

# Susannah Green Tringe

## List of Publications by Year in descending order

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Version: 2024-02-01

172  
papers

32,782  
citations

7672

79  
h-index

5481

169  
g-index

198  
all docs

198  
docs citations

198  
times ranked

30933  
citing authors

#	ARTICLE	IF	CITATIONS
1	Microbial drivers of methane emissions from unrestored industrial salt ponds. ISME Journal, 2022, 16, 284-295.	4.4	24
2	Methylphosphonate Degradation and Salt-Tolerance Genes of Two Novel Halophilic Marivita Metagenome-Assembled Genomes from Unrestored Solar Salterns. Genes, 2022, 13, 148.	1.0	4
3	Exploring the roles of microbes in facilitating plant adaptation to climate change. Biochemical Journal, 2022, 479, 327-335.	1.7	7
4	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. MBio, 2022, 13, .	1.8	18
5	Membrane Bioreactor Pretreatment of High-Salinity O&G Produced Water. ACS ES&T Water, 2022, 2, 484-494.	2.3	9
6	Metagenome-assembled genomes of phytoplankton microbiomes from the Arctic and Atlantic Oceans. Microbiome, 2022, 10, 67.	4.9	17
7	Identification of beneficial and detrimental bacteria impacting sorghum responses to drought using multi-scale and multi-system microbiome comparisons. ISME Journal, 2022, 16, 1957-1969.	4.4	25
8	A toolkit for microbial community editing. Nature Reviews Microbiology, 2022, 20, 383-383.	13.6	3
9	The role of zinc in the adaptive evolution of polar phytoplankton. Nature Ecology and Evolution, 2022, 6, 965-978.	3.4	14
10	A genomic catalog of Earth's microbiomes. Nature Biotechnology, 2021, 39, 499-509.	9.4	457
11	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. ISME Journal, 2021, 15, 421-434.	4.4	46
12	Microbial Community Field Surveys Reveal Abundant Pseudomonas Population in Sorghum Rhizosphere Composed of Many Closely Related Phylotypes. Frontiers in Microbiology, 2021, 12, 598180.	1.5	20
13	Different threats, same response. Nature Plants, 2021, 7, 544-545.	4.7	3
14	Feature selection and causal analysis for microbiome studies in the presence of confounding using standardization. BMC Bioinformatics, 2021, 22, 362.	1.2	3
15	Peatland microbial community responses to plant functional group and drought are depth-dependent. Molecular Ecology, 2021, 30, 5119-5136.	2.0	15
16	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. Nature Communications, 2021, 12, 5483.	5.8	29
17	Restoring wetlands on intensive agricultural lands modifies nitrogen cycling microbial communities and reduces N <sub>2</sub> O production potential. Journal of Environmental Management, 2021, 299, 113562.	3.8	6
18	Methanogenesis and Salt Tolerance Genes of a Novel Halophilic Methanosarcinaceae Metagenome-Assembled Genome from a Former Solar Saltern. Genes, 2021, 12, 1609.	1.0	10

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19	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.	0.9	14
20	Phototrophic Co-cultures From Extreme Environments: Community Structure and Potential Value for Fundamental and Applied Research. <i>Frontiers in Microbiology</i> , 2020, 11, 572131.	1.5	2
21	Plant-microbiome interactions: from community assembly to plant health. <i>Nature Reviews Microbiology</i> , 2020, 18, 607-621.	13.6	1,381
22	Emerging Trends in Biological Treatment of Wastewater From Unconventional Oil and Gas Extraction. <i>Frontiers in Microbiology</i> , 2020, 11, 569019.	1.5	19
23	Clades of huge phages from across Earth's ecosystems. <i>Nature</i> , 2020, 578, 425-431.	13.7	331
24	Niche differentiation is spatially and temporally regulated in the rhizosphere. <i>ISME Journal</i> , 2020, 14, 999-1014.	4.4	135
25	Metagenomes in the Borderline Ecosystems of the Antarctic Cryptoendolithic Communities. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	7
26	Community-Driven Metadata Standards for Agricultural Microbiome Research. <i>Phytobiomes Journal</i> , 2020, 4, 115-121.	1.4	21
27	Geology and climate influence rhizobiome composition of the phenotypically diverse tropical tree <i>Tabebuia heterophylla</i> . <i>PLoS ONE</i> , 2020, 15, e0231083.	1.1	5
28	A layered defense against plant pathogens. <i>Science</i> , 2019, 366, 568-569.	6.0	3
29	Metatranscriptomic Analyses of Diel Metabolic Functions During a Microcystis Bloom in Western Lake Erie (United States). <i>Frontiers in Microbiology</i> , 2019, 10, 2081.	1.5	22
30	mSphere of Influence: the View from the Microbiologists of the Future. <i>MSphere</i> , 2019, 4, .	1.3	0
31	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.	5.3	14
32	Insight into the Bacterial Endophytic Communities of Peach Cultivars Related to Crown Gall Disease Resistance. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	42
33	Metabolomics of sorghum roots during nitrogen stress reveals compromised metabolic capacity for salicylic acid biosynthesis. <i>Plant Direct</i> , 2019, 3, e00122.	0.8	32
34	Unusual Metabolism and Hypervariation in the Genome of a Gracilibacterium (BD1-5) from an Oil-Degrading Community. <i>MBio</i> , 2019, 10, .	1.8	43
35	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.	3.3	191
36	Diversity, evolution, and classification of virophages uncovered through global metagenomics. <i>Microbiome</i> , 2019, 7, 157.	4.9	53

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37	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
38	Deforestation impacts network co-occurrence patterns of microbial communities in Amazon soils. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	34
39	Interactions between plants and soil shaping the root microbiome under abiotic stress. <i>Biochemical Journal</i> , 2019, 476, 2705-2724.	1.7	198
40	Complete Genome Sequence of <i>Agrobacterium</i> sp. Strain 33MFTa1.1, Isolated from <i>Thlaspi arvense</i> Roots. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
41	Landscape topography structures the soil microbiome in arctic polygonal tundra. <i>Nature Communications</i> , 2018, 9, 777.	5.8	105
42	Peatland <i>Acidobacteria</i> with a dissimilatory sulfur metabolism. <i>ISME Journal</i> , 2018, 12, 1729-1742.	4.4	168
43	Community proteogenomics reveals the systemic impact of phosphorus availability on microbial functions in tropical soil. <i>Nature Ecology and Evolution</i> , 2018, 2, 499-509.	3.4	116
44	Genomic features of bacterial adaptation to plants. <i>Nature Genetics</i> , 2018, 50, 138-150.	9.4	480
45	Discovery of enzymes for toluene synthesis from anoxic microbial communities. <i>Nature Chemical Biology</i> , 2018, 14, 451-457.	3.9	47
46	Contrasting patterns of genome-level diversity across distinct co-occurring bacterial populations. <i>ISME Journal</i> , 2018, 12, 742-755.	4.4	76
47	Completion of an Experiment. <i>MSphere</i> , 2018, 3, .	1.3	0
48	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.	1.5	36
49	Recovery of genomes from metagenomes via a dereplication, aggregation and scoring strategy. <i>Nature Microbiology</i> , 2018, 3, 836-843.	5.9	906
50	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.	3.3	435
51	Meta-omics survey of [NiFe]-hydrogenase genes fails to capture drastic variations in H <sub>2</sub> -oxidation activity measured in three soils exposed to H <sub>2</sub> . <i>Soil Biology and Biochemistry</i> , 2018, 125, 239-243.	4.2	7
52	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.	1.5	51
53	Conversion of Amazon rainforest to agriculture alters community traits of methane cycling organisms. <i>Molecular Ecology</i> , 2017, 26, 1547-1556.	2.0	78
54	Genome-Resolved Meta-Omics Ties Microbial Dynamics to Process Performance in Biotechnology for Thiocyanate Degradation. <i>Environmental Science &amp; Technology</i> , 2017, 51, 2944-2953.	4.6	51

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55	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, .	1.4	29
56	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, .	1.4	26
57	Ecophysiology of Freshwater Verrucomicrobia Inferred from Metagenome-Assembled Genomes. <i>MSphere</i> , 2017, 2, .	1.3	87
58	A genomic perspective on stoichiometric regulation of soil carbon cycling. <i>ISME Journal</i> , 2017, 11, 2652-2665.	4.4	97
59	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.	1.6	88
60	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.	9.4	1,512
61	Single-cell genomics for the masses. <i>Nature Biotechnology</i> , 2017, 35, 635-636.	9.4	2
62	Patterns and drivers of fungal community depth stratification in Sphagnum peat. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	28
63	Diurnal cycling of rhizosphere bacterial communities is associated with shifts in carbon metabolism. <i>Microbiome</i> , 2017, 5, 65.	4.9	62
64	A compendium of multi-omic sequence information from the Saanich Inlet water column. <i>Scientific Data</i> , 2017, 4, 170160.	2.4	35
65	Metagenomic analysis of intertidal hypersaline microbial mats from Elkhorn Slough, California, grown with and without molybdate. <i>Standards in Genomic Sciences</i> , 2017, 12, 67.	1.5	5
66	Taxonomic and Functional Diversity of a <i>Quercus pyrenaica</i> Willd. Rhizospheric Microbiome in the Mediterranean Mountains. <i>Forests</i> , 2017, 8, 390.	0.9	8
67	Major changes in microbial diversity and community composition across gut sections of a juvenile <i>Panochlora</i> cockroach. <i>PLoS ONE</i> , 2017, 12, e0177189.	1.1	20
68	Genomic comparisons of a bacterial lineage that inhabits both marine and terrestrial deep subsurface systems. <i>PeerJ</i> , 2017, 5, e3134.	0.9	50
69	Assembly and Succession of Iron Oxide Microbial Mat Communities in Acidic Geothermal Springs. <i>Frontiers in Microbiology</i> , 2016, 7, 25.	1.5	29
70	The Cacti Microbiome: Interplay between Habitat-Filtering and Host-Specificity. <i>Frontiers in Microbiology</i> , 2016, 7, 150.	1.5	219
71	Metagenomic Insights into the Uncultured Diversity and Physiology of Microbes in Four Hypersaline Soda Lake Brines. <i>Frontiers in Microbiology</i> , 2016, 7, 211.	1.5	161
72	<i>Candidatus</i> <i>Adiutrix intracellularis</i> <sup>TM</sup> , an endosymbiont of termite gut flagellates, is the first representative of a deep-branching clade of <i>Deltaproteobacteria</i> and a putative homoacetogen. <i>Environmental Microbiology</i> , 2016, 18, 2548-2564.	1.8	50

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73	Host genotype and age shape the leaf and root microbiomes of a wild perennial plant. <i>Nature Communications</i> , 2016, 7, 12151.	5.8	754
74	In vitro Characterization of Phenylacetate Decarboxylase, a Novel Enzyme Catalyzing Toluene Biosynthesis in an Anaerobic Microbial Community. <i>Scientific Reports</i> , 2016, 6, 31362.	1.6	27
75	Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations. <i>ISME Journal</i> , 2016, 10, 1589-1601.	4.4	226
76	Metatranscriptomic insights on gene expression and regulatory controls in <i>Candidatus</i> <i>Accumulibacter phosphatis</i> . <i>ISME Journal</i> , 2016, 10, 810-822.	4.4	98
77	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.	4.4	159
78	High-resolution phylogenetic microbial community profiling. <i>ISME Journal</i> , 2016, 10, 2020-2032.	4.4	232
79	Plant compartment and biogeography affect microbiome composition in cultivated and native <i>Agave</i> species. <i>New Phytologist</i> , 2016, 209, 798-811.	3.5	663
80	Ecophysiology of an uncultivated lineage of <i>Aigarchaeota</i> from an oxic, hot spring filamentous "streamer" community. <i>ISME Journal</i> , 2016, 10, 210-224.	4.4	94
81	H <sub>2</sub> -saturation of high affinity H <sub>2</sub> -oxidizing bacteria alters the ecological niche of soil microorganisms unevenly among taxonomic groups. <i>PeerJ</i> , 2016, 4, e1782.	0.9	26
82	Proteogenomic analyses indicate bacterial methylotrophy and archaeal heterotrophy are prevalent below the grass root zone. <i>PeerJ</i> , 2016, 4, e2687.	0.9	124
83	Impact of library preparation protocols and template quantity on the metagenomic reconstruction of a mock microbial community. <i>BMC Genomics</i> , 2015, 16, 856.	1.2	79
84	Primer and platform effects on 16S rRNA tag sequencing. <i>Frontiers in Microbiology</i> , 2015, 6, 771.	1.5	435
85	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. <i>Frontiers in Microbiology</i> , 2015, 6, 1205.	1.5	77
86	Elviz " exploration of metagenome assemblies with an interactive visualization tool. <i>BMC Bioinformatics</i> , 2015, 16, 130.	1.2	13
87	Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. <i>Genome Research</i> , 2015, 25, 534-543.	2.4	121
88	High-Throughput Metagenomic Technologies for Complex Microbial Community Analysis: Open and Closed Formats. <i>MBio</i> , 2015, 6, .	1.8	357
89	Microbial dark matter ecogenomics reveals complex synergistic networks in a methanogenic bioreactor. <i>ISME Journal</i> , 2015, 9, 1710-1722.	4.4	360
90	Aquifer environment selects for microbial species cohorts in sediment and groundwater. <i>ISME Journal</i> , 2015, 9, 1846-1856.	4.4	88

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91	Diverse uncultivated ultra-small bacterial cells in groundwater. <i>Nature Communications</i> , 2015, 6, 6372.	5.8	342
92	Genomic Expansion of Domain Archaea Highlights Roles for Organisms from New Phyla in Anaerobic Carbon Cycling. <i>Current Biology</i> , 2015, 25, 690-701.	1.8	522
93	Salicylic acid modulates colonization of the root microbiome by specific bacterial taxa. <i>Science</i> , 2015, 349, 860-864.	6.0	957
94	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.	3.0	8
95	Patterns in Wetland Microbial Community Composition and Functional Gene Repertoire Associated with Methane Emissions. <i>MBio</i> , 2015, 6, e00066-15.	1.8	90
96	Genome Portal, Joint Genome Institute. , 2015, , 222-231.		0
97	FOAM (Functional Ontology Assignments for Metagenomes): a Hidden Markov Model (HMM) database with environmental focus. <i>Nucleic Acids Research</i> , 2014, 42, e145-e145.	6.5	90
98	IMG/M 4 version of the integrated metagenome comparative analysis system. <i>Nucleic Acids Research</i> , 2014, 42, D568-D573.	6.5	270
99	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.	3.3	305
100	Convergent Bacterial Microbiotas in the Fungal Agricultural Systems of Insects. <i>MBio</i> , 2014, 5, e02077.	1.8	96
101	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.	1.5	78
102	Microbial ecology of an Antarctic hypersaline lake: genomic assessment of ecophysiology among dominant haloarchaea. <i>ISME Journal</i> , 2014, 8, 1645-1658.	4.4	54
103	Building the crops of tomorrow: advantages of symbiont-based approaches to improving abiotic stress tolerance. <i>Frontiers in Microbiology</i> , 2014, 5, 283.	1.5	196
104	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.	3.0	266
105	Predominant <i>Acidilobus</i> -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.	1.4	20
106	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.	3.3	98
107	MaxBin: an automated binning method to recover individual genomes from metagenomes using an expectation-maximization algorithm. <i>Microbiome</i> , 2014, 2, 26.	4.9	521
108	Metagenomes from two microbial consortia associated with Santa Barbara seep oil. <i>Marine Genomics</i> , 2014, 18, 97-99.	0.4	14

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109	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.	1.8	9
110	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
111	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.	1.8	246
112	Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. <i>Nature Communications</i> , 2013, 4, 2120.	5.8	201
113	Comparative genomics of two <i>Candidatus Accumulibacter</i> ™ clades performing biological phosphorus removal. <i>ISME Journal</i> , 2013, 7, 2301-2314.	4.4	101
114	High level of intergenera gene exchange shapes the evolution of haloarchaea in an isolated Antarctic lake. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16939-16944.	3.3	105
115	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.	4.9	493
116	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.	3.3	1,594
117	<i>Leucoagaricus gongylophorus</i> Produces Diverse Enzymes for the Degradation of Recalcitrant Plant Polymers in Leaf-Cutter Ant Fungus Gardens. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3770-3778.	1.4	98
118	Relationship between Abundance and Specific Activity of Bacterioplankton in Open Ocean Surface Waters. <i>Applied and Environmental Microbiology</i> , 2013, 79, 177-184.	1.4	127
119	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.	4.4	87
120	Community-wide plasmid gene mobilization and selection. <i>ISME Journal</i> , 2013, 7, 1173-1186.	4.4	124
121	Differences in sequencing technologies improve the retrieval of anammox bacterial genome from metagenomes. <i>BMC Genomics</i> , 2013, 14, 7.	1.2	25
122	Single-cell and metagenomic analyses indicate a fermentative and saccharolytic lifestyle for members of the OP9 lineage. <i>Nature Communications</i> , 2013, 4, 1854.	5.8	199
123	Transcriptional response of bathypelagic marine bacterioplankton to the Deepwater Horizon oil spill. <i>ISME Journal</i> , 2013, 7, 2315-2329.	4.4	172
124	Anoxic carbon flux in photosynthetic microbial mats as revealed by metatranscriptomics. <i>ISME Journal</i> , 2013, 7, 817-829.	4.4	57
125	The YNP metagenome project: environmental parameters responsible for microbial distribution in the Yellowstone geothermal ecosystem. <i>Frontiers in Microbiology</i> , 2013, 4, 67.	1.5	196
126	Comparative Metagenomic and Metatranscriptomic Analysis of Hindgut Paunch Microbiota in Wood- and Dung-Feeding Higher Termites. <i>PLoS ONE</i> , 2013, 8, e61126.	1.1	149



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127	Proteogenomic Analysis of a Thermophilic Bacterial Consortium Adapted to Deconstruct Switchgrass. PLoS ONE, 2013, 8, e68465.	1.1	62
128	Metagenomic Profiling Reveals Lignocellulose Degrading System in a Microbial Community Associated with a Wood-Feeding Beetle. PLoS ONE, 2013, 8, e73827.	1.1	125
129	Metagenome Sequence Analysis of Filamentous Microbial Communities Obtained from Geochemically Distinct Geothermal Channels Reveals Specialization of Three Aquificales Lineages. Frontiers in Microbiology, 2013, 4, 84.	1.5	73
130	Phylogenetic and Functional Analysis of Metagenome Sequence from High-Temperature Archaeal Habitats Demonstrate Linkages between Metabolic Potential and Geochemistry. Frontiers in Microbiology, 2013, 4, 95.	1.5	73
131	Community Structure and Function of High-Temperature Chlorophototrophic Microbial Mats Inhabiting Diverse Geothermal Environments. Frontiers in Microbiology, 2013, 4, 106.	1.5	112
132	The epsomitic phototrophic microbial mat of Hot Lake, Washington: community structural responses to seasonal cycling. Frontiers in Microbiology, 2013, 4, 323.	1.5	75
133	Metagenomes of tropical soil-derived anaerobic switchgrass-adapted consortia with and without iron. Standards in Genomic Sciences, 2013, 7, 382-398.	1.5	12
134	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.	0.9	139
135	Genome Portal, Joint Genome Institute. , 2013, , 1-10.		0
136	Hydrazine Synthase, a Unique Phylomarker with Which To Study the Presence and Biodiversity of Anammox Bacteria. Applied and Environmental Microbiology, 2012, 78, 752-758.	1.4	228
137	The metagenomic basis of anammox metabolism in <i>Candidatus Brocadia fulgida</i> <sup>TM</sup> . Biochemical Society Transactions, 2012, 40, 295-295.	1.6	2
138	Global distribution of a wild alga revealed by targeted metagenomics. Current Biology, 2012, 22, R675-R677.	1.8	65
139	Comparative analyses of foregut and hindgut bacterial communities in hoatzins and cows. ISME Journal, 2012, 6, 531-541.	4.4	186
140	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. ISME Journal, 2012, 6, 1715-1727.	4.4	547
141	Bioprospecting Metagenomics for New Glycoside Hydrolases. Methods in Molecular Biology, 2012, 908, 141-151.	0.4	9
142	Metagenomic analysis of a stable trichloroethene-degrading microbial community. ISME Journal, 2012, 6, 1702-1714.	4.4	58
143	Defining the core <i>Arabidopsis thaliana</i> root microbiome. Nature, 2012, 488, 86-90.	13.7	2,475
144	Microbial Iron Cycling in Acidic Geothermal Springs of Yellowstone National Park: Integrating Molecular Surveys, Geochemical Processes, and Isolation of Novel Fe-Active Microorganisms. Frontiers in Microbiology, 2012, 3, 109.	1.5	82

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145	Metagenomic and metaproteomic insights into bacterial communities in leaf-cutter ant fungus gardens. <i>ISME Journal</i> , 2012, 6, 1688-1701.	4.4	126
146	Phage-bacteria relationships and CRISPR elements revealed by a metagenomic survey of the rumen microbiome. <i>Environmental Microbiology</i> , 2012, 14, 207-227.	1.8	128
147	Deep-sea bacteria enriched by oil and dispersant from the Deepwater Horizon spill. <i>Environmental Microbiology</i> , 2012, 14, 2405-2416.	1.8	275
148	The Metagenome of an Anaerobic Microbial Community Decomposing Poplar Wood Chips. <i>PLoS ONE</i> , 2012, 7, e36740.	1.1	98
149	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.	1.1	30
150	Bioprospecting metagenomics of decaying wood: mining for new glycoside hydrolases. <i>Biotechnology for Biofuels</i> , 2011, 4, 23.	6.2	40
151	The metagenomic basis of anammox metabolism in <i>Candidatus</i> <i>Brocadia fulgida</i> <sup>TM</sup> . <i>Biochemical Society Transactions</i> , 2011, 39, 1799-1804.	1.6	110
152	Metagenomic Discovery of Biomass-Degrading Genes and Genomes from Cow Rumen. <i>Science</i> , 2011, 331, 463-467.	6.0	1,135
153	Multiple syntrophic interactions in a terephthalate-degrading methanogenic consortium. <i>ISME Journal</i> , 2011, 5, 122-130.	4.4	114
154	Structure and dynamics of the microbial communities underlying the carboxylate platform for biofuel production. <i>Applied Microbiology and Biotechnology</i> , 2010, 88, 389-399.	1.7	32
155	Metagenomic insights into evolution of a heavy metal-contaminated groundwater microbial community. <i>ISME Journal</i> , 2010, 4, 660-672.	4.4	332
156	Validation of two ribosomal RNA removal methods for microbial metatranscriptomics. <i>Nature Methods</i> , 2010, 7, 807-812.	9.0	184
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