B Jesse Shapiro

List of Publications by Year in Descending Order

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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	4,115	25	64
papers	citations	h-index	g-index
104	5,094	10.5	5.38
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
70	Fine-Scale Adaptations to Environmental Variation and Growth Strategies Drive Phyllosphere Diversity.. *MBio*, **2022**, e0317521	7.8	1
69	Comparing microscopy and DNA metabarcoding techniques for identifying cyanobacteria assemblages across hundreds of lakes.. *Harmful Algae*, **2022**, 113, 102187	5.3	2
68	Oxidation to Control Cyanobacteria and Cyanotoxins in Drinking Water Treatment Plants: Challenges at the Laboratory and Full-Scale Plants. *Water (Switzerland)*, **2022**, 14, 537	3	0
67	Population Genomics Approaches for Genetic Characterization of SARS-CoV-2 Lineages.. *Frontiers in Medicine*, **2022**, 9, 826746	4.9	1
66	A Glyphosate-Based Herbicide Cross-Selects for Antibiotic Resistance Genes in Bacterioplankton Communities.. *MSystems*, **2022**, e0148221	7.6	1
65	A small number of early introductions seeded widespread transmission of SARS-CoV-2 in Québec, Canada. *Genome Medicine*, **2021**, 13, 169	14.4	6
64	Elevated rates of horizontal gene transfer in the industrialized human microbiome. *Cell*, **2021**, 184, 2053-2067.e18	56.2	31
63	Outbreak investigation of SARS-CoV-2 transmission in an emergency childcare centre. *Canadian Journal of Public Health*, **2021**, 112, 566-575	3.2	2
62	Predicting Vibrio cholerae Infection and Disease Severity Using Metagenomics in a Prospective Cohort Study. *Journal of Infectious Diseases*, **2021**, 223, 342-351	7	13
61	Translational activity is uncoupled from nucleic acid content in bacterial cells of the human gut microbiota. *Gut Microbes*, **2021**, 13, 1-15	8.8	4
60	Can Cyanobacterial Diversity in the Source Predict the Diversity in Sludge and the Risk of Toxin Release in a Drinking Water Treatment Plant?. *Toxins*, **2021**, 13,	4.9	2
59	Genome Evolution in Bacteria Isolated from Million-Year-Old Subseafloor Sediment. *MBio*, **2021**, 12, e0115021	7.8	3
58	Resistance, resilience, and functional redundancy of freshwater bacterioplankton communities facing a gradient of agricultural stressors in a mesocosm experiment. *Molecular Ecology*, **2021**, 30, 4771-4788	5.7	4
57	Widespread agrochemicals differentially affect zooplankton biomass and community structure. *Ecological Applications*, **2021**, 31, e02423	4.9	5
56	A Combination of Metagenomic and Cultivation Approaches Reveals Hypermutator Phenotypes within Vibrio cholerae-Infected Patients. *MSystems*, **2021**, 6, e0088921	7.6	4
55	Single-colony sequencing reveals microbe-by-microbiome phylosymbiosis between the cyanobacterium Microcystis and its associated bacteria. *Microbiome*, **2021**, 9, 194	16.6	3
54	Metagenomic study to evaluate functional capacity of a cyanobacterial bloom during oxidation. *Chemical Engineering Journal Advances*, **2021**, 8, 100151	3.6	1

53	Community rescue in experimental phytoplankton communities facing severe herbicide pollution. *Nature Ecology and Evolution*, **2020**, 4, 578-588	12.3	21
52	Does diversity beget diversity in microbiomes?. *ELife*, **2020**, 9,	8.9	12
51	Two cases of type-a meningitis within the same week in the same hospital are phylogenetically unrelated but recently exchanged capsule genes. *Microbial Genomics*, **2020**, 6,	4.4	2
50	Benchmarking bacterial genome-wide association study methods using simulated genomes and phenotypes. *Microbial Genomics*, **2020**, 6,	4.4	19
49	The evolution of realized niches within freshwater Synechococcus. *Environmental Microbiology*, **2020**, 22, 1238-1250	5.2	5
48	Diversity Assessment of Toxic Cyanobacterial Blooms during Oxidation. *Toxins*, **2020**, 12,	4.9	9
47	A large-scale assessment of lakes reveals a pervasive signal of land use on bacterial communities. *ISME Journal*, **2020**, 14, 3011-3023	11.9	19
46	Functional Diversity: An Epistemic Roadmap. *BioScience*, **2019**, 69, 800-811	5.7	10
45	Trophic structure modulates community rescue following acidification. *Proceedings of the Royal Society B: Biological Sciences*, **2019**, 286, 20190856	4.4	11
44	Microbial evolutionary medicine: from theory to clinical practice. *Lancet Infectious Diseases, The*, **2019**, 19, e273-e283	25.5	6
43	Coherence of Microcystis species revealed through population genomics. *ISME Journal*, **2019**, 13, 2887-2900	11.9	23
42	Reuniting ecology and evolution. *Environmental Microbiology Reports*, **2019**, 11, 13-14	3.7	
41	What Microbial Population Genomics Has Taught Us About Speciation. *Population Genomics*, **2018**, 31-47	1.4	15
40	Niche Separation Increases With Genetic Distance Among Bloom-Forming Cyanobacteria. *Frontiers in Microbiology*, **2018**, 9, 438	5.7	20
39	Cooking and co-ingested polyphenols reduce in vitro methylmercury bioaccessibility from fish and may alter exposure in humans. *Science of the Total Environment*, **2018**, 616-617, 863-874	10.2	19
38	Gut Microbiome of the Canadian Arctic Inuit. *MSphere*, **2017**, 2,	5	28
37	Mitochondrial Recombination and Introgression during Speciation by Hybridization. *Molecular Biology and Evolution*, **2017**, 34, 1947-1959	8.3	36
36	Characterising and predicting cyanobacterial blooms in an 8-year amplicon sequencing time course. *ISME Journal*, **2017**, 11, 1746-1763	11.9	46

35	The Inuit gut microbiome is dynamic over time and shaped by traditional foods. *Microbiome*, **2017**, 5, 151	16.6	32
34	The population genetics of pangenomes. *Nature Microbiology*, **2017**, 2, 1574	26.6	24
33	Vibrio cholerae genomic diversity within and between patients. *Microbial Genomics*, **2017**, 3,	4.4	20
32	Origins of pandemic Vibrio cholerae from environmental gene pools. *Nature Microbiology*, **2016**, 2, 16240	26.6	31
31	Phenotypic differentiation of Streptococcus pyogenes populations is induced by recombination-driven gene-specific sweeps. *Scientific Reports*, **2016**, 6, 36644	4.9	18
30	What Is Speciation?. *PLoS Genetics*, **2016**, 12, e1005860	6	72
29	Environment and host species shape the skin microbiome of captive neotropical bats. *PeerJ*, **2016**, 4, e2430	3.1	32
28	How clonal are bacteria over time?. *Current Opinion in Microbiology*, **2016**, 31, 116-123	7.9	41
27	The advent of genome-wide association studies for bacteria. *Current Opinion in Microbiology*, **2015**, 25, 17-24	7.9	102
26	Population genomics of Mycobacterium tuberculosis in the Inuit. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 13609-14	11.5	59
25	Clinical Sequencing Uncovers Origins and Evolution of Lassa Virus. *Cell*, **2015**, 162, 738-50	56.2	176
24	Microbial Speciation. *Cold Spring Harbor Perspectives in Biology*, **2015**, 7, a018143	10.2	39
23	Ordering microbial diversity into ecologically and genetically cohesive units. *Trends in Microbiology*, **2014**, 22, 235-47	12.4	120
22	Evolutionary consequences of intra-patient phage predation on microbial populations. *ELife*, **2014**, 3, e03497	8.9	82
21	A phylogeny-based sampling strategy and power calculator informs genome-wide associations study design for microbial pathogens. *Genome Medicine*, **2014**, 6, 101	14.4	25
20	Signatures of natural selection and ecological differentiation in microbial genomes. *Advances in Experimental Medicine and Biology*, **2014**, 781, 339-59	3.6	16
19	Genomic analysis identifies targets of convergent positive selection in drug-resistant Mycobacterium tuberculosis. *Nature Genetics*, **2013**, 45, 1183-9	36.3	295
18	Reproducibility of Vibrionaceae population structure in coastal bacterioplankton. *ISME Journal*, **2013**, 7, 509-19	11.9	45

17	Sympatric speciation: when is it possible in bacteria?. *PLoS ONE*, **2013**, 8, e53539	3.7	31
16	Population genomics of early events in the ecological differentiation of bacteria. *Science*, **2012**, 336, 48-51	33.3	366
15	The slow:fast substitution ratio reveals changing patterns of natural selection in gamma-proteobacterial genomes. *ISME Journal*, **2009**, 3, 1180-92	11.9	5
14	Looking for Darwin¥s footprints in the microbial world. *Trends in Microbiology*, **2009**, 17, 196-204	12.4	71
13	Comparing patterns of natural selection across species using selective signatures. *PLoS Genetics*, **2008**, 4, e23	6	32
12	An experimental test of the causes of small-scale phenotypic differentiation in a population of great tits. *Journal of Evolutionary Biology*, **2006**, 19, 176-83	2.3	14
11	VSG switching in Trypanosoma brucei: antigenic variation analysed using RNAi in the absence of immune selection. *Molecular Microbiology*, **2005**, 57, 1608-22	4.1	34
10	An interactional network of genes involved in chitin synthesis in Saccharomyces cerevisiae. *BMC Genetics*, **2005**, 6, 8	2.6	89
9	Analysis of beta-1,3-glucan assembly in Saccharomyces cerevisiae using a synthetic interaction network and altered sensitivity to caspofungin. *Genetics*, **2004**, 167, 35-49	4	138
8	Global mapping of the yeast genetic interaction network. *Science*, **2004**, 303, 808-13	33.3	1700
7	The Action of Certain Organic Accelerators in the Vulcanization of Rubber▯.. *Journal of Industrial & Engineering Chemistry*, **1921**, 13, 67-70		3
6	Single-colony sequencing reveals phylosymbiosis, co-phylogeny, and horizontal gene transfer between the cyanobacterium Microcystis and its microbiome		1
5	Characterizing and predicting cyanobacterial blooms in an 8-year amplicon sequencing time-course		2
4	Vibrio choleraegenomic diversity within and between patients		2
3	Genome evolution in bacteria isolated from million-year-old subseafloor sediment		1
2	Does diversity beget diversity in microbiomes?		1
1	Classic genome-wide association methods are unlikely to identify causal variants in strongly clonal microbial populations		2