

Michael S Robeson

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

16,010
citations

218677
26
h-index

189892
50
g-index

64
all docs

64
docs citations

64
times ranked

20060
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	3.5	2
2	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.	3.5	1
3	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.	4.2	7
4	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.	3.8	14
5	Multi-omics data integration considerations and study design for biological systems and disease. <i>Molecular Omics</i> , 2021, 17, 170-185.	2.8	85
6	Mash-based analyses of <i>Escherichia coli</i> genomes reveal 14 distinct phylogroups. <i>Communications Biology</i> , 2021, 4, 117.	4.4	52
7	Cultivating the Bacterial Microbiota of <i>Populus</i> Roots. <i>MSystems</i> , 2021, 6, e0130620.	3.8	17
8	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. <i>PLoS Computational Biology</i> , 2021, 17, e1009056.	3.2	2
9	Evaluation of DNA extraction protocols from liquid-based cytology specimens for studying cervical microbiota. <i>PLoS ONE</i> , 2021, 16, e0237556.	2.5	4
10	RESCRIPT: Reproducible sequence taxonomy reference database management. <i>PLoS Computational Biology</i> , 2021, 17, e1009581.	3.2	277
11	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.	1.7	9
12	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.	3.0	5
13	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.	2.9	0
14	16S rRNA Gene Amplicon Profiling of Baby and Adult Captive Elephants in Thailand. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	7
15	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.	9.8	21
16	Mixed ancestry from wild and domestic lineages contributes to the rapid expansion of invasive feral swine. <i>Molecular Ecology</i> , 2020, 29, 1103-1119.	3.9	31
17	Measuring the microbiome: Best practices for developing and benchmarking microbiomics methods. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 4048-4062.	4.1	37
18	Genomic characterization of mumps viruses from a large-scale mumps outbreak in Arkansas, 2016. <i>Infection, Genetics and Evolution</i> , 2019, 75, 103965.	2.3	11

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19	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	17.5	11,167
20	Gastrointestinal Tract Dysbiosis Enhances Distal Tumor Progression through Suppression of Leukocyte Trafficking. <i>Cancer Research</i> , 2019, 79, 5999-6009.	0.9	21
21	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.	2.0	9
22	Assessing the utility of metabarcoding for diet analyses of the omnivorous wild pig (<i>Sus</i> Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 T	1.9	63
23	Temporal dynamics of gut microbiota in triclocarban-exposed weaned rats. <i>Environmental Science and Pollution Research</i> , 2018, 25, 14743-14751.	5.3	3
24	Interspecific Plant Interactions Reflected in Soil Bacterial Community Structure and Nitrogen Cycling in Primary Succession. <i>Frontiers in Microbiology</i> , 2018, 9, 128.	3.5	57
25	Cervical microbiome role in outcomes of therapeutic HPV vaccination for cervical intraepithelial neoplasia.. <i>Journal of Clinical Oncology</i> , 2018, 36, 3099-3099.	1.6	3
26	Temporal Dynamics of In-Field Bioreactor Populations Reflect the Groundwater System and Respond Predictably to Perturbation. <i>Environmental Science & Technology</i> , 2017, 51, 2879-2889.	10.0	15
27	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.	8.8	8
28	Hypersaline sapropels act as hotspots for microbial dark matter. <i>Scientific Reports</i> , 2017, 7, 6150.	3.3	15
29	Temporal Development of Gut Microbiota in Triclocarban Exposed Pregnant and Neonatal Rats. <i>Scientific Reports</i> , 2016, 6, 33430.	3.3	25
30	A native and an invasive dune grass share similar, patchily distributed, root-associated fungal communities. <i>Fungal Ecology</i> , 2016, 23, 141-155.	1.6	14
31	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.	3.1	53
32	PanFP: pangenome-based functional profiles for microbial communities. <i>BMC Research Notes</i> , 2015, 8, 479.	1.4	38
33	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.	3.5	60
34	Seasonal Shifts in Diet and Gut Microbiota of the American Bison (<i>Bison bison</i>). <i>PLoS ONE</i> , 2015, 10, e0142409.	2.5	104
35	Microbial community composition and diversity in Caspian Sea sediments. <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-11.	2.7	70
36	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.	3.5	24

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37	Contrasting taxonomic stratification of microbial communities in two hypersaline meromictic lakes. ISME Journal, 2015, 9, 2642-2656.	9.8	82
38	Improved Yield of High Molecular Weight DNA Coincides with Increased Microbial Diversity Access from Iron Oxide Cemented Sub-Surface Clay Environments. PLoS ONE, 2014, 9, e102826.	2.5	25
39	Dispersal, niche breadth and population extinction: colonization ratios predict range size in <scp>N</scp>orth <scp>A</scp>merican dragonflies. Journal of Animal Ecology, 2014, 83, 858-865.	2.8	33
40	Plant host and soil origin influence fungal and bacterial assemblages in the roots of woody plants. Molecular Ecology, 2014, 23, 3356-3370.	3.9	285
41	Characterizing microbial communities through space and time. Current Opinion in Biotechnology, 2012, 23, 431-436.	6.6	98
42	Global Distribution of Polaromonas Phylotypes - Evidence for a Highly Successful Dispersal Capacity. PLoS ONE, 2011, 6, e23742.	2.5	125
43	Phylogeography of microbial phototrophs in the dry valleys of the high Himalayas and Antarctica. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 702-708.	2.6	66
44	Soil rotifer communities are extremely diverse globally but spatially autocorrelated locally. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4406-4410.	7.1	90
45	Functional shifts in unvegetated, perhumid, recently-deglaciated soils do not correlate with shifts in soil bacterial community composition. Journal of Microbiology, 2009, 47, 673-681.	2.8	70
46	Environmental DNA sequencing primers for eutardigrades and bdelloid rotifers. BMC Ecology, 2009, 9, 25.	3.0	25
47	A comprehensive survey of soil acidobacterial diversity using pyrosequencing and clone library analyses. ISME Journal, 2009, 3, 442-453.	9.8	984
48	Soil CO ₂ flux and photoautotrophic community composition in high elevation, "barren" soil. Environmental Microbiology, 2009, 11, 674-686.	3.8	83
49	Insights and inferences about integron evolution from genomic data. BMC Genomics, 2008, 9, 261.	2.8	51
50	PyCogent: a toolkit for making sense from sequence. Genome Biology, 2007, 8, R171.	9.6	170
51	Metagenomic and Small-Subunit rRNA Analyses Reveal the Genetic Diversity of Bacteria, Archaea, Fungi, and Viruses in Soil. Applied and Environmental Microbiology, 2007, 73, 7059-7066.	3.1	480
52	Using DNA Metabarcoding to Examine Wild Pig (Sus scrofa) Diets in a Subtropical Agro-Ecosystem. Proceedings of the Vertebrate Pest Conference, 0, 28, .	0.1	5