## Deborah Jacobs-Sera

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Engineered bacteriophages for treatment of a patient with a disseminated drug-resistant Mycobacterium abscessus. Nature Medicine, 2019, 25, 730-733.	30.7	907
2	A Broadly Implementable Research Course in Phage Discovery and Genomics for First-Year Undergraduate Students. MBio, 2014, 5, e01051-13.	4.1	424
3	Phamerator: a bioinformatic tool for comparative bacteriophage genomics. BMC Bioinformatics, 2011, 12, 395.	2.6	396
4	Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. ELife, 2015, 4, e06416.	6.0	280
5	Comparative Genomic Analysis of 60 Mycobacteriophage Genomes: Genome Clustering, Gene Acquisition, and Gene Size. Journal of Molecular Biology, 2010, 397, 119-143.	4.2	274
6	Exploring the Mycobacteriophage Metaproteome: Phage Genomics as an Educational Platform. PLoS Genetics, 2006, 2, e92.	3.5	239
7	Prophage-mediated defence against viral attack and viral counter-defence. Nature Microbiology, 2017, 2, 16251.	13.3	196
8	On the nature of mycobacteriophage diversity and host preference. Virology, 2012, 434, 187-201.	2.4	159
9	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.	7.1	155
10	Bacteriophages of <i>Gordonia</i> spp. Display a Spectrum of Diversity and Genetic Relationships. MBio, 2017, 8, .	4.1	135
11	Expanding the Diversity of Mycobacteriophages: Insights into Genome Architecture and Evolution. PLoS ONE, 2011, 6, e16329.	2.5	133
12	Annotation of Bacteriophage Genome Sequences Using DNA Master: An Overview. Methods in Molecular Biology, 2018, 1681, 217-229.	0.9	88
13	Genomic Characterization of Mycobacteriophage Giles: Evidence for Phage Acquisition of Host DNA by Illegitimate Recombination. Journal of Bacteriology, 2008, 190, 2172-2182.	2.2	86
14	7-Deazaguanine modifications protect phage DNA from host restriction systems. Nature Communications, 2019, 10, 5442.	12.8	63
15	More Evidence of Collusion: a New Prophage-Mediated Viral Defense System Encoded by Mycobacteriophage Sbash. MBio, 2019, 10, .	4.1	60
16	Cluster K Mycobacteriophages: Insights into the Evolutionary Origins of Mycobacteriophage TM4. PLoS ONE, 2011, 6, e26750.	2.5	60
17	Cluster M Mycobacteriophages Bongo, PegLeg, and Rey with Unusually Large Repertoires of tRNA Isotypes. Journal of Virology, 2014, 88, 2461-2480.	3.4	52
18	Noncanonical DNA polymerization by aminoadenine-based siphoviruses. Science, 2021, 372, 520-524.	12.6	46

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19	Mycobacterium abscessus Strain Morphotype Determines Phage Susceptibility, the Repertoire of Therapeutically Useful Phages, and Phage Resistance. MBio, 2021, 12, .	4.1	43
20	Unlocking the Potential of 46 New Bacteriophages for Biocontrol of Dickeya Solani. Viruses, 2018, 10, 621.	3.3	42
21	Genomics and Proteomics of Mycobacteriophage Patience, an Accidental Tourist in the Mycobacterium Neighborhood. MBio, 2014, 5, e02145.	4.1	39
22	Tales of diversity: Genomic and morphological characteristics of forty-six Arthrobacter phages. PLoS ONE, 2017, 12, e0180517.	2.5	38
23	Yet More Evidence of Collusion: a New Viral Defense System Encoded by <i>Gordonia</i> Phage CarolAnn. MBio, 2019, 10, .	4.1	38
24	Evolutionary Relationships among Actinophages and a Putative Adaptation for Growth in Streptomyces spp. Journal of Bacteriology, 2013, 195, 4924-4935.	2.2	37
25	The Prophage and Plasmid Mobilome as a Likely Driver of Mycobacterium abscessus Diversity. MBio, 2021, 12, .	4.1	32
26	Function, expression, specificity, diversity and incompatibility of actinobacteriophage <i>parABS</i> systems. Molecular Microbiology, 2016, 101, 625-644.	2.5	29
27	Structures of Three Actinobacteriophage Capsids: Roles of Symmetry and Accessory Proteins. Viruses, 2020, 12, 294.	3.3	14
28	Complete Genome Sequences of 38 Gordonia sp. Bacteriophages. Genome Announcements, 2017, 5, .	0.8	7
29	Genome Sequence of Mycobacterium abscessus Phage phiT46-1. Microbiology Resource Announcements, 2021, 10, .	0.6	6
30	A Mycobacteriophage-Based Vaccine Platform: SARS-CoV-2 Antigen Expression and Display. Microorganisms, 2021, 9, 2414.	3.6	6
31	Genome Sequences of 19 Rhodococcus erythropolis Cluster CA Phages. Genome Announcements, 2017, 5, .	0.8	5
32	Complete Genome Sequences of 44 Arthrobacter Phages. Genome Announcements, 2018, 6, .	0.8	3
33	Genome Sequences of 20 Bacteriophages Isolated on Gordonia terrae. Microbiology Resource Announcements, 2020, 9, .	0.6	3
34	Eight Genome Sequences of Cluster BE1 Phages That Infect <i>Streptomyces</i> Species. Genome Announcements, 2018, 6, .	0.8	2
35	Genome Sequence of Mycobacterium abscessus Phage phiT45-1. Microbiology Resource Announcements, 2021, 10, .	0.6	2
36	Genome Sequences of Four Subcluster L2 Mycobacterium Phages, Finemlucis, Miley16, Wilder, and Zakai. Genome Announcements, 2017, 5, .	0.8	1

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37	Genome Sequences of Mycobacteriophages Amgine, Amohnition, Bella96, Cain, DarthP, Hammy, Krueger, LastHope, Peanam, PhelpsODU, Phrank, SirPhilip, Slimphazie, and Unicorn. Genome Announcements, 2017, 5, .	0.8	1
38	Genome Sequences of Four Cluster P Mycobacteriophages. Genome Announcements, 2018, 6, .	0.8	1
39	Genome Sequences of Three Microbacterium Phages Isolated from Flowers. Microbiology Resource Announcements, 2019, 8, .	0.6	Ο
40	Genome Sequence and Characteristics of Cluster C1 Mycobacterium smegmatis Phage EasyJones. Microbiology Resource Announcements, 2021, 10, e0099721.	0.6	0