

Jillian F Banfield

List of Publications by Year in descending order

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Version: 2024-02-01

425
papers

66,516
citations

765

123
h-index

1410

227
g-index

513
all docs

513
docs citations

513
times ranked

54730
citing authors

#	ARTICLE	IF	CITATIONS
1	Polytypism in semi-disordered lizardite and amesite by low-dose HAADF-STEM. <i>American Mineralogist</i> , 2022, 107, 221-232.	0.9	1
2	<i>Microcoleus</i> (Cyanobacteria) form watershed-wide populations without strong gradients in population structure. <i>Molecular Ecology</i> , 2022, 31, 86-103.	2.0	14
3	Global genomic analysis of microbial biotransformation of arsenic highlights the importance of arsenic methylation in environmental and human microbiomes. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 559-572.	1.9	6
4	Soils and sediments host Thermoplasmata archaea encoding novel copper membrane monooxygenases (CuMMOs). <i>ISME Journal</i> , 2022, 16, 1348-1362.	4.4	17
5	Petabase-scale sequence alignment catalyses viral discovery. <i>Nature</i> , 2022, 602, 142-147.	13.7	213
6	Species- and site-specific genome editing in complex bacterial communities. <i>Nature Microbiology</i> , 2022, 7, 34-47.	5.9	127
7	Alum Addition Triggers Hypoxia in an Engineered Pit Lake. <i>Microorganisms</i> , 2022, 10, 510.	1.6	3
8	Phage-encoded ribosomal protein S21 expression is linked to late-stage phage replication. <i>ISME Communications</i> , 2022, 2, .	1.7	10
9	Long-Term Incubation of Lake Water Enables Genomic Sampling of Consortia Involving <i>Planctomycetes</i> and Candidate Phyla Radiation Bacteria. <i>MSystems</i> , 2022, 7, e0022322.	1.7	2
10	From legacy contamination to watershed systems science: a review of scientific insights and technologies developed through DOE-supported research in water and energy security. <i>Environmental Research Letters</i> , 2022, 17, 043004.	2.2	12
11	Saccharibacteria harness light energy using type-1 rhodopsins that may rely on retinal sourced from microbial hosts. <i>ISME Journal</i> , 2022, 16, 2056-2059.	4.4	13
12	Insights into methionine S-methylation in diverse organisms. <i>Nature Communications</i> , 2022, 13, .	5.8	9
13	Widespread stop-codon recoding in bacteriophages may regulate translation of lytic genes. <i>Nature Microbiology</i> , 2022, 7, 918-927.	5.9	25
14	Ion complexation waves emerge at the curved interfaces of layered minerals. <i>Nature Communications</i> , 2022, 13, .	5.8	10
15	Conserved and lineage-specific hypothetical proteins may have played a central role in the rise and diversification of major archaeal groups. <i>BMC Biology</i> , 2022, 20, .	1.7	4
16	Secondary lanthanide phosphate mineralisation in weathering profiles of I, S- and A-type granites. <i>Mineralogical Magazine</i> , 2021, 85, 82-93.	0.6	5
17	Genome-resolved metagenomics reveals site-specific diversity of episymbiotic CPR bacteria and DPANN archaea in groundwater ecosystems. <i>Nature Microbiology</i> , 2021, 6, 354-365.	5.9	109
18	Acetylene-Fueled Trichloroethene Reductive Dechlorination in a Groundwater Enrichment Culture. <i>MBio</i> , 2021, 12, .	1.8	6

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19	Thiocyanate and Organic Carbon Inputs Drive Convergent Selection for Specific Autotrophic Afipia and Thiobacillus Strains Within Complex Microbiomes. <i>Frontiers in Microbiology</i> , 2021, 12, 643368.	1.5	10
20	The NIH Somatic Cell Genome Editing program. <i>Nature</i> , 2021, 592, 195-204.	13.7	84
21	Brockarchaeota, a novel archaeal phylum with unique and versatile carbon cycling pathways. <i>Nature Communications</i> , 2021, 12, 2404.	5.8	32
22	Structural coordination between active sites of a CRISPR reverse transcriptase-integrase complex. <i>Nature Communications</i> , 2021, 12, 2571.	5.8	12
23	Post-translational flavinylation is associated with diverse extracytosolic redox functionalities throughout bacterial life. <i>ELife</i> , 2021, 10, .	2.8	15
24	Meanders as a scaling motif for understanding of floodplain soil microbiome and biogeochemical potential at the watershed scale. <i>Microbiome</i> , 2021, 9, 121.	4.9	11
25	Genome-resolved metagenomics reveals role of iron metabolism in drought-induced rhizosphere microbiome dynamics. <i>Nature Communications</i> , 2021, 12, 3209.	5.8	93
26	Genetic and behavioral adaptation of <i>Candida parapsilosis</i> to the microbiome of hospitalized infants revealed by in situ genomics, transcriptomics, and proteomics. <i>Microbiome</i> , 2021, 9, 142.	4.9	14
27	Protein Family Content Uncovers Lineage Relationships and Bacterial Pathway Maintenance Mechanisms in DPANN Archaea. <i>Frontiers in Microbiology</i> , 2021, 12, 660052.	1.5	20
28	Diverse ATPase Proteins in Mobilomes Constitute a Large Potential Sink for Prokaryotic Host ATP. <i>Frontiers in Microbiology</i> , 2021, 12, 691847.	1.5	11
29	Patterns of Gene Content and Co-occurrence Constrain the Evolutionary Path toward Animal Association in Candidate Phyla Radiation Bacteria. <i>MBio</i> , 2021, 12, e0052121.	1.8	30
30	DNA interference states of the hypercompact CRISPR-Cas1 effector. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 652-661.	3.6	50
31	Closely related Lak megaphages replicate in the microbiomes of diverse animals. <i>IScience</i> , 2021, 24, 102875.	1.9	20
32	Atomic Perspective on the Serpentine-Chlorite Solid-State Transformation. <i>Chemistry of Materials</i> , 2021, 33, 6338-6345.	3.2	2
33	Soil Candidate Phyla Radiation Bacteria Encode Components of Aerobic Metabolism and Co-occur with Nanoarchaea in the Rare Biosphere of Rhizosphere Grassland Communities. <i>MSystems</i> , 2021, 6, e0120520.	1.7	24
34	Stable-Isotope-Informed, Genome-Resolved Metagenomics Uncovers Potential Cross-Kingdom Interactions in Rhizosphere Soil. <i>MSphere</i> , 2021, 6, e0008521.	1.3	34
35	Infant gut strain persistence is associated with maternal origin, phylogeny, and traits including surface adhesion and iron acquisition. <i>Cell Reports Medicine</i> , 2021, 2, 100393.	3.3	39
36	inStrain profiles population microdiversity from metagenomic data and sensitively detects shared microbial strains. <i>Nature Biotechnology</i> , 2021, 39, 727-736.	9.4	238

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37	Transporter genes in biosynthetic gene clusters predict metabolite characteristics and siderophore activity. <i>Genome Research</i> , 2021, 31, 239-250.	2.4	24
38	CRISPR-Cas ϕ from huge phages is a hypercompact genome editor. <i>Science</i> , 2020, 369, 333-337.	6.0	352
39	Groundwater <i>Elusimicrobia</i> are metabolically diverse compared to gut microbiome <i>Elusimicrobia</i> and some have a novel nitrogenase paralog. <i>ISME Journal</i> , 2020, 14, 2907-2922.	4.4	51
40	Diverse Microorganisms in Sediment and Groundwater Are Implicated in Extracellular Redox Processes Based on Genomic Analysis of Bioanode Communities. <i>Frontiers in Microbiology</i> , 2020, 11, 1694.	1.5	9
41	Novel bacterial clade reveals origin of form I Rubisco. <i>Nature Plants</i> , 2020, 6, 1158-1166.	4.7	46
42	Large freshwater phages with the potential to augment aerobic methane oxidation. <i>Nature Microbiology</i> , 2020, 5, 1504-1515.	5.9	66
43	Genome-Resolved Metagenomics and Detailed Geochemical Speciation Analyses Yield New Insights into Microbial Mercury Cycling in Geothermal Springs. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	19
44	Consistent Metagenome-Derived Metrics Verify and Delineate Bacterial Species Boundaries. <i>MSystems</i> , 2020, 5, .	1.7	135
45	Bacterial Secondary Metabolite Biosynthetic Potential in Soil Varies with Phylum, Depth, and Vegetation Type. <i>MBio</i> , 2020, 11, .	1.8	116
46	Accurate and complete genomes from metagenomes. <i>Genome Research</i> , 2020, 30, 315-333.	2.4	263
47	Lipid analysis of CO ₂ -rich subsurface aquifers suggests an autotrophy-based deep biosphere with lysolipids enriched in CPR bacteria. <i>ISME Journal</i> , 2020, 14, 1547-1560.	4.4	29
48	Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut. <i>PLoS ONE</i> , 2020, 15, e0229537.	1.1	8
49	The rise of diversity in metabolic platforms across the Candidate Phyla Radiation. <i>BMC Biology</i> , 2020, 18, 69.	1.7	54
50	A scoutRNA Is Required for Some Type V CRISPR-Cas Systems. <i>Molecular Cell</i> , 2020, 79, 416-424.e5.	4.5	49
51	Subsurface carbon monoxide oxidation capacity revealed through genome-resolved metagenomics of a carboxydrotroph. <i>Environmental Microbiology Reports</i> , 2020, 12, 525-533.	1.0	3
52	Clades of huge phages from across Earth's ecosystems. <i>Nature</i> , 2020, 578, 425-431.	13.7	331
53	Niche differentiation is spatially and temporally regulated in the rhizosphere. <i>ISME Journal</i> , 2020, 14, 999-1014.	4.4	135
54	Increased replication of dissimilatory nitrate-reducing bacteria leads to decreased anammox bioreactor performance. <i>Microbiome</i> , 2020, 8, 7.	4.9	42

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55	Layer size polydispersity in hydrated montmorillonite creates multiscale porosity networks. <i>Applied Clay Science</i> , 2020, 190, 105548.	2.6	9
56	Soil bacterial populations are shaped by recombination and gene-specific selection across a grassland meadow. <i>ISME Journal</i> , 2020, 14, 1834-1846.	4.4	43
57	Structure of the bacterial ribosome at 2 Å... resolution. <i>ELife</i> , 2020, 9, .	2.8	151
58	Title is missing!. , 2020, 15, e0229537.		0
59	Title is missing!. , 2020, 15, e0229537.		0
60	Title is missing!. , 2020, 15, e0229537.		0
61	Title is missing!. , 2020, 15, e0229537.		0
62	Title is missing!. , 2020, 15, e0229537.		0
63	Title is missing!. , 2020, 15, e0229537.		0
64	Title is missing!. , 2020, 15, e0229537.		0
65	Title is missing!. , 2020, 15, e0229537.		0
66	Pathways for the Photoreduction of Fumarate on ZnS. <i>ACS Earth and Space Chemistry</i> , 2019, 3, 2250-2258.	1.2	1
67	Ion exchange selectivity in clay is controlled by nanoscale chemicalâ€mechanical coupling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22052-22057.	3.3	54
68	Putative Mixotrophic Nitrifying-Denitrifying Gammaproteobacteria Implicated in Nitrogen Cycling Within the Ammonia/Oxygen Transition Zone of an Oil Sands Pit Lake. <i>Frontiers in Microbiology</i> , 2019, 10, 2435.	1.5	42
69	The distinction of CPR bacteria from other bacteria based on protein family content. <i>Nature Communications</i> , 2019, 10, 4173.	5.8	112
70	Megaphages infect <i>Prevotella</i> and variants are widespread in gut microbiomes. <i>Nature Microbiology</i> , 2019, 4, 693-700.	5.9	141
71	A Functional Mini-Integrase in a Two-Protein Type V-C CRISPR System. <i>Molecular Cell</i> , 2019, 73, 727-737.e3.	4.5	22
72	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. <i>Nature Communications</i> , 2019, 10, 463.	5.8	87

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73	Revealing the ductility of nanoceramic MgAl ₂ O ₄ . Journal of Materials Research, 2019, 34, 1489-1498.	1.2	6
74	Microbial communities across a hillslope-riparian transect shaped by proximity to the stream, groundwater table, and weathered bedrock. Ecology and Evolution, 2019, 9, 6869-6900.	0.8	24
75	Mediterranean grassland soil C-N compound turnover is dependent on rainfall and depth, and is mediated by genomically divergent microorganisms. Nature Microbiology, 2019, 4, 1356-1367.	5.9	170
76	Metagenomic recovery of two distinct comammox <i>Nitrospira</i> from the terrestrial subsurface. Environmental Microbiology, 2019, 21, 3627-3637.	1.8	69
77	Candidate Phyla Radiation Roizmanbacteria From Hot Springs Have Novel and Unexpectedly Abundant CRISPR-Cas Systems. Frontiers in Microbiology, 2019, 10, 928.	1.5	36
78	An archaeal symbiont-host association from the deep terrestrial subsurface. ISME Journal, 2019, 13, 2135-2139.	4.4	39
79	Wide diversity of methane and short-chain alkane metabolisms in uncultured archaea. Nature Microbiology, 2019, 4, 603-613.	5.9	187
80	Genome-resolved metagenomics of an autotrophic thiocyanate-remediating microbial bioreactor consortium. Water Research, 2019, 158, 106-117.	5.3	11
81	Genome-resolved metagenomics of eukaryotic populations during early colonization of premature infants and in hospital rooms. Microbiome, 2019, 7, 26.	4.9	60
82	Impacts of microbial assemblage and environmental conditions on the distribution of anatoxin-a producing cyanobacteria within a river network. ISME Journal, 2019, 13, 1618-1634.	4.4	60
83	Wide Distribution of Phage That Infect Freshwater SAR11 Bacteria. MSystems, 2019, 4, .	1.7	11
84	Unusual Metabolism and Hypervariation in the Genome of a Gracilibacterium (BD1-5) from an Oil-Degrading Community. MBio, 2019, 10, .	1.8	43
85	Extracellular electron transfer powers flavinylated extracellular reductases in Gram-positive bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26892-26899.	3.3	68
86	Genome-Resolved Proteomic Stable Isotope Probing of Soil Microbial Communities Using ¹³ CO ₂ and ¹³ C-Methanol. Frontiers in Microbiology, 2019, 10, 2706.	1.5	23
87	Metatranscriptomic reconstruction reveals RNA viruses with the potential to shape carbon cycling in soil. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25900-25908.	3.3	165
88	Necrotizing enterocolitis is preceded by increased gut bacterial replication, <i>Klebsiella</i> , and fimbriae-encoding bacteria. Science Advances, 2019, 5, eaax5727.	4.7	120
89	Lateral Gene Transfer Shapes the Distribution of RuBisCO among Candidate Phyla Radiation Bacteria and DPANN Archaea. Molecular Biology and Evolution, 2019, 36, 435-446.	3.5	54
90	Correlative Cryogenic Spectromicroscopy to Investigate Selenium Bioreduction Products. Environmental Science & Technology, 2018, 52, 503-512.	4.6	24

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91	Expanded diversity of microbial groups that shape the dissimilatory sulfur cycle. ISME Journal, 2018, 12, 1715-1728.	4.4	347
92	Major New Microbial Groups Expand Diversity and Alter our Understanding of the Tree of Life. Cell, 2018, 172, 1181-1197.	13.5	498
93	Genome-reconstruction for eukaryotes from complex natural microbial communities. Genome Research, 2018, 28, 569-580.	2.4	163
94	Hospitalized Premature Infants Are Colonized by Related Bacterial Strains with Distinct Proteomic Profiles. MBio, 2018, 9, .	1.8	34
95	Differential depth distribution of microbial function and putative symbionts through sediment-hosted aquifers in the deep terrestrial subsurface. Nature Microbiology, 2018, 3, 328-336.	5.9	227
96	Machine Learning Leveraging Genomes from Metagenomes Identifies Influential Antibiotic Resistance Genes in the Infant Gut Microbiome. MSystems, 2018, 3, .	1.7	68
97	Homologous Recombination and Transposon Propagation Shape the Population Structure of an Organism from the Deep Subsurface with Minimal Metabolism. Genome Biology and Evolution, 2018, 10, 1115-1119.	1.1	24
98	Ecological and genomic profiling of anaerobic methane-oxidizing archaea in a deep granitic environment. ISME Journal, 2018, 12, 31-47.	4.4	59
99	A novel Chromatiales bacterium is a potential sulfide oxidizer in multiple orders of marine sponges. Environmental Microbiology, 2018, 20, 800-814.	1.8	27
100	Atomic Structure, Defects, and Stacking of Clay Particles by Low-Dose, High Resolution (Cryo)-TEM. Microscopy and Microanalysis, 2018, 24, 1958-1959.	0.2	3
101	Programmed DNA destruction by miniature CRISPR-Cas14 enzymes. Science, 2018, 362, 839-842.	6.0	757
102	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome. Genome Research, 2018, 28, 1467-1480.	2.4	117
103	Biosynthetic capacity, metabolic variety and unusual biology in the CPR and DPANN radiations. Nature Reviews Microbiology, 2018, 16, 629-645.	13.6	314
104	Recovery of genomes from metagenomes via a dereplication, aggregation and scoring strategy. Nature Microbiology, 2018, 3, 836-843.	5.9	906
105	Insights into the ecology, evolution, and metabolism of the widespread Woese archaeal lineages. Microbiome, 2018, 6, 102.	4.9	181
106	The developing premature infant gut microbiome is a major factor shaping the microbiome of neonatal intensive care unit rooms. Microbiome, 2018, 6, 112.	4.9	65
107	Stable isotope informed genome-resolved metagenomics reveals that Saccharibacteria utilize microbially-processed plant-derived carbon. Microbiome, 2018, 6, 122.	4.9	156
108	Novel soil bacteria possess diverse genes for secondary metabolite biosynthesis. Nature, 2018, 558, 440-444.	13.7	321

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109	Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO ₂ concentrations. <i>Environmental Microbiology</i> , 2017, 19, 459-474.	1.8	212
110	Genome-Resolved Meta-Omics Ties Microbial Dynamics to Process Performance in Biotechnology for Thiocyanate Degradation. <i>Environmental Science & Technology</i> , 2017, 51, 2944-2953.	4.6	51
111	Asgard archaea illuminate the origin of eukaryotic cellular complexity. <i>Nature</i> , 2017, 541, 353-358.	13.7	882
112	The Source and Evolutionary History of a Microbial Contaminant Identified Through Soil Metagenomic Analysis. <i>MBio</i> , 2017, 8, .	1.8	17
113	Genome-Resolved metagenomics of a bioremediation system for degradation of thiocyanate in mine water containing suspended solid tailings. <i>MicrobiologyOpen</i> , 2017, 6, e00446.	1.2	22
114	Identical bacterial populations colonize premature infant gut, skin, and oral microbiomes and exhibit different in situ growth rates. <i>Genome Research</i> , 2017, 27, 601-612.	2.4	99
115	Disturbances of the Perioperative Microbiome Across Multiple Body Sites in Patients Undergoing Pancreaticoduodenectomy. <i>Pancreas</i> , 2017, 46, 260-267.	0.5	56
116	Unusual respiratory capacity and nitrogen metabolism in a Parcubacterium (OD1) of the Candidate Phyla Radiation. <i>Scientific Reports</i> , 2017, 7, 40101.	1.6	119
117	Candidatus <i>Mycoplasma girerdii</i> replicates, diversifies, and co-occurs with <i>Trichomonas vaginalis</i> in the oral cavity of a premature infant. <i>Scientific Reports</i> , 2017, 7, 3764.	1.6	17
118	Mechanism of Ferric Oxalate Photolysis. <i>ACS Earth and Space Chemistry</i> , 2017, 1, 270-276.	1.2	59
119	Potential for microbial H ₂ and metal transformations associated with novel bacteria and archaea in deep terrestrial subsurface sediments. <i>ISME Journal</i> , 2017, 11, 1915-1929.	4.4	137
120	Retroelement-guided protein diversification abounds in vast lineages of Bacteria and Archaea. <i>Nature Microbiology</i> , 2017, 2, 17045.	5.9	62
121	New CRISPR-Cas systems from uncultivated microbes. <i>Nature</i> , 2017, 542, 237-241.	13.7	471
122	Reply to Delmont and Eren: Strain variants and population structure during the Deepwater Horizon oil spill. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8950-E8952.	3.3	0
123	Analysis of Microbial Communities Associated with Bioremediation Systems for Thiocyanate-Laden Mine Water Effluents. <i>Solid State Phenomena</i> , 2017, 262, 601-604.	0.3	0
124	dRep: a tool for fast and accurate genomic comparisons that enables improved genome recovery from metagenomes through de-replication. <i>ISME Journal</i> , 2017, 11, 2864-2868.	4.4	1,309
125	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
126	Strain-resolved analysis of hospital rooms and infants reveals overlap between the human and room microbiome. <i>Nature Communications</i> , 2017, 8, 1814.	5.8	162

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127	Novel Microbial Diversity and Functional Potential in the Marine Mammal Oral Microbiome. <i>Current Biology</i> , 2017, 27, 3752-3762.e6.	1.8	82
128	Simulation of <i>Deepwater Horizon</i> oil plume reveals substrate specialization within a complex community of hydrocarbon degraders. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7432-7437.	3.3	120
129	Complete 4.55-Megabase-Pair Genome of <i>Candidatus</i> <i>Fluviicola riflensis</i> , Curated from Short-Read Metagenomic Sequences. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
130	Microbial Community Structure and the Persistence of Cyanobacterial Populations in Salt Crusts of the Hyperarid Atacama Desert from Genome-Resolved Metagenomics. <i>Frontiers in Microbiology</i> , 2017, 8, 1435.	1.5	73
131	Genome-resolved metaproteomic characterization of preterm infant gut microbiota development reveals species-specific metabolic shifts and variabilities during early life. <i>Microbiome</i> , 2017, 5, 72.	4.9	36
132	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. <i>Frontiers in Microbiology</i> , 2016, 7, 238.	1.5	66
133	Functional metagenomic selection of ribulose 1, 5-bisphosphate carboxylase/oxygenase from uncultivated bacteria. <i>Environmental Microbiology</i> , 2016, 18, 1187-1199.	1.8	26
134	Genome-Resolved Metagenomic Analysis Reveals Roles for Candidate Phyla and Other Microbial Community Members in Biogeochemical Transformations in Oil Reservoirs. <i>MBio</i> , 2016, 7, e01669-15.	1.8	151
135	Microbial Metagenomics Reveals Climate-Relevant Subsurface Biogeochemical Processes. <i>Trends in Microbiology</i> , 2016, 24, 600-610.	3.5	35
136	RubisCO of a nucleoside pathway known from Archaea is found in diverse uncultivated phyla in bacteria. <i>ISME Journal</i> , 2016, 10, 2702-2714.	4.4	98
137	Pilot study of sources and concentrations of size-resolved airborne particles in a neonatal intensive care unit. <i>Building and Environment</i> , 2016, 106, 10-19.	3.0	11
138	A Model for Nucleation When Nuclei Are Nonstoichiometric: Understanding the Precipitation of Iron Oxyhydroxide Nanoparticles. <i>Crystal Growth and Design</i> , 2016, 16, 5726-5737.	1.4	19
139	Short- and Long-Range Attractive Forces That Influence the Structure of Montmorillonite Osmotic Hydrates. <i>Langmuir</i> , 2016, 32, 12039-12046.	1.6	38
140	Measurement of bacterial replication rates in microbial communities. <i>Nature Biotechnology</i> , 2016, 34, 1256-1263.	9.4	342
141	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. <i>Nature Communications</i> , 2016, 7, 13219.	5.8	994
142	A new view of the tree of life. <i>Nature Microbiology</i> , 2016, 1, 16048.	5.9	1,823
143	Evidence for persistent and shared bacterial strains against a background of largely unique gut colonization in hospitalized premature infants. <i>ISME Journal</i> , 2016, 10, 2817-2830.	4.4	47
144	Metagenomic analysis of a high carbon dioxide subsurface microbial community populated by chemolithoautotrophs and bacteria and archaea from candidate phyla. <i>Environmental Microbiology</i> , 2016, 18, 1686-1703.	1.8	78

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145	Precipitation pathways for ferrihydrite formation in acidic solutions. <i>Geochimica Et Cosmochimica Acta</i> , 2016, 172, 247-264.	1.6	67
146	Critical biogeochemical functions in the subsurface are associated with bacteria from new phyla and little studied lineages. <i>Environmental Microbiology</i> , 2016, 18, 159-173.	1.8	164
147	Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. <i>Nature Communications</i> , 2016, 7, 10613.	5.8	224
148	Metagenomic reconstructions of bacterial CRISPR loci constrain population histories. <i>ISME Journal</i> , 2016, 10, 858-870.	4.4	80
149	Concentrations and Sources of Airborne Particles in a Neonatal Intensive Care Unit. <i>PLoS ONE</i> , 2016, 11, e0154991.	1.1	33
150	Analysis of five complete genome sequences for members of the class Peribacteria in the recently recognized Peregrinibacteria bacterial phylum. <i>PeerJ</i> , 2016, 4, e1607.	0.9	57
151	Proteogenomic analyses indicate bacterial methylotrophy and archaeal heterotrophy are prevalent below the grass root zone. <i>PeerJ</i> , 2016, 4, e2687.	0.9	124
152	Metaproteomics reveals functional shifts in microbial and human proteins during a preterm infant gut colonization case. <i>Proteomics</i> , 2015, 15, 3463-3473.	1.3	54
153	Bioreactor microbial ecosystems for thiocyanate and cyanide degradation unravelled with genome-resolved metagenomics. <i>Environmental Microbiology</i> , 2015, 17, 4929-4941.	1.8	124
154	Strain-resolved microbial community proteomics reveals simultaneous aerobic and anaerobic function during gastrointestinal tract colonization of a preterm infant. <i>Frontiers in Microbiology</i> , 2015, 6, 654.	1.5	24
155	<i>De Novo</i> Sequences of <i>Haloquadratum walsbyi</i> from Lake Tyrrell, Australia, Reveal a Variable Genomic Landscape. <i>Archaea</i> , 2015, 2015, 1-12.	2.3	26
156	CRISPR Immunity Drives Rapid Phage Genome Evolution in <i>Streptococcus thermophilus</i> . <i>MBio</i> , 2015, 6, .	1.8	151
157	Formation and Restacking of Disordered Smectite Osmotic Hydrates. <i>Clays and Clay Minerals</i> , 2015, 63, 432-442.	0.6	26
158	Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. <i>Genome Research</i> , 2015, 25, 534-543.	2.4	121
159	Aquifer environment selects for microbial species cohorts in sediment and groundwater. <i>ISME Journal</i> , 2015, 9, 1846-1856.	4.4	88
160	Diverse uncultivated ultra-small bacterial cells in groundwater. <i>Nature Communications</i> , 2015, 6, 6372.	5.8	342
161	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
162	Crystallization by particle attachment in synthetic, biogenic, and geologic environments. <i>Science</i> , 2015, 349, aaa6760.	6.0	1,467

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163	Molecular Dynamics Simulation Study of the Early Stages of Nucleation of Iron Oxyhydroxide Nanoparticles in Aqueous Solutions. <i>Journal of Physical Chemistry B</i> , 2015, 119, 10630-10642.	1.2	36
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