

# Deborah Jacobs-Sera

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1359509/publications.pdf>

Version: 2024-02-01

40  
papers

4,102  
citations

236925

25  
h-index

315739

38  
g-index

41  
all docs

41  
docs citations

41  
times ranked

3155  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome Sequence of Mycobacterium abscessus Phage phiT46-1. Microbiology Resource Announcements, 2021, 10, .	0.6	6
2	Genome Sequence of Mycobacterium abscessus Phage phiT45-1. Microbiology Resource Announcements, 2021, 10, .	0.6	2
3	The Prophage and Plasmid Mobilome as a Likely Driver of Mycobacterium abscessus Diversity. MBio, 2021, 12, .	4.1	32
4	Mycobacterium abscessus Strain Morphotype Determines Phage Susceptibility, the Repertoire of Therapeutically Useful Phages, and Phage Resistance. MBio, 2021, 12, .	4.1	43
5	Noncanonical DNA polymerization by aminoadenine-based siphoviruses. Science, 2021, 372, 520-524.	12.6	46
6	A Mycobacteriophage-Based Vaccine Platform: SARS-CoV-2 Antigen Expression and Display. Microorganisms, 2021, 9, 2414.	3.6	6
7	Genome Sequence and Characteristics of Cluster C1 Mycobacterium smegmatis Phage EasyJones. Microbiology Resource Announcements, 2021, 10, e0099721.	0.6	0
8	Structures of Three Actinobacteriophage Capsids: Roles of Symmetry and Accessory Proteins. Viruses, 2020, 12, 294.	3.3	14
9	Genome Sequences of 20 Bacteriophages Isolated on Gordonia terrae. Microbiology Resource Announcements, 2020, 9, .	0.6	3
10	Engineered bacteriophages for treatment of a patient with a disseminated drug-resistant Mycobacterium abscessus. Nature Medicine, 2019, 25, 730-733.	30.7	907
11	Yet More Evidence of Collusion: a New Viral Defense System Encoded by <i>Gordonia</i> Phage CarolAnn. MBio, 2019, 10, .	4.1	38
12	More Evidence of Collusion: a New Prophage-Mediated Viral Defense System Encoded by Mycobacteriophage Sbash. MBio, 2019, 10, .	4.1	60
13	Genome Sequences of Three Mycobacterium Phages Isolated from Flowers. Microbiology Resource Announcements, 2019, 8, .	0.6	0
14	7-Deazaguanine modifications protect phage DNA from host restriction systems. Nature Communications, 2019, 10, 5442.	12.8	63
15	Genome Sequences of Four Cluster P Mycobacteriophages. Genome Announcements, 2018, 6, .	0.8	1
16	Annotation of Bacteriophage Genome Sequences Using DNA Master: An Overview. Methods in Molecular Biology, 2018, 1681, 217-229.	0.9	88
17	Unlocking the Potential of 46 New Bacteriophages for Biocontrol of <i>Dickeya Solani</i> . Viruses, 2018, 10, 621.	3.3	42
18	Eight Genome Sequences of Cluster BE1 Phages That Infect <i>Streptomyces</i> Species. Genome Announcements, 2018, 6, .	0.8	2

#	ARTICLE	IF	CITATIONS
19	Complete Genome Sequences of 44 Arthrobacter Phages. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
20	Prophage-mediated defence against viral attack and viral counter-defence. <i>Nature Microbiology</i> , 2017, 2, 16251.	13.3	196
21	Complete Genome Sequences of 38 <i>Gordonia</i> sp. Bacteriophages. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
22	Bacteriophages of <i>Gordonia</i> spp. Display a Spectrum of Diversity and Genetic Relationships. <i>MBio</i> , 2017, 8, .	4.1	135
23	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.	7.1	155
24	Genome Sequences of Four Subcluster L2 Mycobacterium Phages, Finemlucis, Miley16, Wilder, and Zakai. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
25	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
26	Genome Sequences of 19 <i>Rhodococcus erythropolis</i> Cluster CA Phages. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
27	Tales of diversity: Genomic and morphological characteristics of forty-six <i>Arthrobacter</i> phages. <i>PLoS ONE</i> , 2017, 12, e0180517.	2.5	38
28	Function, expression, specificity, diversity and incompatibility of actinobacteriophage <i>parABS</i> systems. <i>Molecular Microbiology</i> , 2016, 101, 625-644.	2.5	29
29	Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. <i>ELife</i> , 2015, 4, e06416.	6.0	280
30	A Broadly Implementable Research Course in Phage Discovery and Genomics for First-Year Undergraduate Students. <i>MBio</i> , 2014, 5, e01051-13.	4.1	424
31	Genomics and Proteomics of Mycobacteriophage Patience, an Accidental Tourist in the Mycobacterium Neighborhood. <i>MBio</i> , 2014, 5, e02145.	4.1	39
32	Cluster M Mycobacteriophages Bongo, PegLeg, and Rey with Unusually Large Repertoires of tRNA Isootypes. <i>Journal of Virology</i> , 2014, 88, 2461-2480.	3.4	52
33	Evolutionary Relationships among Actinophages and a Putative Adaptation for Growth in <i>Streptomyces</i> spp. <i>Journal of Bacteriology</i> , 2013, 195, 4924-4935.	2.2	37
34	On the nature of mycobacteriophage diversity and host preference. <i>Virology</i> , 2012, 434, 187-201.	2.4	159
35	Phamerator: a bioinformatic tool for comparative bacteriophage genomics. <i>BMC Bioinformatics</i> , 2011, 12, 395.	2.6	396
36	Expanding the Diversity of Mycobacteriophages: Insights into Genome Architecture and Evolution. <i>PLoS ONE</i> , 2011, 6, e16329.	2.5	133

#	ARTICLE	IF	CITATIONS
37	Cluster K Mycobacteriophages: Insights into the Evolutionary Origins of Mycobacteriophage TM4. PLoS ONE, 2011, 6, e26750.	2.5	60
38	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
39	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
40	Exploring the Mycobacteriophage Metaproteome: Phage Genomics as an Educational Platform. PLoS Genetics, 2006, 2, e92.	3.5	239