

# Michael S Robeson

## 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.

57  
papers

7,022  
citations

26  
h-index

64  
g-index

64  
ext. papers

11,771  
ext. citations

6.4  
avg, IF

5.04  
L-index

#	Paper	IF	Citations
57	Short-Term Metformin Treatment Enriches in an Obese Liver Steatosis Zucker Rat Model.. <i>Frontiers in Microbiology</i> , <b>2022</b> , 13, 834776	5.7	
56	Bacterial and Fungal Adaptations in Cecum and Distal Colon of Piglets Fed With Dairy-Based Milk Formula in Comparison With Human Milk.. <i>Frontiers in Microbiology</i> , <b>2022</b> , 13, 801854	5.7	
55	Iron deficient diets modify the gut microbiome and reduce the severity of enteric infection in a mouse model of <i>S. Typhimurium</i> -induced enterocolitis. <i>Journal of Nutritional Biochemistry</i> , <b>2022</b> , 109065	6.3	0
54	RESCRIPT: Reproducible sequence taxonomy reference database management. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1009581	5	30
53	Progression of diabetes is associated with changes in the ileal transcriptome and ileal-colon morphology in the UC Davis Type 2 Diabetes Mellitus rat. <i>Physiological Reports</i> , <b>2021</b> , 9, e15102	2.6	0
52	Cultivating the Bacterial Microbiota of Roots. <i>MSystems</i> , <b>2021</b> , 6, e0130620	7.6	5
51	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1009056	5	0
50	Characterization of the bacterial microbiomes of social amoebae and exploration of the roles of host and environment on microbiome composition. <i>Environmental Microbiology</i> , <b>2021</b> , 23, 126-142	5.2	5
49	Multi-omics data integration considerations and study design for biological systems and disease. <i>Molecular Omics</i> , <b>2021</b> , 17, 170-185	4.4	27
48	Mash-based analyses of <i>Escherichia coli</i> genomes reveal 14 distinct phylogroups. <i>Communications Biology</i> , <b>2021</b> , 4, 117	6.7	20
47	Evaluation of DNA extraction protocols from liquid-based cytology specimens for studying cervical microbiota. <i>PLoS ONE</i> , <b>2021</b> , 16, e0237556	3.7	1
46	16S rRNA Gene Amplicon Profiling of Baby and Adult Captive Elephants in Thailand. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	1
45	A phylogenetic model for the recruitment of species into microbial communities and application to studies of the human microbiome. <i>ISME Journal</i> , <b>2020</b> , 14, 1359-1368	11.9	12
44	Mixed ancestry from wild and domestic lineages contributes to the rapid expansion of invasive feral swine. <i>Molecular Ecology</i> , <b>2020</b> , 29, 1103-1119	5.7	10
43	Measuring the microbiome: Best practices for developing and benchmarking microbiomics methods. <i>Computational and Structural Biotechnology Journal</i> , <b>2020</b> , 18, 4048-4062	6.8	15
42	Comparative genomics of hepatitis A virus, hepatitis C virus, and hepatitis E virus provides insights into the evolutionary history of Hepatovirus species. <i>MicrobiologyOpen</i> , <b>2020</b> , 9, e973	3.4	1
41	Genomic characterization of mumps viruses from a large-scale mumps outbreak in Arkansas, 2016. <i>Infection, Genetics and Evolution</i> , <b>2019</b> , 75, 103965	4.5	5

40	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , <b>2019</b> , 37, 852-857	44.5	4050
39	Gastrointestinal Tract Dysbiosis Enhances Distal Tumor Progression through Suppression of Leukocyte Trafficking. <i>Cancer Research</i> , <b>2019</b> , 79, 5999-6009	10.1	16
38	Cervical Microbiome and Response to a Human Papillomavirus Therapeutic Vaccine for Treating High-Grade Cervical Squamous Intraepithelial Lesion. <i>Integrative Cancer Therapies</i> , <b>2019</b> , 18, 15347354193893063		
37	Assessing the utility of metabarcoding for diet analyses of the omnivorous wild pig ( <i>Sus scrofa</i> ). <i>Ecology and Evolution</i> , <b>2018</b> , 8, 185-196	2.8	35
36	Temporal dynamics of gut microbiota in triclocarban-exposed weaned rats. <i>Environmental Science and Pollution Research</i> , <b>2018</b> , 25, 14743-14751	5.1	1
35	Interspecific Plant Interactions Reflected in Soil Bacterial Community Structure and Nitrogen Cycling in Primary Succession. <i>Frontiers in Microbiology</i> , <b>2018</b> , 9, 128	5.7	41
34	Cervical microbiome role in outcomes of therapeutic HPV vaccination for cervical intraepithelial neoplasia.. <i>Journal of Clinical Oncology</i> , <b>2018</b> , 36, 3099-3099	2.2	2
33	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science <b>2018</b> ,		78
32	Temporal Dynamics of In-Field Bioreactor Populations Reflect the Groundwater System and Respond Predictably to Perturbation. <i>Environmental Science &amp; Technology</i> , <b>2017</b> , 51, 2879-2889	10.3	10
31	Scattered far and wide: A broadly distributed temperate dune grass finds familiar fungal root associates in its invasive range. <i>Soil Biology and Biochemistry</i> , <b>2017</b> , 112, 177-190	7.5	6
30	Hypersaline sapropels act as hotspots for microbial dark matter. <i>Scientific Reports</i> , <b>2017</b> , 7, 6150	4.9	7
29	A native and an invasive dune grass share similar, patchily distributed, root-associated fungal communities. <i>Fungal Ecology</i> , <b>2016</b> , 23, 141-155	4.1	13
28	Enrichment of Root Endophytic Bacteria from <i>Populus deltoides</i> and Single-Cell-Genomics Analysis. <i>Applied and Environmental Microbiology</i> , <b>2016</b> , 82, 5698-708	4.8	40
27	Temporal Development of Gut Microbiota in Triclocarban Exposed Pregnant and Neonatal Rats. <i>Scientific Reports</i> , <b>2016</b> , 6, 33430	4.9	18
26	Microbial community composition and diversity in Caspian Sea sediments. <i>FEMS Microbiology Ecology</i> , <b>2015</b> , 91, 1-11	4.3	46
25	Structure, mineralogy, and microbial diversity of geothermal spring microbialites associated with a deep oil drilling in Romania. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 253	5.7	18
24	Contrasting taxonomic stratification of microbial communities in two hypersaline meromictic lakes. <i>ISME Journal</i> , <b>2015</b> , 9, 2642-56	11.9	55
23	PanFP: pangenome-based functional profiles for microbial communities. <i>BMC Research Notes</i> , <b>2015</b> , 8, 479	2.3	28

22	Metabolic functions of <i>Pseudomonas fluorescens</i> strains from <i>Populus deltoides</i> depend on rhizosphere or endosphere isolation compartment. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 1118	5.7	42
21	Seasonal Shifts in Diet and Gut Microbiota of the American Bison ( <i>Bison bison</i> ). <i>PLoS ONE</i> , <b>2015</b> , 10, e0142409	3.7	64
20	Dispersal, niche breadth and population extinction: colonization ratios predict range size in North American dragonflies. <i>Journal of Animal Ecology</i> , <b>2014</b> , 83, 858-65	4.7	24
19	Plant host and soil origin influence fungal and bacterial assemblages in the roots of woody plants. <i>Molecular Ecology</i> , <b>2014</b> , 23, 3356-70	5.7	167
18	Improved yield of high molecular weight DNA coincides with increased microbial diversity access from iron oxide cemented sub-surface clay environments. <i>PLoS ONE</i> , <b>2014</b> , 9, e102826	3.7	18
17	Characterizing microbial communities through space and time. <i>Current Opinion in Biotechnology</i> , <b>2012</b> , 23, 431-6	11.4	73
16	Global distribution of <i>Polaromonas</i> phylotypes--evidence for a highly successful dispersal capacity. <i>PLoS ONE</i> , <b>2011</b> , 6, e23742	3.7	90
15	Phylogeography of microbial phototrophs in the dry valleys of the high Himalayas and Antarctica. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2011</b> , 278, 702-8	4.4	63
14	Soil rotifer communities are extremely diverse globally but spatially autocorrelated locally. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 4406-10	11.5	72
13	Functional shifts in unvegetated, perhumid, recently-deglaciated soils do not correlate with shifts in soil bacterial community composition. <i>Journal of Microbiology</i> , <b>2009</b> , 47, 673-81	3	64
12	Environmental DNA sequencing primers for eutardigrades and bdelloid rotifers. <i>BMC Ecology</i> , <b>2009</b> , 9, 25	2.7	17
11	A comprehensive survey of soil acidobacterial diversity using pyrosequencing and clone library analyses. <i>ISME Journal</i> , <b>2009</b> , 3, 442-53	11.9	727
10	Soil CO <sub>2</sub> flux and photoautotrophic community composition in high-elevation, <del>V</del> arrenVsoil. <i>Environmental Microbiology</i> , <b>2009</b> , 11, 674-86	5.2	65
9	Insights and inferences about integron evolution from genomic data. <i>BMC Genomics</i> , <b>2008</b> , 9, 261	4.5	40
8	Metagenomic and small-subunit rRNA analyses reveal the genetic diversity of bacteria, archaea, fungi, and viruses in soil. <i>Applied and Environmental Microbiology</i> , <b>2007</b> , 73, 7059-66	4.8	406
7	PyCogent: a toolkit for making sense from sequence. <i>Genome Biology</i> , <b>2007</b> , 8, R171	18.3	151
6	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
5	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138

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