Graham F Hatfull

List of Publications by Year
in descending order

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	Engineered bacteriophages for treatment of a patient with a disseminated drug-resistant Mycobacterium abscessus. Nature Medicine, 2019, 25, 730-733.	15.2	907
2	Origins of Highly Mosaic Mycobacteriophage Genomes. Cell, 2003, 113, 171-182.	13.5	609
3	Specialized transduction: an efficient method for generating marked and unmarked targeted gene disruptions in Mycobacterium tuberculosis, M. bovis BCG and M. smegmatis. Microbiology (United) Tj ETQq1 1 0.784314 rg BT /Overlock	[illegible]	[illegible]
4	Recombineering in Mycobacterium tuberculosis. Nature Methods, 2007, 4, 147-152.	9.0	477
5	Growth of <i>Mycobacterium tuberculosis</i> biofilms containing free mycolic acids and harbouring drugâ€tolerant bacteria. Molecular Microbiology, 2008, 69, 164-174.	1.2	454
6	A Broadly Implementable Research Course in Phage Discovery and Genomics for First-Year Undergraduate Students. MBio, 2014, 5, e01051-13.	1.8	424
7	Genomic sequences of bacteriophages HK97 and HK022: pervasive genetic mosaicism in the lambdoid bacteriophages 1 1Edited by M. Gottesman. Journal of Molecular Biology, 2000, 299, 27-51.	2.0	417
8	Bacteriophages and their genomes. Current Opinion in Virology, 2011, 1, 298-303.	2.6	397
9	Phamerator: a bioinformatic tool for comparative bacteriophage genomics. BMC Bioinformatics, 2011, 12, 395.	1.2	396
10	GroEL1: A Dedicated Chaperone Involved in Mycolic Acid Biosynthesis during Biofilm Formation in Mycobacteria. Cell, 2005, 123, 861-873.	13.5	379
11	The origins and ongoing evolution of viruses. Trends in Microbiology, 2000, 8, 504-508.	3.5	348
12	Bacteriophage genomics. Current Opinion in Microbiology, 2008, 11, 447-453.	2.3	330
13	PhagesDB: the actinobacteriophage database. Bioinformatics, 2017, 33, 784-786.	1.8	310
14	Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. ELife, 2015, 4, e06416.	2.8	280
15	Comparative Genomic Analysis of 60 Mycobacteriophage Genomes: Genome Clustering, Gene Acquisition, and Gene Size. Journal of Molecular Biology, 2010, 397, 119-143.	2.0	274
16	Imbroglios of Viral Taxonomy: Genetic Exchange and Failings of Phenetic Approaches. Journal of Bacteriology, 2002, 184, 4891-4905.	1.0	240
17	Exploring the Mycobacteriophage Metaproteome: Phage Genomics as an Educational Platform. PLoS Genetics, 2006, 2, e92.	1.5	239
18	Efficient site-specific integration in Plasmodium falciparum chromosomes mediated by mycobacteriophage Bxb1 integrase. Nature Methods, 2006, 3, 615-621.	9.0	223

#	Article	IF	Citations
19	Dark Matter of the Biosphere: the Amazing World of Bacteriophage Diversity. Journal of Virology, 2015, 89, 8107-8110.	1.5	198
20	Prophage-mediated defence against viral attack and viral counter-defence. Nature Microbiology, 2017, 2, 16251.	5.9	196
21	Bacteriophage evolution differs by host, lifestyle and genome. Nature Microbiology, 2017, 2, 17112.	5.9	192
22	Bacteriophage Mu genome sequence: analysis and comparison with Mu-like prophages in Haemophilus, Neisseria and Deinococcus. Journal of Molecular Biology, 2002, 317, 337-359.	2.0	188
23	The Generalized Transducing Salmonella Bacteriophage ES18: Complete Genome Sequence and DNA Packaging Strategy. Journal of Bacteriology, 2005, 187, 1091-1104.	1.0	185
24	Genome structure of mycobacteriophage D29: implications for phage evolution 1 1Edited by J. Karn. Journal of Molecular Biology, 1998, 279, 143-164.	2.0	182
25	Phage Therapy for Antibiotic-Resistant Bacterial Infections. Annual Review of Medicine, 2022, 73, 197-211.	5.0	182
26	Proline isomerism in staphylococcal nuclease characterized by NMR and site-directed mutagenesis. Nature, 1987, 329, 266-268.	13.7	180
27	BRED: A Simple and Powerful Tool for Constructing Mutant and Recombinant Bacteriophage Genomes. PLoS ONE, 2008, 3, e3957.	1.1	166
28	Superinfection immunity of mycobacteriophage L5: applications for genetic transformation of mycobacteria. Molecular Microbiology, 1993, 7, 407-417.	1.2	161
29	A new cell division operon inEscherichia coli. Molecular Genetics and Genomics, 1986, 205, 134-145.	2.4	159
30	On the nature of mycobacteriophage diversity and host preference. Virology, 2012, 434, 187-201.	1.1	159
31	Genomic and structural analysis of Syn9, a cyanophage infecting marineProchlorococcusandSynechococcus. Environmental Microbiology, 2007, 9, 1675-1695.	1.8	158
32	An inclusive Research Education Community (iREC): Impact of the SEA-PHAGES program on research outcomes and student learning. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 13531-13536.	3.3	155
33	The role of iron in <i>Mycobacterium smegmatis</i> biofilm formation: the exochelin siderophore is essential in limiting iron conditions for biofilm formation but not for planktonic growth. Molecular Microbiology, 2007, 66, 468-483.	1.2	154
34	Bacteriophages of <i>Gordonia</i> spp. Display a Spectrum of Diversity and Genetic Relationships. MBio, 2017, 8, .	1.8	135
35	Expanding the Diversity of Mycobacteriophages: Insights into Genome Architecture and Evolution. PLoS ONE, 2011, 6, e16329.	1.1	133
36	Teaching Scientific Inquiry. Science, 2006, 314, 1880-1881.	6.0	128

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37	Efficient point mutagenesis in mycobacteria using singleâ€stranded DNA recombineering: characterization of antimycobacterial drug targets. Molecular Microbiology, 2008, 67, 1094-1107.	1.2	126
38	Mycobacteriophage Lysin B is a novel mycolylarabinogalactan esterase. Molecular Microbiology, 2009, 73, 367-381.	1.2	123
39	The Orientation of Mycobacteriophage Bxb1 Integration Is Solely Dependent on the Central Dinucleotide of attP and attB. Molecular Cell, 2003, 12, 1101-1111.	4.5	122
40	Recombineering mycobacteria and their phages. Nature Reviews Microbiology, 2008, 6, 851-857.	13.6	122
41	The Î³Î´ resolvase induces an unusual DNA structure at the recombinational crossover point. Cell, 1987, 49, 103-110.	13.5	121
42	The crystal structure of the catalytic domain of the site-specific recombination enzyme Î³Î´ resolvase at 2.7 Å… resolution. Cell, 1990, 63, 1323-1329.	13.5	121
43	Genomic sequence and analysis of the atypical temperate bacteriophage N15 1 1Edited by M. Gottesman. Journal of Molecular Biology, 2000, 299, 53-73.	2.0	121
44	The Genome of Bacillus subtilis Bacteriophage SPO1. Journal of Molecular Biology, 2009, 388, 48-70.	2.0	120
45	Control of Phage Bxb1 Excision by a Novel Recombination Directionality Factor. PLoS Biology, 2006, 4, e186.	2.6	118
46	Mycobacteriophage Bxb1 integrates into the Mycobacterium smegmatis groEL1 gene. Molecular Microbiology, 2003, 50, 463-473.	1.2	117
47	Enzymatic Hydrolysis of Trehalose Dimycolate Releases Free Mycolic Acids during Mycobacterial Growth in Biofilms. Journal of Biological Chemistry, 2010, 285, 17380-17389.	1.6	113
48	Mycobacteriophage Endolysins: Diverse and Modular Enzymes with Multiple Catalytic Activities. PLoS ONE, 2012, 7, e34052.	1.1	112
49	A peptidoglycan hydrolase motif within the mycobacteriophage TM4 tape measure protein promotes efficient infection of stationary phase cells. Molecular Microbiology, 2006, 62, 1569-1585.	1.2	110
50	Exploring the prokaryotic virosphere. Research in Microbiology, 2008, 159, 306-313.	1.0	109
51	Phage Therapy of <i>Mycobacterium</i> Infections: Compassionate Use of Phages in 20 Patients With Drug-Resistant Mycobacterial Disease. Clinical Infectious Diseases, 2023, 76, 103-112.	2.9	109
52	A Measure of College Student Persistence in the Sciences (PITS). CBE Life Sciences Education, 2016, 15, ar54.	1.1	106
53	The Secret Lives of Mycobacteriophages. Advances in Virus Research, 2012, 82, 179-288.	0.9	103
54	Keto-Mycolic Acid-Dependent Pellicle Formation Confers Tolerance to Drug-Sensitive Mycobacterium tuberculosis. MBio, 2013, 4, e00222-13.	1.8	103

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55	Mycobacteriophages: Genes and Genomes. Annual Review of Microbiology, 2010, 64, 331-356.	2.9	101
56	Mycobacterium smegmatis RNA polymerase: DNA supercoiling, action of rifampicin and mechanism of rifampicin resistance. Molecular Microbiology, 1993, 8, 277-285.	1.2	98
57	The pKO2 Linear Plasmid Prophage of Klebsiella oxytoca. Journal of Bacteriology, 2004, 186, 1818-1832.	1.0	98
58	Potent antibody-mediated neutralization limits bacteriophage treatment of a pulmonary Mycobacterium abscessus infection. Nature Medicine, 2021, 27, 1357-1361.	15.2	94
59	Fluoromycobacteriophages for Rapid, Specific, and Sensitive Antibiotic Susceptibility Testing of Mycobacterium tuberculosis. PLoS ONE, 2009, 4, e4870.	1.1	94
60	Host and pathogen response to bacteriophage engineered against Mycobacterium abscessus lung infection. Cell, 2022, 185, 1860-1874.e12.	13.5	93
61	Genome Sequence, Structural Proteins, and Capsid Organization of the Cyanophage Syn5: A â€œHornedâ€• Bacteriophage of Marine Synechococcus. Journal of Molecular Biology, 2007, 368, 966-981.	2.0	92
62	Mycobacterial Recombineering. Methods in Molecular Biology, 2008, 435, 203-215.	0.4	92
63	Evaluation of a Transposase Protocol for Rapid Generation of Shotgun High-Throughput Sequencing Libraries from Nanogram Quantities of DNA. Applied and Environmental Microbiology, 2011, 77, 8071-8079.	1.4	89
64	Propionibacterium acnes Bacteriophages Display Limited Genetic Diversity and Broad Killing Activity against Bacterial Skin Isolates. MBio, 2012, 3, .	1.8	89
65	Recombineering. Bacteriophage, 2012, 2, 5-14.	1.9	88
66	Bacteriophages with tails: chasing their origins and evolution. Research in Microbiology, 2003, 154, 253-257.	1.0	87
67	Synapsis in Phage Bxb1 Integration: Selection Mechanism for the Correct Pair of Recombination Sites. Journal of Molecular Biology, 2005, 349, 331-348.	2.0	87
68	Cooperativity mutants of the Î³Î´ resolvase identify an essential interdimer interaction. Cell, 1990, 63, 1331-1338.	13.5	86
69	Genomic Characterization of Mycobacteriophage Giles: Evidence for Phage Acquisition of Host DNA by Illegitimate Recombination. Journal of Bacteriology, 2008, 190, 2172-2182.	1.0	86
70	Rapid Film-Based Determination of Antibiotic Susceptibilities of Mycobacterium tuberculosis Strains by Using a Luciferase Reporter Phage and the Bronx Box. Journal of Clinical Microbiology, 1999, 37, 1144-1149.	1.8	86
71	Actinobacteriophages: Genomics, Dynamics, and Applications. Annual Review of Virology, 2020, 7, 37-61.	3.0	85
72	Complete Genomic Sequence of the Virulent Salmonella Bacteriophage SP6. Journal of Bacteriology, 2004, 186, 1933-1944.	1.0	84

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73	Comparative genomic analysis of mycobacteriophage Tweety: evolutionary insights and construction of compatible site-specific integration vectors for mycobacteria. Microbiology (United Kingdom), 2007, 153, 2711-2723.	0.7	83
74	Genome organization and characterization of mycobacteriophage Bxb1. Molecular Microbiology, 2002, 38, 955-970.	1.2	81
75	Exponential-Phase Glycogen Recycling Is Essential for Growth of <i>Mycobacterium smegmatis</i>. Journal of Bacteriology, 1999, 181, 6670-6678.	1.0	81
76	Transcriptional silencing by the mycobacteriophage L5 repressor. EMBO Journal, 1997, 16, 5914-5921.	3.5	79
77	Mycobacteriophages: Windows into Tuberculosis. PLoS Pathogens, 2014, 10, e1003953.	2.1	79
78	Mobilization of the non-conjugative plasmid RSF1010: A genetic and DNA sequence analysis of the mobilization region. Molecular Genetics and Genomics, 1987, 206, 161-168.	2.4	75
79	Integration-Dependent Bacteriophage Immunity Provides Insights into the Evolution of Genetic Switches. Molecular Cell, 2013, 49, 237-248.	4.5	75
80	Molecular Genetics of Mycobacteriophages. Microbiology Spectrum, 2014, 2, .	1.2	74
81	Integration and excision by the large serine recombinase ï†Rv1 integrase. Molecular Microbiology, 2005, 55, 1896-1910.	1.2	73
82	Do mycobacteria produce endospores?. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 878-881.	3.3	73
83	Mycobacteriophages. Microbiology Spectrum, 2018, 6, .	1.2	72
84	Anti-Tuberculosis Bacteriophage D29 Delivery with a Vibrating Mesh Nebulizer, Jet Nebulizer, and Soft Mist Inhaler. Pharmaceutical Research, 2017, 34, 2084-2096.	1.7	71
85	Integration and excision of the Mycobacterium tuberculosis prophage-like element, ï†Rv1. Molecular Microbiology, 2002, 45, 1515-1526.	1.2	70
86	Comparative genomics of the mycobacteriophages: insights into bacteriophage evolution. Research in Microbiology, 2008, 159, 332-339.	1.0	70
87	ï• ² GFP10, a High-Intensity Fluorophage, Enables Detection and Rapid Drug Susceptibility Testing of Mycobacterium tuberculosis Directly from Sputum Samples. Journal of Clinical Microbiology, 2012, 50, 1362-1369.	1.8	69
88	Complete Genome Sequences of 138 Mycobacteriophages. Journal of Virology, 2012, 86, 2382-2384.	1.5	69
89	Construction of D29 shuttle phasmids and luciferase reporter phages for detection of mycobacteria. Gene, 1996, 183, 129-136.	1.0	68
90	Transcriptional regulation of repressor synthesis in mycobacteriophage L5. Molecular Microbiology, 1995, 17, 1045-1056.	1.2	65

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91	Characterization of the mycobacteriophage L5 attachment site, attP 1 1 Edited by M. Gottesman. Journal of Molecular Biology, 1997, 266, 76-92.	2.0	65
92	Corrected Sequence of the Bacteriophage P22 Genome. Journal of Bacteriology, 2003, 185, 1475-1477.	1.0	65
93	Single-molecule analysis reveals the molecular bearing mechanism of DNA strand exchange by a serine recombinase. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7419-7424.	3.3	63
94	7-Deazaguanine modifications protect phage DNA from host restriction systems. Nature Communications, 2019, 10, 5442.	5.8	63
95	More Evidence of Collusion: a New Prophage-Mediated Viral Defense System Encoded by Mycobacteriophage Sbash. MBio, 2019, 10, .	1.8	60
96	Cluster K Mycobacteriophages: Insights into the Evolutionary Origins of Mycobacteriophage TM4. PLoS ONE, 2011, 6, e26750.	1.1	60
97	Toward a Phage Cocktail for Tuberculosis: Susceptibility and Tuberculocidal Action of Mycobacteriophages against Diverse Mycobacterium tuberculosis Strains. MBio, 2021, 12, .	1.8	56
98	Bacteriophage treatment of disseminated cutaneous Mycobacterium chelonae infection. Nature Communications, 2022, 13, 2313.	5.8	56
99	Bxz1, a new generalized transducing phage for mycobacteria. FEMS Microbiology Letters, 2004, 241, 271-276.	0.7	55
100	Functional requirements for bacteriophage growth: gene essentiality and expression in mycobacteriophage <scp>G</scp>iles. Molecular Microbiology, 2013, 88, 577-589.	1.2	53
101	Mycobacteriophages BPs, Angel and Halo: comparative genomics reveals a novel class of ultra-small mobile genetic elements. Microbiology (United Kingdom), 2009, 155, 2962-2977.	0.7	53
102	Rapid identification and susceptibility testing of Mycobacterium tuberculosis from MGIT cultures with luciferase reporter mycobacteriophages. Journal of Medical Microbiology, 2003, 52, 557-561.	0.7	52
103	Cluster M Mycobacteriophages Bongo, PegLeg, and Rey with Unusually Large Repertoires of tRNA Isotypes. Journal of Virology, 2014, 88, 2461-2480.	1.5	52
104	Evolution of Superinfection Immunity in Cluster A Mycobacteriophages. MBio, 2019, 10, .	1.8	52
105	Snapshot of haloarchaeal tailed virus genomes. RNA Biology, 2013, 10, 803-816.	1.5	51
106	Genomic diversity of bacteriophages infecting Microbacterium spp. PLoS ONE, 2020, 15, e0234636.	1.1	50
107	Control of Directionality in L5 Integrase-mediated Site-specific Recombination. Journal of Molecular Biology, 2003, 326, 805-821.	2.0	49
108	Two-step site selection for serine-integrase-mediated excision: DNA-directed integrase conformation and central dinucleotide proofreading. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3238-3243.	3.3	49

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109	Staphylococci phages display vast genomic diversity and evolutionary relationships. BMC Genomics, 2019, 20, 357.	1.2	49
110	Prophylaxis of Mycobacterium tuberculosis H37Rv Infection in a Preclinical Mouse Model via Inhalation of Nebulized Bacteriophage D29. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	48
111	Noncanonical DNA polymerization by aminoadenine-based siphoviruses. Science, 2021, 372, 520-524.	6.0	46
112	Mycobacteriophage Exploit NHEJ to Facilitate Genome Circularization. Molecular Cell, 2006, 23, 743-748.	4.5	45
113	Genetic transformation of mycobacteria. Trends in Microbiology, 1993, 1, 310-314.	3.5	44
114	Mycobacteriophages. , 1998, 101, 145-174.		44
115	Molecular Genetics of Mycobacteriophages. Microbiology Spectrum, 2014, 2, 1-36.	1.2	44
116	Mycobacteriophage L5 infection of Mycobacterium bovis BCG: implications for phage genetics in the slowâ€growing mycobacteria. Molecular Microbiology, 1997, 26, 755-766.	1.2	43
117	Mycobacterium abscessus Strain Morphotype Determines Phage Susceptibility, the Repertoire of Therapeutically Useful Phages, and Phage Resistance. MBio, 2021, 12, .	1.8	43
118	Identification and characterization of mycobacteriophage L5 excisionase. Molecular Microbiology, 2000, 35, 350-360.	1.2	42
119	Unlocking the Potential of 46 New Bacteriophages for Biocontrol of Dickeya Solani. Viruses, 2018, 10, 621.	1.5	42
120	Genomics and Proteomics of Mycobacteriophage Patience, an Accidental Tourist in the Mycobacterium Neighborhood. MBio, 2014, 5, e02145.	1.8	39
121	Tales of diversity: Genomic and morphological characteristics of forty-six Arthrobacter phages. PLoS ONE, 2017, 12, e0180517.	1.1	38
122	Mycobacteriophage Fruitloop gp52 inactivates Wag31 (DivIVA) to prevent heterotypic superinfection. Molecular Microbiology, 2018, 108, 443-460.	1.2	38
123	Yet More Evidence of Collusion: a New Viral Defense System Encoded by <i>Gordonia</i> Phage CarolAnn. MBio, 2019, 10, .	1.8	38
124	Characterization of a Mycobacterium smegmatis gene that confers resistance to phages L5 and D29 when overexpressed. Molecular Microbiology, 1996, 21, 159-170.	1.2	37
125	Evaluation of Fluoromycobacteriophages for Detecting Drug Resistance in Mycobacterium tuberculosis. Journal of Clinical Microbiology, 2011, 49, 1838-1842.	1.8	37
126	Evolutionary Relationships among Actinophages and a Putative Adaptation for Growth in Streptomyces spp. Journal of Bacteriology, 2013, 195, 4924-4935.	1.0	37

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127	Attachment Site Selection and Identity in Bxb1 Serine Integrase-Mediated Site-Specific Recombination. PLoS Genetics, 2013, 9, e1003490.	1.5	37
128	Innovations in Undergraduate Science Education: Going Viral. Journal of Virology, 2015, 89, 8111-8113.	1.5	36
129	Mycobacteriophage ZoeJ: A broad host-range close relative of mycobacteriophage TM4. Tuberculosis, 2019, 115, 14-23.	0.8	35
130	Mycobacteriophages: From Petri dish to patient. PLoS Pathogens, 2022, 18, e1010602.	2.1	35
131	CRISPY-BRED and CRISPY-BRIP: efficient bacteriophage engineering. Scientific Reports, 2021, 11, 6796.	1.6	34
132	The Prophage and Plasmid Mobilome as a Likely Driver of Mycobacterium abscessus Diversity. MBio, 2021, 12, .	1.8	32
133	Molecular Genetics of Mycobacteriophages. , 0, , 81-119.		32
134	Fluorescent Reporter DS6A Mycobacteriophages Reveal Unique Variations in Infectibility and Phage Production in Mycobacteria. Journal of Bacteriology, 2016, 198, 3220-3232.	1.0	31
135	Transcriptional regulation and immunity in mycobacteriophage Bxb1. Molecular Microbiology, 2002, 38, 971-985.	1.2	30
136	Measuring Networking as an Outcome Variable in Undergraduate Research Experiences. CBE Life Sciences Education, 2015, 14, ar38.	1.1	30
137	Function, expression, specificity, diversity and incompatibility of actinobacteriophage <i>parABS</i> systems. Molecular Microbiology, 2016, 101, 625-644.	1.2	29
138	Successive and Targeted DNA Integrations in the <i>Drosophila</i> Genome by Bxb1 and Ï†C31 Integrases. Genetics, 2011, 189, 391-395.	1.2	28
139	Reporter Phage and Breath Tests: Emerging Phenotypic Assays for Diagnosing Active Tuberculosis, Antibiotic Resistance, and Treatment Efficacy. Journal of Infectious Diseases, 2011, 204, S1142-S1150.	1.9	28
140	Cluster J Mycobacteriophages: Intron Splicing in Capsid and Tail Genes. PLoS ONE, 2013, 8, e69273.	1.1	28
141	Characterization of the dnaG Locus in Mycobacterium smegmatis Reveals Linkage of DNA Replication and Cell Division. Journal of Bacteriology, 1998, 180, 65-72.	1.0	27
142	Characterization and induction of prophages in human gut-associated Bifidobacterium hosts. Scientific Reports, 2018, 8, 12772.	1.6	26
143	Characterization of the mIHF Gene of Mycobacterium smegmatis. Journal of Bacteriology, 1998, 180, 5473-5477.	1.0	26
144	Remote control of DNA-acting enzymes by varying the Brownian dynamics of a distant DNA end. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16546-16551.	3.3	25

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145	Mycobacteriophage Marvin: a New Singleton Phage with an Unusual Genome Organization. Journal of Virology, 2012, 86, 4762-4775.	1.5	25
146	Complete Genome Sequences of 63 Mycobacteriophages. Genome Announcements, 2013, 1, .	0.8	25
147	Enhanced Specialized Transduction Using Recombineering in Mycobacterium tuberculosis. MBio, 2014, 5, e01179-14.	1.8	25
148	Genome Sequence of Salmonella Phage Ï‡. Genome Announcements, 2015, 3, .	0.8	25
149	Expression and evolutionary patterns of mycobacteriophage D29 and its temperate close relatives. BMC Microbiology, 2017, 17, 225.	1.3	24
150	Uncoupling of the recombination and topoisomerase activities of the Î³Î´ resolvase by a mutation at the crossover point. Nature, 1988, 332, 861-863.	13.7	23
151	The Bxb1 gp47 recombination directionality factor is required not only for prophage excision, but also for phage DNA replication. Gene, 2012, 495, 42-48.	1.0	23
152	The sequence of the distal end of theE. coliribosomal RNA rrnE operon indicates conserved features are shared by rrn operons. Nucleic Acids Research, 1985, 13, 5515-5525.	6.5	22
153	Mycobacteriophage D29 integrase-mediated recombination: specificity of mycobacteriophage integration. Gene, 1998, 225, 143-151.	1.0	22
154	Exposing the Secrets of Two Well-Known Lactobacillus casei Phages, J-1 and PL-1, by Genomic and Structural Analysis. Applied and Environmental Microbiology, 2014, 80, 7107-7121.	1.4	22
155	Comparative Genomics of Cluster O Mycobacteriophages. PLoS ONE, 2015, 10, e0118725.	1.1	22
156	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
157	Mycobacteriophageâ€“antibiotic therapy promotes enhanced clearance of drug-resistant <i>Mycobacterium abscessus</i>. DMM Disease Models and Mechanisms, 2021, 14, .	1.2	22
158	Genetic Dissection of Mycobacterial Biofilms. Methods in Molecular Biology, 2015, 1285, 215-226.	0.4	22
159	Protein-DNA Complexes in Mycobacteriophage L5 Integrative Recombination. Journal of Bacteriology, 1999, 181, 454-461.	1.0	22
160	Application of BRED technology to construct recombinant D29 reporter phage expressing EGFP. FEMS Microbiology Letters, 2013, 344, 166-172.	0.7	21
161	Mycobacteriophage-repressor-mediated immunity as a selectable genetic marker: Adephagia and BPs repressor selection. Microbiology (United Kingdom), 2015, 161, 1539-1551.	0.7	21
162	Characterization of a Mycobacterium smegmatis Mutant That Is Simultaneously Resistant to d -Cycloserine and Vancomycin. Antimicrobial Agents and Chemotherapy, 2000, 44, 1701-1704.	1.4	20

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163	A Mycobacterial Systems Resource for the Research Community. MBio, 2021, 12, .	1.8	20
164	Genetic Analysis of Peptidoglycan Biosynthesis in Mycobacteria: Characterization of a ddlA Mutant ofMycobacterium smegmatis. Journal of Bacteriology, 2000, 182, 6854-6856.	1.0	19
165	Temperature-dependent Regulation of Mycolic Acid Cyclopropanation in Saprophytic Mycobacteria. Journal of Biological Chemistry, 2010, 285, 21698-21707.	1.6	19
166	Generation of Affinity-Tagged Fluoromycobacteriophages by Mixed Assembly of Phage Capsids. Applied and Environmental Microbiology, 2013, 79, 5608-5615.	1.4	18
167	Fluoromycobacteriophages Can Detect Viable Mycobacterium tuberculosis and Determine Phenotypic Rifampicin Resistance in 3â€“5 Days From Sputum Collection. Frontiers in Microbiology, 2018, 9, 1471.	1.5	18
168	The Structure of Xis Reveals the Basis for Filament Formation and Insight into DNA Bending within a Mycobacteriophage Intasome. Journal of Molecular Biology, 2014, 426, 412-422.	2.0	17
169	Mycobacteriophages: Cornerstones of Mycobacterial Research. , 0, , 163-183.		17
170	Genome Sequence of <i>Salmonella</i> Phage 9NA. Genome Announcements, 2014, 2, .	0.8	16
171	The Protein Interactome of Mycobacteriophage Giles Predicts Functions for Unknown Proteins. Journal of Bacteriology, 2015, 197, 2508-2516.	1.0	16
172	Genome Sequence of Salmonella enterica Phage Det7. Genome Announcements, 2015, 3, .	0.8	16
173	Protein-Mediated and RNA-Based Origins of Replication of Extrachromosomal Mycobacterial Prophages. MBio, 2020, 11, .	1.8	16
174	Mycobacteriophages to Treat Tuberculosis: Dream or Delusion?. Respiration, 2022, 101, 1-15.	1.2	16
175	Virus-host protein-protein interactions of mycobacteriophage Giles. Scientific Reports, 2017, 7, 16514.	1.6	15
176	Identification of mycobacteriophage toxic genes reveals new features of mycobacterial physiology and morphology. Scientific Reports, 2020, 10, 14670.	1.6	15
177	Application of Bacteriophages for Mycobacterial Infections, from Diagnosis to Treatment. Microorganisms, 2021, 9, 2366.	1.6	15
178	The cohesive ends of mycobacteriophage L5 DNA. Nucleic Acids Research, 1992, 20, 3251-3251.	6.5	14
179	Cross-talk between Diverse Serine Integrases. Journal of Molecular Biology, 2014, 426, 318-331.	2.0	14
180	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

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