

Graham F Hatfull

List of Publications by Year in descending order

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264
papers

18,669
citations

9234

74
h-index

16605

123
g-index

270
all docs

270
docs citations

270
times ranked

10969
citing authors

#	ARTICLE	IF	CITATIONS
1	Phage Therapy of <i>Mycobacterium</i> Infections: Compassionate Use of Phages in 20 Patients With Drug-Resistant Mycobacterial Disease. <i>Clinical Infectious Diseases</i> , 2023, 76, 103-112.	2.9	109
2	Phage Therapy for Antibiotic-Resistant Bacterial Infections. <i>Annual Review of Medicine</i> , 2022, 73, 197-211.	5.0	182
3	Mycobacteriophages to Treat Tuberculosis: Dream or Delusion?. <i>Respiration</i> , 2022, 101, 1-15.	1.2	16
4	Instructional Models for Course-Based Research Experience (CRE) Teaching. <i>CBE Life Sciences Education</i> , 2022, 21, ar8.	1.1	7
5	DEPhT: a novel approach for efficient prophage discovery and precise extraction. <i>Nucleic Acids Research</i> , 2022, 50, e75-e75.	6.5	13
6	Nebulized Bacteriophage in a Patient With Refractory <i>Mycobacterium abscessus</i> Lung Disease. <i>Open Forum Infectious Diseases</i> , 2022, 9, .	0.4	10
7	Complete Genome Sequences of Lambdoid Phages 21, 434, and 434B and Several Lambda Hybrids. <i>Microbiology Resource Announcements</i> , 2022, 11, e0012022.	0.3	3
8	Host and pathogen response to bacteriophage engineered against <i>Mycobacterium abscessus</i> lung infection. <i>Cell</i> , 2022, 185, 1860-1874.e12.	13.5	93
9	Bacteriophage treatment of disseminated cutaneous <i>Mycobacterium chelonae</i> infection. <i>Nature Communications</i> , 2022, 13, 2313.	5.8	56
10	Mycobacteriophages: From Petri dish to patient. <i>PLoS Pathogens</i> , 2022, 18, e1010602.	2.1	35
11	pdm_utils: a SEA-PHAGES MySQL phage database management toolkit. <i>Bioinformatics</i> , 2021, 37, 2464-2466.	1.8	11
12	Bacteriophage Discovery and Genomics. , 2021, , 219-230.		0
13	Genome Sequence of <i>Mycobacterium abscessus</i> Phage phiT46-1. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	6
14	CRISPY-BRED and CRISPY-BRIP: efficient bacteriophage engineering. <i>Scientific Reports</i> , 2021, 11, 6796.	1.6	34
15	Genome Sequence of <i>Mycobacterium abscessus</i> Phage phiT45-1. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
16	The Prophage and Plasmid Mobilome as a Likely Driver of <i>Mycobacterium abscessus</i> Diversity. <i>MBio</i> , 2021, 12, .	1.8	32
17	<i>Mycobacterium abscessus</i> Strain Morphotype Determines Phage Susceptibility, the Repertoire of Therapeutically Useful Phages, and Phage Resistance. <i>MBio</i> , 2021, 12, .	1.8	43
18	A Mycobacterial Systems Resource for the Research Community. <i>MBio</i> , 2021, 12, .	1.8	20

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19	Noncanonical DNA polymerization by aminoadenine-based siphoviruses. <i>Science</i> , 2021, 372, 520-524.	6.0	46
20	Toward a Phage Cocktail for Tuberculosis: Susceptibility and Tuberculocidal Action of Mycobacteriophages against Diverse Mycobacterium tuberculosis Strains. <i>MBio</i> , 2021, 12, .	1.8	56
21	Potent antibody-mediated neutralization limits bacteriophage treatment of a pulmonary Mycobacterium abscessus infection. <i>Nature Medicine</i> , 2021, 27, 1357-1361.	15.2	94
22	Wildy Prize Lecture, 2020â€“2021: Who wouldnâ€™t want to discover a new virus?. <i>Microbiology (United Kingdom)</i> , 2021, 157, 1-10.	0.7	5
23	Mycobacteriophageâ€“antibiotic therapy promotes enhanced clearance of drug-resistant Mycobacterium abscessus. <i>DMM Disease Models and Mechanisms</i> , 2021, 14, .	1.2	22
24	Genome analysis of Salmonella enterica serovar Typhimurium bacteriophage L, indicator for StySA (StyLT2III) restriction-modification system action. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	7
25	A Mycobacteriophage-Based Vaccine Platform: SARS-CoV-2 Antigen Expression and Display. <i>Microorganisms</i> , 2021, 9, 2414.	1.6	6
26	Application of Bacteriophages for Mycobacterial Infections, from Diagnosis to Treatment. <i>Microorganisms</i> , 2021, 9, 2366.	1.6	15
27	Set Phages to Kill: An Interview with Graham Hatfull, PhD. <i>Phage</i> , 2020, 1, 4-9.	0.8	3
28	Identification of mycobacteriophage toxic genes reveals new features of mycobacterial physiology and morphology. <i>Scientific Reports</i> , 2020, 10, 14670.	1.6	15
29	Protein-Mediated and RNA-Based Origins of Replication of Extrachromosomal Mycobacterial Prophages. <i>MBio</i> , 2020, 11, .	1.8	16
30	Genomic diversity of bacteriophages infecting Mycobacterium spp. <i>PLoS ONE</i> , 2020, 15, e0234636.	1.1	50
31	Structures of Three Actinobacteriophage Capsids: Roles of Symmetry and Accessory Proteins. <i>Viruses</i> , 2020, 12, 294.	1.5	14
32	Genome Sequences of 20 Bacteriophages Isolated on Gordonia terrae. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	3
33	Actinobacteriophages: Genomics, Dynamics, and Applications. <i>Annual Review of Virology</i> , 2020, 7, 37-61.	3.0	85
34	Prophylaxis of Mycobacterium tuberculosis H37Rv Infection in a Preclinical Mouse Model via Inhalation of Nebulized Bacteriophage D29. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	48
35	Mycobacteriophage Zoelj: A broad host-range close relative of mycobacteriophage TM4. <i>Tuberculosis</i> , 2019, 115, 14-23.	0.8	35
36	Complete Genome Sequence of Mycobacterium foliorum NRRL B-24224, a Host for Bacteriophage Discovery. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	12

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37	Evolution of Superinfection Immunity in Cluster A Mycobacteriophages. MBio, 2019, 10, .	1.8	52
38	Engineered bacteriophages for treatment of a patient with a disseminated drug-resistant Mycobacterium abscessus. Nature Medicine, 2019, 25, 730-733.	15.2	907
39	Yet More Evidence of Collusion: a New Viral Defense System Encoded by <i>Gordonia</i> Phage CarolAnn. MBio, 2019, 10, .	1.8	38
40	Staphylococci phages display vast genomic diversity and evolutionary relationships. BMC Genomics, 2019, 20, 357.	1.2	49
41	More Evidence of Collusion: a New Prophage-Mediated Viral Defense System Encoded by Mycobacteriophage Sbash. MBio, 2019, 10, .	1.8	60
42	Genome Sequences of Three Microbacterium Phages Isolated from Flowers. Microbiology Resource Announcements, 2019, 8, .	0.3	0
43	7-Deazaguanine modifications protect phage DNA from host restriction systems. Nature Communications, 2019, 10, 5442.	5.8	63
44	Fluoromycobacteriophages for Drug Susceptibility Testing (DST) of Mycobacteria. Methods in Molecular Biology, 2019, 1898, 27-36.	0.4	6
45	Genetic Manipulation of Lytic Bacteriophages with BRED: Bacteriophage Recombineering of Electroporated DNA. Methods in Molecular Biology, 2019, 1898, 69-80.	0.4	13
46	Roger Hendrix: Gentle Provocateur. Journal of Bacteriology, 2018, 200, .	1.0	2
47	Mycobacteriophage Fruitloop gp52 inactivates Wag31 (DivIVA) to prevent heterotypic superinfection. Molecular Microbiology, 2018, 108, 443-460.	1.2	38
48	Genome Sequences of Four Cluster P Mycobacteriophages. Genome Announcements, 2018, 6, .	0.8	1
49	Complete genomic sequences of Propionibacterium freudenreichii phages from Swiss cheese reveal greater diversity than Cutibacterium (formerly Propionibacterium) acnes phages. BMC Microbiology, 2018, 18, 19.	1.3	13
50	Unlocking the Potential of 46 New Bacteriophages for Biocontrol of Dickeya Solani. Viruses, 2018, 10, 621.	1.5	42
51	Mycobacteriophages. Microbiology Spectrum, 2018, 6, .	1.2	72
52	Eight Genome Sequences of Cluster BE1 Phages That Infect <i>Streptomyces</i> Species. Genome Announcements, 2018, 6, .	0.8	2
53	Fluoromycobacteriophages Can Detect Viable Mycobacterium tuberculosis and Determine Phenotypic Rifampicin Resistance in 3-5 Days From Sputum Collection. Frontiers in Microbiology, 2018, 9, 1471.	1.5	18
54	Characterization and induction of prophages in human gut-associated Bifidobacterium hosts. Scientific Reports, 2018, 8, 12772.	1.6	26

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55	Complete Genome Sequences of 44 Arthrobacter Phages. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
56	Prophage-mediated defence against viral attack and viral counter-defence. <i>Nature Microbiology</i> , 2017, 2, 16251.	5.9	196
57	Complete Genome Sequences of 38 <i>Gordonia</i> sp. Bacteriophages. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
58	Genome Sequences of Mycobacteriophages Kerberos, Pomar16, and StarStuff. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
59	Genome Sequence of Mycobacterium Phage CrystalP. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
60	Bacteriophages of <i>Gordonia</i> spp. Display a Spectrum of Diversity and Genetic Relationships. <i>MBio</i> , 2017, 8, .	1.8	135
61	Virus-host protein-protein interactions of mycobacteriophage Giles. <i>Scientific Reports</i> , 2017, 7, 16514.	1.6	15
62	An inclusive Research Education Community (iREC): Impact of the SEA-PHAGES program on research outcomes and student learning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13531-13536.	3.3	155
63	Genome Sequences of 12 Cluster AN Arthrobacter Phages. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
64	Genome Sequences of Four Subcluster L2 Mycobacterium Phages, Finemlucis, Miley16, Wilder, and Zakai. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
65	Anti-Tuberculosis Bacteriophage D29 Delivery with a Vibrating Mesh Nebulizer, Jet Nebulizer, and Soft Mist Inhaler. <i>Pharmaceutical Research</i> , 2017, 34, 2084-2096.	1.7	71
66	Bacteriophage evolution differs by host, lifestyle and genome. <i>Nature Microbiology</i> , 2017, 2, 17112.	5.9	192
67	PhagesDB: the actinobacteriophage database. <i>Bioinformatics</i> , 2017, 33, 784-786.	1.8	310
68	Complete Genome Sequences of Mycobacteriophages Clautastrophe, Kingsolomon, Krypton555, and Nicholas. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
69	Genome Sequences of Mycobacteriophages Amgine, Amohnition, Bella96, Cain, DarthP, Hammy, Krueger, LastHope, Peanam, PhelpsODU, Phrank, SirPhilip, Slimphazie, and Unicorn. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
70	Genome Sequences of Chancellor, Mitti, and Wintermute, Three Subcluster K4 Phages Isolated Using <i>Mycobacterium smegmatis</i> mc 2 155. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
71	Genome Sequences of Three Cluster AU Arthrobacter Phages, Caterpillar, Nightmare, and Teacup. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
72	Genome Sequences of Mycobacteriophages Findley, Hurricane, and TBond007. <i>Genome Announcements</i> , 2017, 5, .	0.8	0

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73	Complete Genome Sequences of <i>Arthrobacter</i> Phages Beans, Franzy, Jordan, Piccoletto, Shade, and Timinator. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
74	Complete Genome Sequences of Cluster A Mycobacteriophages BobSwaget, Fred313, KADY, Lokk, MyraDee, Stagni, and StepMih. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
75	Genome Sequences of 19 <i>Rhodococcus erythropolis</i> Cluster CA Phages. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
76	Tales of diversity: Genomic and morphological characteristics of forty-six <i>Arthrobacter</i> phages. <i>PLoS ONE</i> , 2017, 12, e0180517.	1.1	38
77	Expression and evolutionary patterns of mycobacteriophage D29 and its temperate close relatives. <i>BMC Microbiology</i> , 2017, 17, 225.	1.3	24
78	Genome Sequences of Subcluster K5 Mycobacteriophages AlleyCat, Edugator, and Guillsminger. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
79	<i>Bacteriophage Discovery and Genomics.</i> , 2017, , 1-13.		0
80	Genome Sequences of <i>Gordonia</i> Phages Bowser and Schwabeltier. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
81	Genome Sequences of Newly Isolated Mycobacteriophages Forming Cluster S. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
82	Genome Sequences of <i>Gordonia terrae</i> Phages Benczkowski14 and Katyusha. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
83	Genome Sequences of <i>Gordonia</i> Phages BaxterFox, Kita, Nymphadora, and Yeezy. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
84	Genome Sequence of <i>Gordonia</i> Phage BetterKatz. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
85	Genome Sequence of <i>Gordonia</i> Phage Emalyn. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
86	Genome Sequences of <i>Gordonia</i> Phages Hotorobo, Woes, and Monty. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
87	Complete Genome Sequences of 61 Mycobacteriophages. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
88	Function, expression, specificity, diversity and incompatibility of actinobacteriophage <i>parABS</i> systems. <i>Molecular Microbiology</i> , 2016, 101, 625-644.	1.2	29
89	Genome Sequences of <i>Gordonia terrae</i> Phages Attis and SoilAssassin. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
90	Genome Sequence of <i>Gordonia</i> Phage Yvonnetastic. <i>Genome Announcements</i> , 2016, 4, .	0.8	1

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91	A Measure of College Student Persistence in the Sciences (PITS). CBE Life Sciences Education, 2016, 15, ar54.	1.1	106
92	Genome Sequences of <i>Gordonia terrae</i> Bacteriophages Phinally and Vivi2. Genome Announcements, 2016, 4, .	0.8	1
93	Characterization of mycobacteria and mycobacteriophages isolated from compost at the São Paulo Zoo Park Foundation in Brazil and creation of the new mycobacteriophage Cluster U. BMC Microbiology, 2016, 16, 111.	1.3	12
94	Genome Sequences of <i>Gordonia</i> Bacteriophages Obliviate, UmaThurman, and Guacamole. Genome Announcements, 2016, 4, .	0.8	2
95	Fluorescent Reporter DS6A Mycobacteriophages Reveal Unique Variations in Infectibility and Phage Production in Mycobacteria. Journal of Bacteriology, 2016, 198, 3220-3232.	1.0	31
96	Crossover-site sequence and DNA torsional stress control strand interchanges by the Bxb1 site-specific serine recombinase. Nucleic Acids Research, 2016, 44, 8921-8932.	6.5	14
97	Characterization of prophages containing â€œevolvedâ€•Dit/Tal modules in the genome of Lactobacillus casei BL23. Applied Microbiology and Biotechnology, 2016, 100, 9201-9215.	1.7	22
98	Genome Sequence of <i>Gordonia</i> Bacteriophage Lucky10. Genome Announcements, 2016, 4, .	0.8	1
99	A Diversified Portfolio. Annual Review of Virology, 2016, 3, vi-viii.	3.0	4
100	Complete Genome Sequence of Gordonia terrae 3612. Genome Announcements, 2016, 4, .	0.8	6
101	Brujita Integrase: A Simple, Arm-Less, Directionless, and Promiscuous Tyrosine Integrase System. Journal of Molecular Biology, 2016, 428, 2289-2306.	2.0	7
102	Complete Genome Sequence of Arthrobacter sp. ATCC 21022, a Host for Bacteriophage Discovery. Genome Announcements, 2016, 4, .	0.8	11
103	Rapid Whole-Cell Assay of Antitubercular Drugs Using Second-Generation Fluoromycobacteriophages. Antimicrobial Agents and Chemotherapy, 2016, 60, 3253-3256.	1.4	13
104	In the Trenches of Microbial Warfare: Identification of Genes and Pathways Contributing to Bacteriophage Infection by Quantitative Selection Analysis. Journal of Molecular Biology, 2016, 428, 413-415.	2.0	0
105	Measuring Networking as an Outcome Variable in Undergraduate Research Experiences. CBE Life Sciences Education, 2015, 14, ar38.	1.1	30
106	Comparative Genomics of Cluster O Mycobacteriophages. PLoS ONE, 2015, 10, e0118725.	1.1	22
107	An Unusual Phage Repressor Encoded by Mycobacteriophage BPs. PLoS ONE, 2015, 10, e0137187.	1.1	12
108	The Protein Interactome of Mycobacteriophage Giles Predicts Functions for Unknown Proteins. Journal of Bacteriology, 2015, 197, 2508-2516.	1.0	16

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109	Genome Sequences of Mycobacteriophages AlanGrant, Bae, Corofin, OrangeOswald, and Vincenzo, New Members of Cluster B. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
110	Genome Sequences of Cluster G Mycobacteriophages Cambiare, FlagStaff, and MOOREtheMARYer. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
111	Genome Sequence of Mycobacteriophage Mindy. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
112	Genome Sequence of a Newly Isolated Mycobacteriophage, ShedlockHolmes. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
113	Genome Sequence of Mycobacteriophage Phayonce. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
114	Genome Sequences of Mycobacteriophages Luchador and Nerujay. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
115	Adding pieces to the puzzle: New insights into bacteriophage diversity from integrated research-education programs. <i>Bacteriophage</i> , 2015, 5, e1084073.	1.9	12
116	Dark Matter of the Biosphere: the Amazing World of Bacteriophage Diversity. <i>Journal of Virology</i> , 2015, 89, 8107-8110.	1.5	198
117	Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. <i>ELife</i> , 2015, 4, e06416.	2.8	280
118	Mycobacteriophage-repressor-mediated immunity as a selectable genetic marker: Adephagia and BPs repressor selection. <i>Microbiology (United Kingdom)</i> , 2015, 161, 1539-1551.	0.7	21
119	Genome Sequence of Salmonella enterica Phage Det7. <i>Genome Announcements</i> , 2015, 3, .	0.8	16
120	Genome Sequence of Salmonella Phage ĩ. <i>Genome Announcements</i> , 2015, 3, .	0.8	25
121	Innovations in Undergraduate Science Education: Going Viral. <i>Journal of Virology</i> , 2015, 89, 8111-8113.	1.5	36
122	Genetic Dissection of Mycobacterial Biofilms. <i>Methods in Molecular Biology</i> , 2015, 1285, 215-226.	0.4	22
123	Mycobacteriophages: Windows into Tuberculosis. <i>PLoS Pathogens</i> , 2014, 10, e1003953.	2.1	79
124	A Broadly Implementable Research Course in Phage Discovery and Genomics for First-Year Undergraduate Students. <i>MBio</i> , 2014, 5, e01051-13.	1.8	424
125	Genomics and Proteomics of Mycobacteriophage Patience, an Accidental Tourist in the Mycobacterium Neighborhood. <i>MBio</i> , 2014, 5, e02145.	1.8	39
126	Genome Sequence of Salmonella Phage 9NA. <i>Genome Announcements</i> , 2014, 2, .	0.8	16

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127	PHIRE and TWiV: Experiences in Bringing Virology to New Audiences. <i>Annual Review of Virology</i> , 2014, 1, 37-53.	3.0	8
128	The Structure of Xis Reveals the Basis for Filament Formation and Insight into DNA Bending within a Mycobacteriophage Intasome. <i>Journal of Molecular Biology</i> , 2014, 426, 412-422.	2.0	17
129	Cross-talk between Diverse Serine Integrases. <i>Journal of Molecular Biology</i> , 2014, 426, 318-331.	2.0	14
130	Enhanced Specialized Transduction Using Recombineering in <i>Mycobacterium tuberculosis</i> . <i>MBio</i> , 2014, 5, e01179-14.	1.8	25
131	Cluster M Mycobacteriophages Bongo, PegLeg, and Rey with Unusually Large Repertoires of tRNA Isoypes. <i>Journal of Virology</i> , 2014, 88, 2461-2480.	1.5	52
132	Exposing the Secrets of Two Well-Known <i>Lactobacillus casei</i> Phages, J-1 and PL-1, by Genomic and Structural Analysis. <i>Applied and Environmental Microbiology</i> , 2014, 80, 7107-7121.	1.4	22
133	Mutational Analysis of the Mycobacteriophage BPs Promoter PR Reveals Context-Dependent Sequences for Mycobacterial Gene Expression. <i>Journal of Bacteriology</i> , 2014, 196, 3589-3597.	1.0	12
134	Molecular Genetics of Mycobacteriophages. <i>Microbiology Spectrum</i> , 2014, 2, .	1.2	74
135	Molecular Genetics of Mycobacteriophages. <i>Microbiology Spectrum</i> , 2014, 2, 1-36.	1.2	44
136	Evolutionary Relationships among Actinophages and a Putative Adaptation for Growth in <i>Streptomyces</i> spp. <i>Journal of Bacteriology</i> , 2013, 195, 4924-4935.	1.0	37
137	Integration-Dependent Bacteriophage Immunity Provides Insights into the Evolution of Genetic Switches. <i>Molecular Cell</i> , 2013, 49, 237-248.	4.5	75
138	Application of BRED technology to construct recombinant D29 reporter phage expressing EGFP. <i>FEMS Microbiology Letters</i> , 2013, 344, 166-172.	0.7	21
139	Complete Genome Sequences of 63 Mycobacteriophages. <i>Genome Announcements</i> , 2013, 1, .	0.8	25
140	Attachment Site Selection and Identity in Bxb1 Serine Integrase-Mediated Site-Specific Recombination. <i>PLoS Genetics</i> , 2013, 9, e1003490.	1.5	37
141	Keto-Mycolic Acid-Dependent Pellicle Formation Confers Tolerance to Drug-Sensitive <i>Mycobacterium tuberculosis</i> . <i>MBio</i> , 2013, 4, e00222-13.	1.8	103
142	Generation of Affinity-Tagged Fluoromycobacteriophages by Mixed Assembly of Phage Capsids. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5608-5615.	1.4	18
143	Functional requirements for bacteriophage growth: gene essentiality and expression in mycobacteriophage <i>φ</i> CP1. <i>Molecular Microbiology</i> , 2013, 88, 577-589.	1.2	53
144	Evolution of genetic switch complexity. <i>Bacteriophage</i> , 2013, 3, e24186.	1.9	12

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145	Snapshot of haloarchaeal tailed virus genomes. <i>RNA Biology</i> , 2013, 10, 803-816.	1.5	51
146	Cluster J Mycobacteriophages: Intron Splicing in Capsid and Tail Genes. <i>PLoS ONE</i> , 2013, 8, e69273.	1.1	28
147	Ĥ ² GFP10, a High-Intensity Fluorophage, Enables Detection and Rapid Drug Susceptibility Testing of <i>Mycobacterium tuberculosis</i> Directly from Sputum Samples. <i>Journal of Clinical Microbiology</i> , 2012, 50, 1362-1369.	1.8	69
148	Remote control of DNA-acting enzymes by varying the Brownian dynamics of a distant DNA end. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16546-16551.	3.3	25
149	Complete Genome Sequences of 138 Mycobacteriophages. <i>Journal of Virology</i> , 2012, 86, 2382-2384.	1.5	69
150	Mycobacteriophage Marvin: a New Singleton Phage with an Unusual Genome Organization. <i>Journal of Virology</i> , 2012, 86, 4762-4775.	1.5	25
151	On the nature of mycobacteriophage diversity and host preference. <i>Virology</i> , 2012, 434, 187-201.	1.1	159
152	The Bxb1 gp47 recombination directionality factor is required not only for prophage excision, but also for phage DNA replication. <i>Gene</i> , 2012, 495, 42-48.	1.0	23
153	The Secret Lives of Mycobacteriophages. <i>Advances in Virus Research</i> , 2012, 82, 179-288.	0.9	103
154	Mycobacteriophage Endolysins: Diverse and Modular Enzymes with Multiple Catalytic Activities. <i>PLoS ONE</i> , 2012, 7, e34052.	1.1	112
155	Recombineering. <i>Bacteriophage</i> , 2012, 2, 5-14.	1.9	88
156	<i>Propionibacterium acnes</i> Bacteriophages Display Limited Genetic Diversity and Broad Killing Activity against Bacterial Skin Isolates. <i>MBio</i> , 2012, 3, .	1.8	89
157	Single-molecule analysis reveals the molecular bearing mechanism of DNA strand exchange by a serine recombinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7419-7424.	3.3	63
158	Evaluation of Fluoromycobacteriophages for Detecting Drug Resistance in <i>Mycobacterium tuberculosis</i> . <i>Journal of Clinical Microbiology</i> , 2011, 49, 1838-1842.	1.8	37
159	Bacteriophages and their genomes. <i>Current Opinion in Virology</i> , 2011, 1, 298-303.	2.6	397
160	Phamerator: a bioinformatic tool for comparative bacteriophage genomics. <i>BMC Bioinformatics</i> , 2011, 12, 395.	1.2	396
161	Successive and Targeted DNA Integrations in the <i>Drosophila</i> Genome by Bxb1 and ĤC31 Integrases. <i>Genetics</i> , 2011, 189, 391-395.	1.2	28
162	Reporter Phage and Breath Tests: Emerging Phenotypic Assays for Diagnosing Active Tuberculosis, Antibiotic Resistance, and Treatment Efficacy. <i>Journal of Infectious Diseases</i> , 2011, 204, S1142-S1150.	1.9	28

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