

# Robert M Bowers

## List of Publications by Year in descending order

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Version: 2024-02-01

34  
papers

5,110  
citations

236925

25  
h-index

377865

34  
g-index

34  
all docs

34  
docs citations

34  
times ranked

7019  
citing authors

#	ARTICLE	IF	CITATIONS
1	Metagenomes and Metagenome-Assembled Genomes from Substrate-Amended Hot Spring Sediment Incubations from Yellowstone National Park. <i>Microbiology Resource Announcements</i> , 2022, 11, e0106521.	0.6	2
2	Dissecting the dominant hot spring microbial populations based on community-wide sampling at single-cell genomic resolution. <i>ISME Journal</i> , 2022, 16, 1337-1347.	9.8	15
3	High Potential for Biomass-Degrading Enzymes Revealed by Hot Spring Metagenomics. <i>Frontiers in Microbiology</i> , 2021, 12, 668238.	3.5	16
4	Zymomonas diversity and potential for biofuel production. <i>Biotechnology for Biofuels</i> , 2021, 14, 112.	6.2	10
5	Function-driven single-cell genomics uncovers cellulose-degrading bacteria from the rare biosphere. <i>ISME Journal</i> , 2020, 14, 659-675.	9.8	69
6	Ecological and genomic analyses of candidate phylum <sc>WPS</sc> bacteria in an unvegetated soil. <i>Environmental Microbiology</i> , 2020, 22, 3143-3157.	3.8	42
7	A pipeline for targeted metagenomics of environmental bacteria. <i>Microbiome</i> , 2020, 8, 21.	11.1	39
8	Community ecology across bacteria, archaea and microbial eukaryotes in the sediment and seawater of coastal Puerto Nuevo, Baja California. <i>PLoS ONE</i> , 2019, 14, e0212355.	2.5	44
9	Sequencing of Genomes from Environmental Single Cells. <i>Methods in Molecular Biology</i> , 2018, 1712, 97-111.	0.9	1
10	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	17.5	1,512
11	Towards a balanced view of the bacterial tree of life. <i>Microbiome</i> , 2017, 5, 140.	11.1	102
12	Analysis of single-cell genome sequences of bacteria and archaea. <i>Emerging Topics in Life Sciences</i> , 2017, 1, 249-255.	2.6	10
13	Next generation sequencing data of a defined microbial mock community. <i>Scientific Data</i> , 2016, 3, 160081.	5.3	90
14	Insights into the single cell draft genome of <i>Candidatus Achromatium palustre</i> . <i>Standards in Genomic Sciences</i> , 2016, 11, 28.	1.5	13
15	Novel microbial assemblages inhabiting crustal fluids within mid-ocean ridge flank subsurface basalt. <i>ISME Journal</i> , 2016, 10, 2033-2047.	9.8	59
16	High-resolution phylogenetic microbial community profiling. <i>ISME Journal</i> , 2016, 10, 2020-2032.	9.8	232
17	Impact of library preparation protocols and template quantity on the metagenomic reconstruction of a mock microbial community. <i>BMC Genomics</i> , 2015, 16, 856.	2.8	79
18	Activity and phylogenetic diversity of sulfate-reducing microorganisms in low-temperature subsurface fluids within the upper oceanic crust. <i>Frontiers in Microbiology</i> , 2014, 5, 748.	3.5	53

#	ARTICLE	IF	CITATIONS
19	Seasonal Variability in Bacterial and Fungal Diversity of the Near-Surface Atmosphere. <i>Environmental Science &amp; Technology</i> , 2013, 47, 12097-12106.	10.0	349
20	Co-habiting amphibian species harbor unique skin bacterial communities in wild populations. <i>ISME Journal</i> , 2012, 6, 588-596.	9.8	282
21	Seasonal variability in airborne bacterial communities at a high-elevation site. <i>Atmospheric Environment</i> , 2012, 50, 41-49.	4.1	226
22	Effect of template on generating a standard curve for absolute quantification of an RNA virus by real-time reverse transcriptase-polymerase chain reaction. <i>Molecular and Cellular Probes</i> , 2011, 25, 60-64.	2.1	20
23	Spatial variability in airborne bacterial communities across land-use types and their relationship to the bacterial communities of potential source environments. <i>ISME Journal</i> , 2011, 5, 601-612.	9.8	385
24	Sources of Bacteria in Outdoor Air across Cities in the Midwestern United States. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6350-6356.	3.1	237
25	Fungal growth on a common wood substrate across a tropical elevation gradient: Temperature sensitivity, community composition, and potential for above-ground decomposition. <i>Soil Biology and Biochemistry</i> , 2010, 42, 1083-1090.	8.8	61
26	Expression of a foreign epitope on infectious pancreatic necrosis virus VP2 capsid protein subviral particle (SVP) and immunogenicity in rainbow trout. <i>Antiviral Research</i> , 2010, 85, 525-531.	4.1	27
27	The ecology of the phyllosphere: geographic and phylogenetic variability in the distribution of bacteria on tree leaves. <i>Environmental Microbiology</i> , 2010, 12, 2885-2893.	3.8	574
28	The contribution of biological particles to observed particulate organic carbon at a remote high altitude site. <i>Atmospheric Environment</i> , 2009, 43, 4278-4282.	4.1	41
29	Validation of reference genes for quantitative measurement of immune gene expression in shrimp. <i>Molecular Immunology</i> , 2009, 46, 1688-1695.	2.2	78
30	Characterization of Airborne Microbial Communities at a High-Elevation Site and Their Potential To Act as Atmospheric Ice Nuclei. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5121-5130.	3.1	273
31	Detection and quantification of infectious hematopoietic necrosis virus in rainbow trout ( <i>Oncorhynchus mykiss</i> ) by SYBR Green real-time reverse transcriptase-polymerase chain reaction. <i>Journal of Virological Methods</i> , 2008, 147, 157-166.	2.1	26
32	Detection and quantitation of infectious pancreatic necrosis virus by real-time reverse transcriptase-polymerase chain reaction using lethal and non-lethal tissue sampling. <i>Journal of Virological Methods</i> , 2008, 147, 226-234.	2.1	76
33	cDNA Microarrays as a Tool for Identification of Biomineralization Proteins in the Coccolithophorid <i>Emiliana huxleyi</i> (Haptophyta). <i>Applied and Environmental Microbiology</i> , 2006, 72, 5512-5526.	3.1	36
34	Suppressive Subtractive Hybridization of and Differences in Gene Expression Content of Calcifying and Noncalcifying Cultures of <i>Emiliana huxleyi</i> Strain 1516. <i>Applied and Environmental Microbiology</i> , 2005, 71, 2564-2575.	3.1	31