

# Michael S Robeson

## List of Publications by Year in descending order

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Version: 2024-02-01

52  
papers

16,010  
citations

218381

26  
h-index

189595

50  
g-index

64  
all docs

64  
docs citations

64  
times ranked

20060  
citing authors

#	ARTICLE	IF	CITATIONS
1	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
2	A comprehensive survey of soil acidobacterial diversity using pyrosequencing and clone library analyses. <i>ISME Journal</i> , 2009, 3, 442-453.	4.4	984
3	Metagenomic and Small-Subunit rRNA Analyses Reveal the Genetic Diversity of Bacteria, Archaea, Fungi, and Viruses in Soil. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7059-7066.	1.4	480
4	Plant host and soil origin influence fungal and bacterial assemblages in the roots of woody plants. <i>Molecular Ecology</i> , 2014, 23, 3356-3370.	2.0	285
5	RESCRIPT: Reproducible sequence taxonomy reference database management. <i>PLoS Computational Biology</i> , 2021, 17, e1009581.	1.5	277
6	PyCogent: a toolkit for making sense from sequence. <i>Genome Biology</i> , 2007, 8, R171.	13.9	170
7	Global Distribution of Polaromonas Phylotypes - Evidence for a Highly Successful Dispersal Capacity. <i>PLoS ONE</i> , 2011, 6, e23742.	1.1	125
8	Seasonal Shifts in Diet and Gut Microbiota of the American Bison ( <i>Bison bison</i> ). <i>PLoS ONE</i> , 2015, 10, e0142409.	1.1	104
9	Characterizing microbial communities through space and time. <i>Current Opinion in Biotechnology</i> , 2012, 23, 431-436.	3.3	98
10	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> , 2011, 108, 4406-4410.	3.3	90
11	Multi-omics data integration considerations and study design for biological systems and disease. <i>Molecular Omics</i> , 2021, 17, 170-185.	1.4	85
12	Soil CO <sub>2</sub> flux and photoautotrophic community composition in high-elevation, barren soil. <i>Environmental Microbiology</i> , 2009, 11, 674-686.	1.8	83
13	Contrasting taxonomic stratification of microbial communities in two hypersaline meromictic lakes. <i>ISME Journal</i> , 2015, 9, 2642-2656.	4.4	82
14	Functional shifts in unvegetated, perhumid, recently-deglaciated soils do not correlate with shifts in soil bacterial community composition. <i>Journal of Microbiology</i> , 2009, 47, 673-681.	1.3	70
15	Microbial community composition and diversity in Caspian Sea sediments. <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-11.	1.3	70
16	Phylogeography of microbial phototrophs in the dry valleys of the high Himalayas and Antarctica. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 702-708.	1.2	66
17	Assessing the utility of metabarcoding for diet analyses of the omnivorous wild pig ( <i>Sus</i> )	0.8	63
18	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> , 2015, 6, 1118.	1.5	60

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19	Interspecific Plant Interactions Reflected in Soil Bacterial Community Structure and Nitrogen Cycling in Primary Succession. <i>Frontiers in Microbiology</i> , 2018, 9, 128.	1.5	57
20	Enrichment of Root Endophytic Bacteria from <i>Populus deltoides</i> and Single-Cell-Genomics Analysis. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5698-5708.	1.4	53
21	Mash-based analyses of <i>Escherichia coli</i> genomes reveal 14 distinct phylogroups. <i>Communications Biology</i> , 2021, 4, 117.	2.0	52
22	Insights and inferences about integron evolution from genomic data. <i>BMC Genomics</i> , 2008, 9, 261.	1.2	51
23	PanFP: pangenome-based functional profiles for microbial communities. <i>BMC Research Notes</i> , 2015, 8, 479.	0.6	38
24	Measuring the microbiome: Best practices for developing and benchmarking microbiomics methods. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 4048-4062.	1.9	37
25	Dispersal, niche breadth and population extinction: colonization ratios predict range size in North American dragonflies. <i>Journal of Animal Ecology</i> , 2014, 83, 858-865.	1.3	33
26	Mixed ancestry from wild and domestic lineages contributes to the rapid expansion of invasive feral swine. <i>Molecular Ecology</i> , 2020, 29, 1103-1119.	2.0	31
27	Environmental DNA sequencing primers for eutardigrades and bdelloid rotifers. <i>BMC Ecology</i> , 2009, 9, 25.	3.0	25
28	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> , 2014, 9, e102826.	1.1	25
29	Temporal Development of Gut Microbiota in Triclocarban Exposed Pregnant and Neonatal Rats. <i>Scientific Reports</i> , 2016, 6, 33430.	1.6	25
30	Structure, mineralogy, and microbial diversity of geothermal spring microbialites associated with a deep oil drilling in Romania. <i>Frontiers in Microbiology</i> , 2015, 6, 253.	1.5	24
31	Gastrointestinal Tract Dysbiosis Enhances Distal Tumor Progression through Suppression of Leukocyte Trafficking. <i>Cancer Research</i> , 2019, 79, 5999-6009.	0.4	21
32	A phylogenetic model for the recruitment of species into microbial communities and application to studies of the human microbiome. <i>ISME Journal</i> , 2020, 14, 1359-1368.	4.4	21
33	Cultivating the Bacterial Microbiota of <i>Populus</i> Roots. <i>MSystems</i> , 2021, 6, e0130620.	1.7	17
34	Temporal Dynamics of In-Field Bioreactor Populations Reflect the Groundwater System and Respond Predictably to Perturbation. <i>Environmental Science &amp; Technology</i> , 2017, 51, 2879-2889.	4.6	15
35	Hypersaline sapropels act as hotspots for microbial dark matter. <i>Scientific Reports</i> , 2017, 7, 6150.	1.6	15
36	A native and an invasive dune grass share similar, patchily distributed, root-associated fungal communities. <i>Fungal Ecology</i> , 2016, 23, 141-155.	0.7	14

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37	Characterization of the bacterial microbiomes of social amoebae and exploration of the roles of host and environment on microbiome composition. <i>Environmental Microbiology</i> , 2021, 23, 126-142.	1.8	14
38	Genomic characterization of mumps viruses from a large-scale mumps outbreak in Arkansas, 2016. <i>Infection, Genetics and Evolution</i> , 2019, 75, 103965.	1.0	11
39	Cervical Microbiome and Response to a Human Papillomavirus Therapeutic Vaccine for Treating High-Grade Cervical Squamous Intraepithelial Lesion. <i>Integrative Cancer Therapies</i> , 2019, 18, 153473541989306.	0.8	9
40	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> , 2021, 9, e15102.	0.7	9
41	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> , 2017, 112, 177-190.	4.2	8
42	16S rRNA Gene Amplicon Profiling of Baby and Adult Captive Elephants in Thailand. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	7
43	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> , 2022, 107, 109065.	1.9	7
44	Comparative genomics of hepatitis A virus, hepatitis C virus, and hepatitis E virus provides insights into the evolutionary history of <i>Hepatovirus</i> species. <i>MicrobiologyOpen</i> , 2020, 9, e973.	1.2	5
45	Using DNA Metabarcoding to Examine Wild Pig ( <i>Sus scrofa</i> ) Diets in a Subtropical Agro-Ecosystem. <i>Proceedings of the Vertebrate Pest Conference</i> , 0, 28, .	0.1	5
46	Evaluation of DNA extraction protocols from liquid-based cytology specimens for studying cervical microbiota. <i>PLoS ONE</i> , 2021, 16, e0237556.	1.1	4
47	Temporal dynamics of gut microbiota in triclocarban-exposed weaned rats. <i>Environmental Science and Pollution Research</i> , 2018, 25, 14743-14751.	2.7	3
48	Cervical microbiome role in outcomes of therapeutic HPV vaccination for cervical intraepithelial neoplasia. <i>Journal of Clinical Oncology</i> , 2018, 36, 3099-3099.	0.8	3
49	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. <i>PLoS Computational Biology</i> , 2021, 17, e1009056.	1.5	2
50	Short-Term Metformin Treatment Enriches <i>Bacteroides dorei</i> in an Obese Liver Steatosis Zucker Rat Model. <i>Frontiers in Microbiology</i> , 2022, 13, 834776.	1.5	2
51	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> , 2022, 13, 801854.	1.5	1
52	Microbial composition in the nose of children with and without viruses during asthma exacerbations. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, AB179.	1.5	0