the International Committee on Taxonomy of Viruses (2016). <i>Archives of Virology</i> , 2016, 161, 2921-2949.	0.9	263
49	Possibility and Challenges of Conversion of Current Virus Species Names to Linnaean Binomials. <i>Systematic Biology</i> , 2016, 66, syw096.	2.7	17
50	Genome Sequence of vB_AbaS_TRS1, a Viable Prophage Isolated from <i>Acinetobacter baumannii</i> Strain A118. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
51	Draft Whole-Genome Sequences of 25 <i>Salmonella enterica</i> Strains Representing 24 Serovars. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
52	Taxonomy of prokaryotic viruses: update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2016, 161, 1095-1099.	0.9	83
53	Comparative analysis of multiple inducible phages from <i>Mannheimia haemolytica</i> . <i>BMC Microbiology</i> , 2015, 15, 175.	1.3	18
54	A proposed new bacteriophage subfamily: <i>Jerseyvirinae</i> . <i>Archives of Virology</i> , 2015, 160, 1021-1033.	0.9	22

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55	A Suggested New Bacteriophage Genus, <i>â€œKp34likevirusâ€</i> , within the Autographivirinae Subfamily of Podoviridae. <i>Viruses</i> , 2015, 7, 1804-1822.	1.5	38
56	Multilocus Sequence Typing and Virulence Gene Profiles Associated with <i>Escherichia coli</i> from Human and Animal Sources. <i>Foodborne Pathogens and Disease</i> , 2015, 12, 302-310.	0.8	74
57	Taxonomic reassessment of N4-like viruses using comparative genomics and proteomics suggests a new subfamily - <i>â€œEnquartavirinaeâ€</i> . <i>Archives of Virology</i> , 2015, 160, 3053-3062.	0.9	36
58	Campylobacter group II phage CP21 is the prototype of a new subgroup revealing a distinct modular genome organization and host specificity. <i>BMC Genomics</i> , 2015, 16, 629.	1.2	16
59	Complete Genome Sequence of <i>Pseudomonas aeruginosa</i> Phage <i>vB_PaeM_CEB_DP1</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	6
60	Integration of genomic and proteomic analyses in the classification of the Siphoviridae family. <i>Virology</i> , 2015, 477, 144-154.	1.1	52
61	Salmonella Phages and Prophages: Genomics, Taxonomy, and Applied Aspects. <i>Methods in Molecular Biology</i> , 2015, 1225, 237-287.	0.4	31
62	Complete genome sequence of bacteriophage <i>vB_YenP_AP5</i> which infects <i>Yersinia enterocolitica</i> of serotype O:3. <i>Virology Journal</i> , 2014, 11, 188.	1.4	20
63	Characterization of Newly Isolated Lytic Bacteriophages Active against <i>Acinetobacter baumannii</i> . <i>PLoS ONE</i> , 2014, 9, e104853.	1.1	80
64	Bacteriophage behavioral ecology. <i>Bacteriophage</i> , 2014, 4, e29866.	1.9	71
65	A suggested classification for two groups of <i>Campylobacter myoviruses</i> . <i>Archives of Virology</i> , 2014, 159, 181-190.	0.9	63
66	UFV-P2 as a member of the <i>Luz24likevirus</i> genus: a new overview on comparative functional genome analyses of the <i>LUZ24-like</i> phages. <i>BMC Genomics</i> , 2014, 15, 7.	1.2	27
67	Three proposed new bacteriophage genera of staphylococcal phages: <i>â€œ3alikevirusâ€</i> , <i>â€œ77likevirusâ€</i> and <i>â€œPhietalikevirusâ€</i> . <i>Archives of Virology</i> , 2014, 159, 389-398.	0.9	22
68	Isolation and characterization of a new <i>Staphylococcus epidermidis</i> broad-spectrum bacteriophage. <i>Journal of General Virology</i> , 2014, 95, 506-515.	1.3	59
69	Multi-laboratory evaluation of the rapid genosertyping array (SGSA) for the identification of <i>Salmonella</i> serovars. <i>Diagnostic Microbiology and Infectious Disease</i> , 2014, 80, 185-190.	0.8	27
70	Characterization of <i>Staphylococcus epidermidis</i> phage <i>vB_SepS_SEP9</i> â€“ a unique member of the Siphoviridae family. <i>Research in Microbiology</i> , 2014, 165, 679-685.	1.0	21
71	Efficiency of bacteriophage therapy against <i>Cronobacter sakazakii</i> in <i>Galleria mellonella</i> (greater wax) Tj ETQq1 1 0.784314 rgBT /Ov	0.9	80
72	Isolation and characterization of a novel bacteriophage against <i>Mycobacterium avium</i> subspecies paratuberculosis. <i>Archives of Virology</i> , 2014, 159, 2659-2674.	0.9	15

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73	Supersize me: Cronobacter sakazakii phage GAP32. <i>Virology</i> , 2014, 460-461, 138-146.	1.1	46
74	Four Escherichia coli O157:H7 Phages: A New Bacteriophage Genus and Taxonomic Classification of T1-Like Phages. <i>PLoS ONE</i> , 2014, 9, e100426.	1.1	55
75	The genome and proteome of Serratia bacteriophage $\hat{\iota}$ which forms unstable lysogens. <i>Virology Journal</i> , 2014, 11, 6.	1.4	15
76	What Does the Talking?: Quorum Sensing Signalling Genes Discovered in a Bacteriophage Genome. <i>PLoS ONE</i> , 2014, 9, e85131.	1.1	123
77	Characterising the biology of novel lytic bacteriophages infecting multidrug resistant <i>Klebsiella pneumoniae</i> . <i>Virology Journal</i> , 2013, 10, 100.	1.4	112
78	The host-range, genomics and proteomics of Escherichia coli O157:H7 bacteriophage rV5. <i>Virology Journal</i> , 2013, 10, 76.	1.4	55
79	Genome sequence and analysis of a broad-host range lytic bacteriophage that infects the <i>Bacillus cereus</i> group. <i>Virology Journal</i> , 2013, 10, 48.	1.4	44
80	Efficacy of bacteriophage LISTEX $\hat{\alpha}$, Φ P100 combined with chemical antimicrobials in reducing <i>Listeria monocytogenes</i> in cooked turkey and roast beef. <i>International Journal of Food Microbiology</i> , 2013, 167, 208-214.	2.1	125
81	New temperate <i>Pseudomonas aeruginosa</i> phage, phi297: Specific features of genome structure. <i>Russian Journal of Genetics</i> , 2013, 49, 806-818.	0.2	8
82	Romulus and Remus, Two Phage Isolates Representing a Distinct Clade within the Twortlikevirus Genus, Display Suitable Properties for Phage Therapy Applications. <i>Journal of Virology</i> , 2013, 87, 3237-3247.	1.5	79
83	The Genome of Cronobacter sakazakii Bacteriophage vB_CsaP_GAP227 Suggests a New Genus within the Autographivirinae. <i>Genome Announcements</i> , 2013, 1, .	0.8	10
84	Genome Sequence of Cronobacter sakazakii Myovirus vB_CsaM_GAP31. <i>Journal of Virology</i> , 2012, 86, 13830-13831.	1.5	9
85	Complete Genome Sequence of <i>Actinobacillus suis</i> H91-0380, a Virulent Serotype O2 Strain. <i>Journal of Bacteriology</i> , 2012, 194, 6686-6687.	1.0	13
86	Genome Sequence of the Broad-Host-Range <i>Pseudomonas</i> Phage $\hat{\iota}_1$ -S1. <i>Journal of Virology</i> , 2012, 86, 10239-10239.	1.5	11
87	Complete Genome Sequence of the Giant Virus OBP and Comparative Genome Analysis of the Diverse $\hat{\iota}$ -KZ-Related Phages. <i>Journal of Virology</i> , 2012, 86, 1844-1852.	1.5	75
88	Complete Genome Sequence of the Giant <i>Pseudomonas</i> Phage Lu11. <i>Journal of Virology</i> , 2012, 86, 6369-6370.	1.5	25
89	Bacteriophage cocktail significantly reduces <i>Escherichia coli</i> O157. <i>Bacteriophage</i> , 2012, 2, 178-185.	1.9	118
90	<i>Escherichia coli</i> O157:H7 Typing Phage V7 Is a T4-Like Virus. <i>Journal of Virology</i> , 2012, 86, 10246-10246.	1.5	10

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91	Complete Genome Sequence of <i>Vibrio parahaemolyticus</i> Bacteriophage vB_VpaM_MAR. <i>Journal of Virology</i> , 2012, 86, 13138-13139.	1.5	17
92	Complete Genome Sequence of <i>Cronobacter sakazakii</i> Bacteriophage vB_CsaM_GAP161. <i>Journal of Virology</i> , 2012, 86, 13806-13807.	1.5	12
93	Genome Sequence of Temperate <i>Vibrio parahaemolyticus</i> Bacteriophage vB_VpaS_MAR10. <i>Journal of Virology</i> , 2012, 86, 13851-13852.	1.5	15
94	A suggested new bacteriophage genus: <i>Viunalikevirus</i> . <i>Archives of Virology</i> , 2012, 157, 2035-2046.	0.9	77
95	Properties of the new D3-like <i>Pseudomonas aeruginosa</i> bacteriophage phiPMG1: Genome structure and prospects for the use in phage therapy. <i>Russian Journal of Genetics</i> , 2012, 48, 902-911.	0.2	7
96	Genome and proteome analysis of 7-7-1, a flagellotropic phage infecting <i>Agrobacterium</i> sp H13-3. <i>Virology Journal</i> , 2012, 9, 102.	1.4	23
97	Endemic bacteriophages: a cautionary tale for evaluation of bacteriophage therapy and other interventions for infection control in animals. <i>Virology Journal</i> , 2012, 9, 207.	1.4	24
98	Genomic, Proteomic and Physiological Characterization of a T5-like Bacteriophage for Control of Shiga Toxin-Producing <i>Escherichia coli</i> O157:H7. <i>PLoS ONE</i> , 2012, 7, e34585.	1.1	64
99	Bacteriophages with the Ability to Degrade Uropathogenic <i>Escherichia Coli</i> Biofilms. <i>Viruses</i> , 2012, 4, 471-487.	1.5	94
100	Isolation and characterization of a novel indigenous intestinal N4-related coliphage vB_EcoP_G7C. <i>Virology</i> , 2012, 426, 93-99.	1.1	49
101	The genome and proteome of a <i>Campylobacter coli</i> bacteriophage vB_CcoM-IBB_35 reveal unusual features. <i>Virology Journal</i> , 2012, 9, 35.	1.4	19
102	Genome Sequencing and Analysis of a Type A <i>Clostridium perfringens</i> Isolate from a Case of Bovine Clostridial Abomasitis. <i>PLoS ONE</i> , 2012, 7, e32271.	1.1	27
103	T4-Related Bacteriophage LIMeStone Isolates for the Control of Soft Rot on Potato Caused by <i>Dickeya solani</i> . <i>PLoS ONE</i> , 2012, 7, e33227.	1.1	169
104	Selection and Characterization of a Candidate Therapeutic Bacteriophage That Lyses the <i>Escherichia coli</i> O104:H4 Strain from the 2011 Outbreak in Germany. <i>PLoS ONE</i> , 2012, 7, e52709.	1.1	48
105	Genomic and Proteomic Characterization of the Broad-Host-Range <i>Salmonella</i> Phage PVP-SE1: Creation of a New Phage Genus. <i>Journal of Virology</i> , 2011, 85, 11265-11273.	1.5	80
106	Identification of <i>Salmonella enterica</i> species- and subgroup-specific genomic regions using Panseq 2.0. <i>Infection, Genetics and Evolution</i> , 2011, 11, 2151-2161.	1.0	10
107	Complete genome sequence of the lytic <i>Pseudomonas fluorescens</i> phage Φ -IBB-PF7A. <i>Virology Journal</i> , 2011, 8, 142.	1.4	11
108	A <i>Shigella boydii</i> bacteriophage which resembles <i>Salmonella</i> phage Φ VII. <i>Virology Journal</i> , 2011, 8, 242.	1.4	62

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109	Bacteriophage phi297, a new species of <i>Pseudomonas aeruginosa</i> temperate phages with a mosaic genome: Potential use in phage therapy. <i>Russian Journal of Genetics</i> , 2011, 47, 794-798.	0.2	8
110	<i>Clostridium perfringens</i> bacteriophages $\hat{\phi}$ CP390 and $\hat{\phi}$ CP26F: genomic organization and proteomic analysis of the virions. <i>Archives of Virology</i> , 2011, 156, 25-35.	0.9	32
111	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
112	Isolation and characterisation of KP34â€”a novel $\hat{\phi}$ KMV-like bacteriophage for <i>Klebsiella pneumoniae</i> . <i>Applied Microbiology and Biotechnology</i> , 2011, 90, 1333-1345.	1.7	62
113	Characterization of a ϕ Vil-like Phage Specific to <i>Escherichia coli</i> O157:H7. <i>Virology Journal</i> , 2011, 8, 430.	1.4	60
114	Evidence of a Dominant Lineage of <i>Vibrio cholerae</i> -Specific Lytic Bacteriophages Shed by Cholera Patients over a 10-Year Period in Dhaka, Bangladesh. <i>MBio</i> , 2011, 2, e00334-10.	1.8	115
115	Gene Cluster Conferring Streptomycin, Sulfonamide, and Tetracycline Resistance in <i>Escherichia coli</i> O157:H7 Phage Types 23, 45, and 67. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1900-1903.	1.4	14
116	Genome and Proteome of <i>Campylobacter jejuni</i> Bacteriophage NCTC 12673. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8265-8271.	1.4	61
117	Rapid Genoserotyping Tool for Classification of <i>Salmonella</i> Serovars. <i>Journal of Clinical Microbiology</i> , 2011, 49, 2954-2965.	1.8	46
118	T1-like Viruses. , 2011, , 1821-1830.		2
119	Pan-genome sequence analysis using Panseq: an online tool for the rapid analysis of core and accessory genomic regions. <i>BMC Bioinformatics</i> , 2010, 11, 461.	1.2	249
120	Genome sequence of adherent-invasive <i>Escherichia coli</i> and comparative genomic analysis with other <i>E. coli</i> pathotypes. <i>BMC Genomics</i> , 2010, 11, 667.	1.2	193
121	Molecular and physiological analysis of three <i>Pseudomonas aeruginosa</i> phages belonging to the ϕ N4-like viruses. <i>Virology</i> , 2010, 405, 26-30.	1.1	86
122	The O28 Antigen Gene Clusters of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Dakar and Serovar Pomona Are Different. <i>International Journal of Microbiology</i> , 2010, 2010, 1-8.	0.9	2
123	Lineage and Host Source Are Both Correlated with Levels of Shiga Toxin 2 Production by <i>Escherichia coli</i> O157:H7 Strains. <i>Applied and Environmental Microbiology</i> , 2010, 76, 474-482.	1.4	51
124	Complete Genomic Sequence of Bacteriophage Felix O1. <i>Viruses</i> , 2010, 2, 710-730.	1.5	72
125	<i>Escherichia coli</i> O123 O antigen genes and polysaccharide structure are conserved in some <i>Salmonella enterica</i> serogroups. <i>Journal of Medical Microbiology</i> , 2009, 58, 884-894.	0.7	8
126	Complete Genome of the Broad-Host-Range <i>Erwinia amylovora</i> Phage $\hat{\phi}$ 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

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127	Classification of Myoviridae bacteriophages using protein sequence similarity. <i>BMC Microbiology</i> , 2009, 9, 224.	1.3	245
128	Characterization of the cell surface glycolipid from <i>Spirochaeta aurantia</i> . <i>Glycoconjugate Journal</i> , 2009, 26, 1097-1108.	1.4	2
129	Position paper: The creation of a rational scheme for the nomenclature of viruses of <i>Bacteria</i> and <i>Archaea</i> . <i>Environmental Microbiology</i> , 2009, 11, 2775-2777.	1.8	184
130	Comparative analysis of the widespread and conserved PB14-like viruses infecting <i>Pseudomonas aeruginosa</i> . <i>Environmental Microbiology</i> , 2009, 11, 2874-2883.	1.8	85
131	The genome and proteome of a virulent <i>Escherichia coli</i> O157:H7 bacteriophage closely resembling <i>Salmonella</i> phage Felix O1. <i>Virology Journal</i> , 2009, 6, 41.	1.4	34
132	Bacteriophage Enrichment from Water and Soil. <i>Methods in Molecular Biology</i> , 2009, 501, 15-21.	0.4	166
133	Enumeration of Bacteriophages by Double Agar Overlay Plaque Assay. <i>Methods in Molecular Biology</i> , 2009, 501, 69-76.	0.4	645
134	Measurement of the Rate of Attachment of Bacteriophage to Cells. <i>Methods in Molecular Biology</i> , 2009, 501, 151-155.	0.4	102
135	Measurement of the Bacteriophage Inactivation Kinetics with Purified Receptors. <i>Methods in Molecular Biology</i> , 2009, 501, 157-160.	0.4	9
136	Approaches to the Compositional Analysis of DNA. <i>Methods in Molecular Biology</i> , 2009, 502, 11-17.	0.4	1
137	In Sffamily Identification of Genes in Bacteriophage DNA. <i>Methods in Molecular Biology</i> , 2009, 502, 57-89.	0.4	25
138	Internet Resources of Interest to Bacteriophage Workers. <i>Methods in Molecular Biology</i> , 2009, 502, 365-373.	0.4	0
139	Methods in molecular biology. Introduction. <i>Methods in Molecular Biology</i> , 2009, 502, xiii-xxii.	0.4	1
140	Genomic analysis of bacteriophage μ 34 of <i>Salmonella entericaserovar Anatum</i> (15+). <i>BMC Microbiology</i> , 2008, 8, 227.	1.3	34
141	The genome and proteome of the <i>Kluyvera</i> bacteriophage Kvp1 – another member of the T7-like Autographivirinae. <i>Virology Journal</i> , 2008, 5, 122.	1.4	12
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