

B Jesse Shapiro

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

70
papers

4,115
citations

25
h-index

64
g-index

104
ext. papers

5,094
ext. citations

10.5
avg, IF

5.38
L-index

#	Paper	IF	Citations
70	Global mapping of the yeast genetic interaction network. <i>Science</i> , 2004 , 303, 808-13	33.3	1700
69	Population genomics of early events in the ecological differentiation of bacteria. <i>Science</i> , 2012 , 336, 48-51	33.3	366
68	Genomic analysis identifies targets of convergent positive selection in drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2013 , 45, 1183-9	36.3	295
67	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. <i>Cell</i> , 2015 , 162, 738-50	56.2	176
66	Analysis of beta-1,3-glucan assembly in <i>Saccharomyces cerevisiae</i> using a synthetic interaction network and altered sensitivity to caspofungin. <i>Genetics</i> , 2004 , 167, 35-49	4	138
65	Ordering microbial diversity into ecologically and genetically cohesive units. <i>Trends in Microbiology</i> , 2014 , 22, 235-47	12.4	120
64	The advent of genome-wide association studies for bacteria. <i>Current Opinion in Microbiology</i> , 2015 , 25, 17-24	7.9	102
63	An interactional network of genes involved in chitin synthesis in <i>Saccharomyces cerevisiae</i> . <i>BMC Genetics</i> , 2005 , 6, 8	2.6	89
62	Evolutionary consequences of intra-patient phage predation on microbial populations. <i>ELife</i> , 2014 , 3, e03497	8.9	82
61	What Is Speciation?. <i>PLoS Genetics</i> , 2016 , 12, e1005860	6	72
60	Looking for Darwin's footprints in the microbial world. <i>Trends in Microbiology</i> , 2009 , 17, 196-204	12.4	71
59	Population genomics of <i>Mycobacterium tuberculosis</i> in the Inuit. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 13609-14	11.5	59
58	Characterising and predicting cyanobacterial blooms in an 8-year amplicon sequencing time course. <i>ISME Journal</i> , 2017 , 11, 1746-1763	11.9	46
57	Reproducibility of Vibrionaceae population structure in coastal bacterioplankton. <i>ISME Journal</i> , 2013 , 7, 509-19	11.9	45
56	How clonal are bacteria over time?. <i>Current Opinion in Microbiology</i> , 2016 , 31, 116-123	7.9	41
55	Microbial Speciation. <i>Cold Spring Harbor Perspectives in Biology</i> , 2015 , 7, a018143	10.2	39
54	Mitochondrial Recombination and Introgression during Speciation by Hybridization. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1947-1959	8.3	36

53	VSG switching in <i>Trypanosoma brucei</i> : antigenic variation analysed using RNAi in the absence of immune selection. <i>Molecular Microbiology</i> , 2005 , 57, 1608-22	4.1	34
52	The Inuit gut microbiome is dynamic over time and shaped by traditional foods. <i>Microbiome</i> , 2017 , 5, 151	16.6	32
51	Comparing patterns of natural selection across species using selective signatures. <i>PLoS Genetics</i> , 2008 , 4, e23	6	32
50	Environment and host species shape the skin microbiome of captive neotropical bats. <i>PeerJ</i> , 2016 , 4, e2430	3.1	32
49	Elevated rates of horizontal gene transfer in the industrialized human microbiome. <i>Cell</i> , 2021 , 184, 2053-2067.e18	5.6	31
48	Origins of pandemic <i>Vibrio cholerae</i> from environmental gene pools. <i>Nature Microbiology</i> , 2016 , 2, 1624-1636	6.6	31
47	Sympatric speciation: when is it possible in bacteria?. <i>PLoS ONE</i> , 2013 , 8, e53539	3.7	31
46	Gut Microbiome of the Canadian Arctic Inuit. <i>MSphere</i> , 2017 , 2,	5	28
45	A phylogeny-based sampling strategy and power calculator informs genome-wide associations study design for microbial pathogens. <i>Genome Medicine</i> , 2014 , 6, 101	14.4	25
44	The population genetics of pangenomes. <i>Nature Microbiology</i> , 2017 , 2, 1574	26.6	24
43	Coherence of <i>Microcystis</i> species revealed through population genomics. <i>ISME Journal</i> , 2019 , 13, 2887-2900	20	23
42	Community rescue in experimental phytoplankton communities facing severe herbicide pollution. <i>Nature Ecology and Evolution</i> , 2020 , 4, 578-588	12.3	21
41	Niche Separation Increases With Genetic Distance Among Bloom-Forming Cyanobacteria. <i>Frontiers in Microbiology</i> , 2018 , 9, 438	5.7	20
40	<i>Vibrio cholerae</i> genomic diversity within and between patients. <i>Microbial Genomics</i> , 2017 , 3,	4.4	20
39	Benchmarking bacterial genome-wide association study methods using simulated genomes and phenotypes. <i>Microbial Genomics</i> , 2020 , 6,	4.4	19
38	A large-scale assessment of lakes reveals a pervasive signal of land use on bacterial communities. <i>ISME Journal</i> , 2020 , 14, 3011-3023	11.9	19
37	Cooking and co-ingested polyphenols reduce in vitro methylmercury bioaccessibility from fish and may alter exposure in humans. <i>Science of the Total Environment</i> , 2018 , 616-617, 863-874	10.2	19
36	Phenotypic differentiation of <i>Streptococcus pyogenes</i> populations is induced by recombination-driven gene-specific sweeps. <i>Scientific Reports</i> , 2016 , 6, 36644	4.9	18

35	Signatures of natural selection and ecological differentiation in microbial genomes. <i>Advances in Experimental Medicine and Biology</i> , 2014 , 781, 339-59	3.6	16
34	What Microbial Population Genomics Has Taught Us About Speciation. <i>Population Genomics</i> , 2018 , 31-47	1.4	15
33	An experimental test of the causes of small-scale phenotypic differentiation in a population of great tits. <i>Journal of Evolutionary Biology</i> , 2006 , 19, 176-83	2.3	14
32	Predicting <i>Vibrio cholerae</i> Infection and Disease Severity Using Metagenomics in a Prospective Cohort Study. <i>Journal of Infectious Diseases</i> , 2021 , 223, 342-351	7	13
31	Does diversity beget diversity in microbiomes?. <i>ELife</i> , 2020 , 9,	8.9	12
30	Trophic structure modulates community rescue following acidification. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019 , 286, 20190856	4.4	11
29	Functional Diversity: An Epistemic Roadmap. <i>BioScience</i> , 2019 , 69, 800-811	5.7	10
28	Diversity Assessment of Toxic Cyanobacterial Blooms during Oxidation. <i>Toxins</i> , 2020 , 12,	4.9	9
27	Microbial evolutionary medicine: from theory to clinical practice. <i>Lancet Infectious Diseases</i> , 2019 , 19, e273-e283	25.5	6
26	A small number of early introductions seeded widespread transmission of SARS-CoV-2 in Québec, Canada. <i>Genome Medicine</i> , 2021 , 13, 169	14.4	6
25	The slow:fast substitution ratio reveals changing patterns of natural selection in gamma-proteobacterial genomes. <i>ISME Journal</i> , 2009 , 3, 1180-92	11.9	5
24	The evolution of realized niches within freshwater <i>Synechococcus</i> . <i>Environmental Microbiology</i> , 2020 , 22, 1238-1250	5.2	5
23	Widespread agrochemicals differentially affect zooplankton biomass and community structure. <i>Ecological Applications</i> , 2021 , 31, e02423	4.9	5
22	Translational activity is uncoupled from nucleic acid content in bacterial cells of the human gut microbiota. <i>Gut Microbes</i> , 2021 , 13, 1-15	8.8	4
21	Resistance, resilience, and functional redundancy of freshwater bacterioplankton communities facing a gradient of agricultural stressors in a mesocosm experiment. <i>Molecular Ecology</i> , 2021 , 30, 4771-4788	5.7	4
20	A Combination of Metagenomic and Cultivation Approaches Reveals Hypermutator Phenotypes within <i>Vibrio cholerae</i> -Infected Patients. <i>MSystems</i> , 2021 , 6, e0088921	7.6	4
19	The Action of Certain Organic Accelerators in the Vulcanization of Rubber. <i>Journal of Industrial & Engineering Chemistry</i> , 1921 , 13, 67-70		3
18	Genome Evolution in Bacteria Isolated from Million-Year-Old Subseafloor Sediment. <i>MBio</i> , 2021 , 12, e0115021	1.5	3

17	Single-colony sequencing reveals microbe-by-microbiome phyllosymbiosis between the cyanobacterium <i>Microcystis</i> and its associated bacteria. <i>Microbiome</i> , 2021 , 9, 194	16.6	3
16	Comparing microscopy and DNA metabarcoding techniques for identifying cyanobacteria assemblages across hundreds of lakes.. <i>Harmful Algae</i> , 2022 , 113, 102187	5.3	2
15	Two cases of type-a meningitis within the same week in the same hospital are phylogenetically unrelated but recently exchanged capsule genes. <i>Microbial Genomics</i> , 2020 , 6,	4.4	2
14	Characterizing and predicting cyanobacterial blooms in an 8-year amplicon sequencing time-course		2
13	<i>Vibrio cholerae</i> genomic diversity within and between patients		2
12	Outbreak investigation of SARS-CoV-2 transmission in an emergency childcare centre. <i>Canadian Journal of Public Health</i> , 2021 , 112, 566-575	3.2	2
11	Classic genome-wide association methods are unlikely to identify causal variants in strongly clonal microbial populations		2
10	Can Cyanobacterial Diversity in the Source Predict the Diversity in Sludge and the Risk of Toxin Release in a Drinking Water Treatment Plant?. <i>Toxins</i> , 2021 , 13,	4.9	2
9	Fine-Scale Adaptations to Environmental Variation and Growth Strategies Drive Phyllosphere Diversity.. <i>MBio</i> , 2022 , e0317521	7.8	1
8	Single-colony sequencing reveals phyllosymbiosis, co-phylogeny, and horizontal gene transfer between the cyanobacterium <i>Microcystis</i> and its microbiome		1
7	Genome evolution in bacteria isolated from million-year-old subseafloor sediment		1
6	Does diversity beget diversity in microbiomes?		1
5	Metagenomic study to evaluate functional capacity of a cyanobacterial bloom during oxidation. <i>Chemical Engineering Journal Advances</i> , 2021 , 8, 100151	3.6	1
4	Population Genomics Approaches for Genetic Characterization of SARS-CoV-2 Lineages.. <i>Frontiers in Medicine</i> , 2022 , 9, 826746	4.9	1
3	A Glyphosate-Based Herbicide Cross-Selects for Antibiotic Resistance Genes in Bacterioplankton Communities.. <i>MSystems</i> , 2022 , e0148221	7.6	1
2	Oxidation to Control Cyanobacteria and Cyanotoxins in Drinking Water Treatment Plants: Challenges at the Laboratory and Full-Scale Plants. <i>Water (Switzerland)</i> , 2022 , 14, 537	3	0
1	Reuniting ecology and evolution. <i>Environmental Microbiology Reports</i> , 2019 , 11, 13-14	3.7	