

Susannah Green Tringe

List of Publications by Year in descending order

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Version: 2024-02-01

172
papers

32,782
citations

6613

79
h-index

4774

169
g-index

198
all docs

198
docs citations

198
times ranked

27668
citing authors

#	ARTICLE	IF	CITATIONS
1	Defining the core <i>Arabidopsis thaliana</i> root microbiome. <i>Nature</i> , 2012, 488, 86-90.	27.8	2,475
2	Diversity and heritability of the maize rhizosphere microbiome under field conditions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 6548-6553.	7.1	1,594
3	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
4	Comparative Metagenomics of Microbial Communities. <i>Science</i> , 2005, 308, 554-557.	12.6	1,432
5	Plant-microbiome interactions: from community assembly to plant health. <i>Nature Reviews Microbiology</i> , 2020, 18, 607-621.	28.6	1,381
6	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007, 450, 560-565.	27.8	1,181
7	Metagenomic Discovery of Biomass-Degrading Genes and Genomes from Cow Rumen. <i>Science</i> , 2011, 331, 463-467.	12.6	1,135
8	Salicylic acid modulates colonization of the root microbiome by specific bacterial taxa. <i>Science</i> , 2015, 349, 860-864.	12.6	957
9	Recovery of genomes from metagenomes via a dereplication, aggregation and scoring strategy. <i>Nature Microbiology</i> , 2018, 3, 836-843.	13.3	906
10	Host genotype and age shape the leaf and root microbiomes of a wild perennial plant. <i>Nature Communications</i> , 2016, 7, 12151.	12.8	754
11	Plant compartment and biogeography affect microbiome composition in cultivated and native <i>Agave</i> species. <i>New Phytologist</i> , 2016, 209, 798-811.	7.3	663
12	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2012, 6, 1715-1727.	9.8	547
13	Genomic Expansion of Domain Archaea Highlights Roles for Organisms from New Phyla in Anaerobic Carbon Cycling. <i>Current Biology</i> , 2015, 25, 690-701.	3.9	522
14	MaxBin: an automated binning method to recover individual genomes from metagenomes using an expectation-maximization algorithm. <i>Microbiome</i> , 2014, 2, 26.	11.1	521
15	Community genomic analyses constrain the distribution of metabolic traits across the Chloroflexi phylum and indicate roles in sediment carbon cycling. <i>Microbiome</i> , 2013, 1, 22.	11.1	493
16	Metagenomics: DNA sequencing of environmental samples. <i>Nature Reviews Genetics</i> , 2005, 6, 805-814.	16.3	488
17	Genomic features of bacterial adaptation to plants. <i>Nature Genetics</i> , 2018, 50, 138-150.	21.4	480
18	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457

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19	Primer and platform effects on 16S rRNA tag sequencing. <i>Frontiers in Microbiology</i> , 2015, 6, 771.	3.5	435
20	Large-scale replicated field study of maize rhizosphere identifies heritable microbes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7368-7373.	7.1	435
21	A renaissance for the pioneering 16S rRNA gene. <i>Current Opinion in Microbiology</i> , 2008, 11, 442-446.	5.1	418
22	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
23	Microbial dark matter ecogenomics reveals complex synergistic networks in a methanogenic bioreactor. <i>ISME Journal</i> , 2015, 9, 1710-1722.	9.8	360
24	High-Throughput Metagenomic Technologies for Complex Microbial Community Analysis: Open and Closed Formats. <i>MBio</i> , 2015, 6, .	4.1	357
25	Diverse uncultivated ultra-small bacterial cells in groundwater. <i>Nature Communications</i> , 2015, 6, 6372.	12.8	342
26	Metagenomic insights into evolution of a heavy metal-contaminated groundwater microbial community. <i>ISME Journal</i> , 2010, 4, 660-672.	9.8	332
27	Clades of huge phages from across Earth's ecosystems. <i>Nature</i> , 2020, 578, 425-431.	27.8	331
28	Metagenome of a Versatile Chemolithoautotroph from Expanding Oceanic Dead Zones. <i>Science</i> , 2009, 326, 578-582.	12.6	312
29	Tackling soil diversity with the assembly of large, complex metagenomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4904-4909.	7.1	305
30	Deep-sea bacteria enriched by oil and dispersant from the Deepwater Horizon spill. <i>Environmental Microbiology</i> , 2012, 14, 2405-2416.	3.8	275
31	IMG/M 4 version of the integrated metagenome comparative analysis system. <i>Nucleic Acids Research</i> , 2014, 42, D568-D573.	14.5	270
32	Natural soil microbes alter flowering phenology and the intensity of selection on flowering time in a wild <i>Arabidopsis</i> relative. <i>Ecology Letters</i> , 2014, 17, 717-726.	6.4	266
33	Targeted metagenomics and ecology of globally important uncultured eukaryotic phytoplankton. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14679-14684.	7.1	257
34	High-resolution metagenomics targets specific functional types in complex microbial communities. <i>Nature Biotechnology</i> , 2008, 26, 1029-1034.	17.5	254
35	The metagenome of the marine anammox bacterium <i>Candidatus Scalindua profunda</i> illustrates the versatility of this globally important nitrogen cycle bacterium. <i>Environmental Microbiology</i> , 2013, 15, 1275-1289.	3.8	246
36	High-resolution phylogenetic microbial community profiling. <i>ISME Journal</i> , 2016, 10, 2020-2032.	9.8	232

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37	Hydrazine Synthase, a Unique Phylomarker with Which To Study the Presence and Biodiversity of Anammox Bacteria. <i>Applied and Environmental Microbiology</i> , 2012, 78, 752-758.	3.1	228
38	Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. <i>ISME Journal</i> , 2016, 10, 1589-1601.	9.8	226
39	The Cacti Microbiome: Interplay between Habitat-Filtering and Host-Specificity. <i>Frontiers in Microbiology</i> , 2016, 7, 150.	3.5	219
40	An Insect Herbivore Microbiome with High Plant Biomass-Degrading Capacity. <i>PLoS Genetics</i> , 2010, 6, e1001129.	3.5	213
41	Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. <i>Nature Communications</i> , 2013, 4, 2120.	12.8	201
42	Single-cell and metagenomic analyses indicate a fermentative and saccharolytic lifestyle for members of the OP9 lineage. <i>Nature Communications</i> , 2013, 4, 1854.	12.8	199
43	Interactions between plants and soil shaping the root microbiome under abiotic stress. <i>Biochemical Journal</i> , 2019, 476, 2705-2724.	3.7	198
44	The YNP metagenome project: environmental parameters responsible for microbial distribution in the Yellowstone geothermal ecosystem. <i>Frontiers in Microbiology</i> , 2013, 4, 67.	3.5	196
45	Building the crops of tomorrow: advantages of symbiont-based approaches to improving abiotic stress tolerance. <i>Frontiers in Microbiology</i> , 2014, 5, 283.	3.5	196
46	Biocorrosive Thermophilic Microbial Communities in Alaskan North Slope Oil Facilities. <i>Environmental Science & Technology</i> , 2009, 43, 7977-7984.	10.0	195
47	The Airborne Metagenome in an Indoor Urban Environment. <i>PLoS ONE</i> , 2008, 3, e1862.	2.5	192
48	Division of labor in honey bee gut microbiota for plant polysaccharide digestion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25909-25916.	7.1	191
49	Comparative analyses of foregut and hindgut bacterial communities in hoatzins and cows. <i>ISME Journal</i> , 2012, 6, 531-541.	9.8	186
50	Validation of two ribosomal RNA removal methods for microbial metatranscriptomics. <i>Nature Methods</i> , 2010, 7, 807-812.	19.0	184
51	Transcriptional response of bathypelagic marine bacterioplankton to the Deepwater Horizon oil spill. <i>ISME Journal</i> , 2013, 7, 2315-2329.	9.8	172
52	Peatland <i>Acidobacteria</i> with a dissimilatory sulfur metabolism. <i>ISME Journal</i> , 2018, 12, 1729-1742.	9.8	168
53	Metagenomic Insights into the Uncultured Diversity and Physiology of Microbes in Four Hypersaline Soda Lake Brines. <i>Frontiers in Microbiology</i> , 2016, 7, 211.	3.5	161
54	Consortia of low-abundance bacteria drive sulfate reduction-dependent degradation of fermentation products in peat soil microcosms. <i>ISME Journal</i> , 2016, 10, 2365-2375.	9.8	159

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55	Comparative Metagenomic and Metatranscriptomic Analysis of Hindgut Paunch Microbiota in Wood- and Dung-Feeding Higher Termites. PLoS ONE, 2013, 8, e61126.	2.5	149
56	A metagenomic insight into freshwater methane-utilizing communities and evidence for cooperation between the <i>Methylococcaceae</i> and the <i>Methylophilaceae</i> . PeerJ, 2013, 1, e23.	2.0	139
57	Niche differentiation is spatially and temporally regulated in the rhizosphere. ISME Journal, 2020, 14, 999-1014.	9.8	135
58	Phage-bacteria relationships and CRISPR elements revealed by a metagenomic survey of the rumen microbiome. Environmental Microbiology, 2012, 14, 207-227.	3.8	128
59	Relationship between Abundance and Specific Activity of Bacterioplankton in Open Ocean Surface Waters. Applied and Environmental Microbiology, 2013, 79, 177-184.	3.1	127
60	Metagenomic and metaproteomic insights into bacterial communities in leaf-cutter ant fungus gardens. ISME Journal, 2012, 6, 1688-1701.	9.8	126
61	Metagenomic Profiling Reveals Lignocellulose Degrading System in a Microbial Community Associated with a Wood-Feeding Beetle. PLoS ONE, 2013, 8, e73827.	2.5	125
62	Community-wide plasmid gene mobilization and selection. ISME Journal, 2013, 7, 1173-1186.	9.8	124
63	Proteogenomic analyses indicate bacterial methylotrophy and archaeal heterotrophy are prevalent below the grass root zone. PeerJ, 2016, 4, e2687.	2.0	124
64	Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. Genome Research, 2015, 25, 534-543.	5.5	121
65	Community proteogenomics reveals the systemic impact of phosphorus availability on microbial functions in tropical soil. Nature Ecology and Evolution, 2018, 2, 499-509.	7.8	116
66	Multiple syntrophic interactions in a terephthalate-degrading methanogenic consortium. ISME Journal, 2011, 5, 122-130.	9.8	114
67	Community Structure and Function of High-Temperature Chlorophototrophic Microbial Mats Inhabiting Diverse Geothermal Environments. Frontiers in Microbiology, 2013, 4, 106.	3.5	112
68	The metagenomic basis of anammox metabolism in <i>Candidatus</i> <i>Brocadia fulgida</i> TM . Biochemical Society Transactions, 2011, 39, 1799-1804.	3.4	110
69	High level of intergenera gene exchange shapes the evolution of haloarchaea in an isolated Antarctic lake. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16939-16944.	7.1	105
70	Landscape topography structures the soil microbiome in arctic polygonal tundra. Nature Communications, 2018, 9, 777.	12.8	105
71	Comparative genomics of two <i>Candidatus</i> <i>Accumulibacter</i> TM clades performing biological phosphorus removal. ISME Journal, 2013, 7, 2301-2314.	9.8	101
72	<i>Leucoagaricus gongylophorus</i> Produces Diverse Enzymes for the Degradation of Recalcitrant Plant Polymers in Leaf-Cutter Ant Fungus Gardens. Applied and Environmental Microbiology, 2013, 79, 3770-3778.	3.1	98

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73	Gill bacteria enable a novel digestive strategy in a wood-feeding mollusk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5096-104.	7.1	98
74	Metatranscriptomic insights on gene expression and regulatory controls in <i>Candidatus</i> <i>Accumulibacter phosphatis</i> . <i>ISME Journal</i> , 2016, 10, 810-822.	9.8	98
75	The Metagenome of an Anaerobic Microbial Community Decomposing Poplar Wood Chips. <i>PLoS ONE</i> , 2012, 7, e36740.	2.5	98
76	A genomic perspective on stoichiometric regulation of soil carbon cycling. <i>ISME Journal</i> , 2017, 11, 2652-2665.	9.8	97
77	Convergent Bacterial Microbiotas in the Fungal Agricultural Systems of Insects. <i>MBio</i> , 2014, 5, e02077.	4.1	96
78	Ecophysiology of an uncultivated lineage of Aigarchaeota from an oxic, hot spring filamentous "streamer" community. <i>ISME Journal</i> , 2016, 10, 210-224.	9.8	94
79	FOAM (Functional Ontology Assignments for Metagenomes): a Hidden Markov Model (HMM) database with environmental focus. <i>Nucleic Acids Research</i> , 2014, 42, e145-e145.	14.5	90
80	Patterns in Wetland Microbial Community Composition and Functional Gene Repertoire Associated with Methane Emissions. <i>MBio</i> , 2015, 6, e00066-15.	4.1	90
81	Aquifer environment selects for microbial species cohorts in sediment and groundwater. <i>ISME Journal</i> , 2015, 9, 1846-1856.	9.8	88
82	The rhizosphere microbiome of burned holm-oak: potential role of the genus <i>Arthrobacter</i> in the recovery of burned soils. <i>Scientific Reports</i> , 2017, 7, 6008.	3.3	88
83	Geoarchaeota: a new candidate phylum in the Archaea from high-temperature acidic iron mats in Yellowstone National Park. <i>ISME Journal</i> , 2013, 7, 622-634.	9.8	87
84	Ecophysiology of Freshwater Verrucomicrobia Inferred from Metagenome-Assembled Genomes. <i>MSphere</i> , 2017, 2, .	2.9	87
85	Microbial Iron Cycling in Acidic Geothermal Springs of Yellowstone National Park: Integrating Molecular Surveys, Geochemical Processes, and Isolation of Novel Fe-Active Microorganisms. <i>Frontiers in Microbiology</i> , 2012, 3, 109.	3.5	82
86	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
87	Temporal dynamics of fibrolytic and methanogenic rumen microorganisms during in situ incubation of switchgrass determined by 16S rRNA gene profiling. <i>Frontiers in Microbiology</i> , 2014, 5, 307.	3.5	78
88	Conversion of Amazon rainforest to agriculture alters community traits of methane-cycling organisms. <i>Molecular Ecology</i> , 2017, 26, 1547-1556.	3.9	78
89	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. <i>Frontiers in Microbiology</i> , 2015, 6, 1205.	3.5	77
90	Contrasting patterns of genome-level diversity across distinct co-occurring bacterial populations. <i>ISME Journal</i> , 2018, 12, 742-755.	9.8	76

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91	The epsomitic phototrophic microbial mat of Hot Lake, Washington: community structural responses to seasonal cycling. <i>Frontiers in Microbiology</i> , 2013, 4, 323.	3.5	75
92	Metagenome Sequence Analysis of Filamentous Microbial Communities Obtained from Geochemically Distinct Geothermal Channels Reveals Specialization of Three Aquificales Lineages. <i>Frontiers in Microbiology</i> , 2013, 4, 84.	3.5	73
93	Phylogenetic and Functional Analysis of Metagenome Sequence from High-Temperature Archaeal Habitats Demonstrate Linkages between Metabolic Potential and Geochemistry. <i>Frontiers in Microbiology</i> , 2013, 4, 95.	3.5	73
94	Global distribution of a wild alga revealed by targeted metagenomics. <i>Current Biology</i> , 2012, 22, R675-R677.	3.9	65
95	Proteogenomic Analysis of a Thermophilic Bacterial Consortium Adapted to Deconstruct Switchgrass. <i>PLoS ONE</i> , 2013, 8, e68465.	2.5	62
96	Diurnal cycling of rhizosphere bacterial communities is associated with shifts in carbon metabolism. <i>Microbiome</i> , 2017, 5, 65.	11.1	62
97	Metagenomic analysis of a stable trichloroethene-degrading microbial community. <i>ISME Journal</i> , 2012, 6, 1702-1714.	9.8	58
98	Anoxic carbon flux in photosynthetic microbial mats as revealed by metatranscriptomics. <i>ISME Journal</i> , 2013, 7, 817-829.	9.8	57
99	Microbial ecology of an Antarctic hypersaline lake: genomic assessment of ecophysiology among dominant haloarchaea. <i>ISME Journal</i> , 2014, 8, 1645-1658.	9.8	54
100	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , 2019, 7, 157.	11.1	53
101	Genome-Resolved Meta-Omics Ties Microbial Dynamics to Process Performance in Biotechnology for Thiocyanate Degradation. <i>Environmental Science & Technology</i> , 2017, 51, 2944-2953.	10.0	51
102	New Biological Insights Into How Deforestation in Amazonia Affects Soil Microbial Communities Using Metagenomics and Metagenome-Assembled Genomes. <i>Frontiers in Microbiology</i> , 2018, 9, 1635.	3.5	51
103	â€ˆ <i>Candidatus</i> <i>Adiutrix intracellularis</i> â€™™, an endosymbiont of termite gut flagellates, is the first representative of a deepâ€ˆbranching clade of <i>Deltaproteobacteria</i> and a putative homoacetogen. <i>Environmental Microbiology</i> , 2016, 18, 2548-2564.	3.8	50
104	Genomic comparisons of a bacterial lineage that inhabits both marine and terrestrial deep subsurface systems. <i>PeerJ</i> , 2017, 5, e3134.	2.0	50
105	PlanarXY-model dynamics in a nematic liquid crystal system. <i>Physical Review E</i> , 1994, 49, 4250-4257.	2.1	49
106	Discovery of enzymes for toluene synthesis from anoxic microbial communities. <i>Nature Chemical Biology</i> , 2018, 14, 451-457.	8.0	47
107	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. <i>ISME Journal</i> , 2021, 15, 421-434.	9.8	46
108	Unusual Metabolism and Hypervariation in the Genome of a Gracilibacterium (BD1-5) from an Oil-Degrading Community. <i>MBio</i> , 2019, 10, .	4.1	43

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109	Insight into the Bacterial Endophytic Communities of Peach Cultivars Related to Crown Gall Disease Resistance. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	42
110	Bioprospecting metagenomics of decaying wood: mining for new glycoside hydrolases. <i>Biotechnology for Biofuels</i> , 2011, 4, 23.	6.2	40
111	Microbial Community Structure and Functional Potential in Cultivated and Native Tallgrass Prairie Soils of the Midwestern United States. <i>Frontiers in Microbiology</i> , 2018, 9, 1775.	3.5	36
112	A compendium of multi-omic sequence information from the Saanich Inlet water column. <i>Scientific Data</i> , 2017, 4, 170160.	5.3	35
113	Deforestation impacts network co-occurrence patterns of microbial communities in Amazon soils. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	34
114	A call for standardized classification of metagenome projects. <i>Environmental Microbiology</i> , 2010, 12, 1803-1805.	3.8	33
115	Structure and dynamics of the microbial communities underlying the carboxylate platform for biofuel production. <i>Applied Microbiology and Biotechnology</i> , 2010, 88, 389-399.	3.6	32
116	Metabolomics of sorghum roots during nitrogen stress reveals compromised metabolic capacity for salicylic acid biosynthesis. <i>Plant Direct</i> , 2019, 3, e00122.	1.9	32
117	Metagenomic analysis of microbial consortium from natural crude oil that seeps into the marine ecosystem offshore Southern California. <i>Standards in Genomic Sciences</i> , 2014, 9, 1259-1274.	1.5	31
118	Mesophilic and Thermophilic Conditions Select for Unique but Highly Parallel Microbial Communities to Perform Carboxylate Platform Biomass Conversion. <i>PLoS ONE</i> , 2012, 7, e39689.	2.5	30
119	Assembly and Succession of Iron Oxide Microbial Mat Communities in Acidic Geothermal Springs. <i>Frontiers in Microbiology</i> , 2016, 7, 25.	3.5	29
120	Metagenomic and Metatranscriptomic Analyses Reveal the Structure and Dynamics of a Dechlorinating Community Containing <i>Dehalococcoides mccartyi</i> and Corrinoid-Providing Microorganisms under Cobalamin-Limited Conditions. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	29
121	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. <i>Nature Communications</i> , 2021, 12, 5483.	12.8	29
122	Patterns and drivers of fungal community depth stratification in Sphagnum peat. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	28
123	In vitro Characterization of Phenylacetate Decarboxylase, a Novel Enzyme Catalyzing Toluene Biosynthesis in an Anaerobic Microbial Community. <i>Scientific Reports</i> , 2016, 6, 31362.	3.3	27
124	The Tale of a Neglected Energy Source: Elevated Hydrogen Exposure Affects both Microbial Diversity and Function in Soil. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	26
125	H ₂ -saturation of high affinity H ₂ -oxidizing bacteria alters the ecological niche of soil microorganisms unevenly among taxonomic groups. <i>PeerJ</i> , 2016, 4, e1782.	2.0	26
126	Differences in sequencing technologies improve the retrieval of anammox bacterial genome from metagenomes. <i>BMC Genomics</i> , 2013, 14, 7.	2.8	25

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127	Identification of beneficial and detrimental bacteria impacting sorghum responses to drought using multi-scale and multi-system microbiome comparisons. <i>ISME Journal</i> , 2022, 16, 1957-1969.	9.8	25
128	Microbial drivers of methane emissions from unrestored industrial salt ponds. <i>ISME Journal</i> , 2022, 16, 284-295.	9.8	24
129	p53 Checkpoint-Defective Cells Are Sensitive to X Rays, but Not Hypoxia. <i>Experimental Cell Research</i> , 2000, 258, 82-91.	2.6	22
130	Metatranscriptomic Analyses of Diel Metabolic Functions During a Microcystis Bloom in Western Lake Erie (United States). <i>Frontiers in Microbiology</i> , 2019, 10, 2081.	3.5	22
131	Community-Driven Metadata Standards for Agricultural Microbiome Research. <i>Phytobiomes Journal</i> , 2020, 4, 115-121.	2.7	21
132	Predominant Acidilobus-Like Populations from Geothermal Environments in Yellowstone National Park Exhibit Similar Metabolic Potential in Different Hypoxic Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2014, 80, 294-305.	3.1	20
133	Microbial Community Field Surveys Reveal Abundant Pseudomonas Population in Sorghum Rhizosphere Composed of Many Closely Related Phylotypes. <i>Frontiers in Microbiology</i> , 2021, 12, 598180.	3.5	20
134	Major changes in microbial diversity and community composition across gut sections of a juvenile Panchlora cockroach. <i>PLoS ONE</i> , 2017, 12, e0177189.	2.5	20
135	Emerging Trends in Biological Treatment of Wastewater From Unconventional Oil and Gas Extraction. <i>Frontiers in Microbiology</i> , 2020, 11, 569019.	3.5	19
136	Defining the <i>Sphagnum</i> Core Microbiome across the North American Continent Reveals a Central Role for Diazotrophic Methanotrophs in the Nitrogen and Carbon Cycles of Boreal Peatland Ecosystems. <i>MBio</i> , 2022, 13, .	4.1	18
137	Metagenome-assembled genomes of phytoplankton microbiomes from the Arctic and Atlantic Oceans. <i>Microbiome</i> , 2022, 10, 67.	11.1	17
138	Peatland microbial community responses to plant functional group and drought are depth-dependent. <i>Molecular Ecology</i> , 2021, 30, 5119-5136.	3.9	15
139	Metagenomes from two microbial consortia associated with Santa Barbara seep oil. <i>Marine Genomics</i> , 2014, 18, 97-99.	1.1	14
140	Structural dynamics and transcriptomic analysis of <i>Dehalococcoides mccartyi</i> within a TCE-Dechlorinating community in a completely mixed flow reactor. <i>Water Research</i> , 2019, 158, 146-156.	11.3	14
141	Hidden diversity in the oomycete genus <i>Olpidiopsis</i> is a potential hazard to red algal cultivation and conservation worldwide. <i>European Journal of Phycology</i> , 2020, 55, 162-171.	2.0	14
142	The role of zinc in the adaptive evolution of polar phytoplankton. <i>Nature Ecology and Evolution</i> , 2022, 6, 965-978.	7.8	14
143	Elviz – exploration of metagenome assemblies with an interactive visualization tool. <i>BMC Bioinformatics</i> , 2015, 16, 130.	2.6	13
144	Metagenomes of tropical soil-derived anaerobic switchgrass-adapted consortia with and without iron. <i>Standards in Genomic Sciences</i> , 2013, 7, 382-398.	1.5	12

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145	Enriching for direct regulatory targets in perturbed gene-expression profiles. <i>Genome Biology</i> , 2004, 5, R29.	9.6	10
146	Methanogenesis and Salt Tolerance Genes of a Novel Halophilic Methanosarcinaceae Metagenome-Assembled Genome from a Former Solar Saltern. <i>Genes</i> , 2021, 12, 1609.	2.4	10
147	Bioprospecting Metagenomics for New Glycoside Hydrolases. <i>Methods in Molecular Biology</i> , 2012, 908, 141-151.	0.9	9
148	Rearrangement of a Large Novel <i>Pseudomonas aeruginosa</i> Gene Island in Strains Isolated from a Patient Developing Ventilator-Associated Pneumonia. <i>Journal of Clinical Microbiology</i> , 2014, 52, 2430-2438.	3.9	9
149	Membrane Bioreactor Pretreatment of High-Salinity O&G Produced Water. <i>ACS ES&T Water</i> , 2022, 2, 484-494.	4.6	9
150	Corrigendum to Wagner et al.: Natural soil microbes alter flowering phenology and the intensity of selection on flowering time in a wild <i>Arabidopsis</i> relative. <i>Ecology Letters</i> , 2015, 18, 218-220.	6.4	8
151	Taxonomic and Functional Diversity of a <i>Quercus pyrenaica</i> Willd. Rhizospheric Microbiome in the Mediterranean Mountains. <i>Forests</i> , 2017, 8, 390.	2.1	8
152	Meta-omics survey of [NiFe]-hydrogenase genes fails to capture drastic variations in H ₂ -oxidation activity measured in three soils exposed to H ₂ . <i>Soil Biology and Biochemistry</i> , 2018, 125, 239-243.	8.8	7
153	Metagenomes in the Borderline Ecosystems of the Antarctic Cryptoendolithic Communities. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	7
154	Exploring the roles of microbes in facilitating plant adaptation to climate change. <i>Biochemical Journal</i> , 2022, 479, 327-335.	3.7	7
155	Restoring wetlands on intensive agricultural lands modifies nitrogen cycling microbial communities and reduces N ₂ O production potential. <i>Journal of Environmental Management</i> , 2021, 299, 113562.	7.8	6
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