

# 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  | Short-Term Metformin Treatment Enriches <i>Bacteroides doei</i> in an Obese Liver Steatosis Zucker Rat Model. <i>Frontiers in Microbiology</i> , 2022, 13, 834776.  | 1.5 | 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.                                   | 1.5 | 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. | 1.9 | 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.                        | 1.8 | 14        |
| 5  | Multi-omics data integration considerations and study design for biological systems and disease. <i>Molecular Omics</i> , 2021, 17, 170-185.  | 1.4 | 85        |
| 6  | Mash-based analyses of <i>Escherichia coli</i> genomes reveal 14 distinct phylogroups. <i>Communications Biology</i> , 2021, 4, 117.  | 2.0 | 52        |
| 7  | Cultivating the Bacterial Microbiota of <i>Populus</i> Roots. <i>MSystems</i> , 2021, 6, e0130620.  | 1.7 | 17        |
| 8  | Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. <i>PLoS Computational Biology</i> , 2021, 17, e1009056.   | 1.5 | 2         |
| 9  | Evaluation of DNA extraction protocols from liquid-based cytology specimens for studying cervical microbiota. <i>PLoS ONE</i> , 2021, 16, e0237556.   | 1.1 | 4         |
| 10 | RESCRIPT: Reproducible sequence taxonomy reference database management. <i>PLoS Computational Biology</i> , 2021, 17, e1009581.   | 1.5 | 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.                        | 0.7 | 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.                   | 1.2 | 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.   | 1.5 | 0         |
| 14 | 16S rRNA Gene Amplicon Profiling of Baby and Adult Captive Elephants in Thailand. <i>Microbiology Resource Announcements</i> , 2020, 9, .   | 0.3 | 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.   | 4.4 | 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.  | 2.0 | 31        |
| 17 | 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        |
| 18 | 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        |

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|----|---|-----|-----------|
| 19 | Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.  | 9.4 | 11,167    |
| 20 | Gastrointestinal Tract Dysbiosis Enhances Distal Tumor Progression through Suppression of Leukocyte Trafficking. <i>Cancer Research</i> , 2019, 79, 5999-6009.  | 0.4 | 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. | 0.8 | 9         |
| 22 | Assessing the utility of metabarcoding for diet analyses of the omnivorous wild pig ( <i>Sus</i> ). <i>Overlook 10 Tf 50 622 T</i>  | 0.8 | 63        |
| 23 | Temporal dynamics of gut microbiota in triclocarban-exposed weaned rats. <i>Environmental Science and Pollution Research</i> , 2018, 25, 14743-14751.   | 2.7 | 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.                                     | 1.5 | 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.  | 0.8 | 3         |
| 26 | 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        |
| 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.                        | 4.2 | 8         |
| 28 | Hypersaline sapropels act as hotspots for microbial dark matter. <i>Scientific Reports</i> , 2017, 7, 6150.   | 1.6 | 15        |
| 29 | Temporal Development of Gut Microbiota in Triclocarban Exposed Pregnant and Neonatal Rats. <i>Scientific Reports</i> , 2016, 6, 33430.  | 1.6 | 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.   | 0.7 | 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.                                      | 1.4 | 53        |
| 32 | PanFP: pangenome-based functional profiles for microbial communities. <i>BMC Research Notes</i> , 2015, 8, 479.   | 0.6 | 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.          | 1.5 | 60        |
| 34 | Seasonal Shifts in Diet and Gut Microbiota of the American Bison ( <i>Bison bison</i> ). <i>PLoS ONE</i> , 2015, 10, e0142409.  | 1.1 | 104       |
| 35 | Microbial community composition and diversity in Caspian Sea sediments. <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-11.  | 1.3 | 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.                                | 1.5 | 24        |

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|----|--|------|-----------|
| 37 | Contrasting taxonomic stratification of microbial communities in two hypersaline meromictic lakes. <i>ISME Journal</i> , 2015, 9, 2642-2656.   | 4.4  | 82        |
| 38 | 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        |
| 39 | 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        |
| 40 | 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       |
| 41 | Characterizing microbial communities through space and time. <i>Current Opinion in Biotechnology</i> , 2012, 23, 431-436.  | 3.3  | 98        |
| 42 | Global Distribution of Polaromonas Phylotypes - Evidence for a Highly Successful Dispersal Capacity. <i>PLoS ONE</i> , 2011, 6, e23742.  | 1.1  | 125       |
| 43 | 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        |
| 44 | 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        |
| 45 | 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        |
| 46 | Environmental DNA sequencing primers for eutardigrades and bdelloid rotifers. <i>BMC Ecology</i> , 2009, 9, 25.  | 3.0  | 25        |
| 47 | A comprehensive survey of soil acidobacterial diversity using pyrosequencing and clone library analyses. <i>ISME Journal</i> , 2009, 3, 442-453.   | 4.4  | 984       |
| 48 | 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        |
| 49 | Insights and inferences about integron evolution from genomic data. <i>BMC Genomics</i> , 2008, 9, 261.  | 1.2  | 51        |
| 50 | PyCogent: a toolkit for making sense from sequence. <i>Genome Biology</i> , 2007, 8, R171.   | 13.9 | 170       |
| 51 | 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       |
| 52 | 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         |