

# Jillian F Banfield

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1534815/publications.pdf>

Version: 2024-02-01

427  
papers

66,516  
citations

643

123  
h-index

1222

227  
g-index

513  
all docs

513  
docs citations

513  
times ranked

48826  
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.	1.9	1
2	<i>Microcoleus</i> (Cyanobacteria) form watershed-wide populations without strong gradients in population structure. <i>Molecular Ecology</i> , 2022, 31, 86-103.	3.9	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.	4.1	6
4	Soils and sediments host Thermoplasmata archaea encoding novel copper membrane monooxygenases (CuMMOs). <i>ISME Journal</i> , 2022, 16, 1348-1362.	9.8	17
5	Petabase-scale sequence alignment catalyses viral discovery. <i>Nature</i> , 2022, 602, 142-147.	27.8	213
6	Species- and site-specific genome editing in complex bacterial communities. <i>Nature Microbiology</i> , 2022, 7, 34-47.	13.3	127
7	Alum Addition Triggers Hypoxia in an Engineered Pit Lake. <i>Microorganisms</i> , 2022, 10, 510.	3.6	3
8	Phage-encoded ribosomal protein S21 expression is linked to late-stage phage replication. <i>ISME Communications</i> , 2022, 2, .	4.2	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.	3.8	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.	5.2	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.	9.8	13
12	Insights into methionine S-methylation in diverse organisms. <i>Nature Communications</i> , 2022, 13, .	12.8	9
13	Widespread stop-codon recoding in bacteriophages may regulate translation of lytic genes. <i>Nature Microbiology</i> , 2022, 7, 918-927.	13.3	25
14	Ion complexation waves emerge at the curved interfaces of layered minerals. <i>Nature Communications</i> , 2022, 13, .	12.8	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, .	3.8	4
16	Secondary lanthanide phosphate mineralisation in weathering profiles of I-, S- and A-type granites. <i>Mineralogical Magazine</i> , 2021, 85, 82-93.	1.4	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.	13.3	109
18	Acetylene-Fueled Trichloroethene Reductive Dechlorination in a Groundwater Enrichment Culture. <i>MBio</i> , 2021, 12, .	4.1	6

#	ARTICLE	IF	CITATIONS
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.	3.5	10
20	The NIH Somatic Cell Genome Editing program. <i>Nature</i> , 2021, 592, 195-204.	27.8	84
21	Brockarchaeota, a novel archaeal phylum with unique and versatile carbon cycling pathways. <i>Nature Communications</i> , 2021, 12, 2404.	12.8	32
22	Structural coordination between active sites of a CRISPR reverse transcriptase-integrase complex. <i>Nature Communications</i> , 2021, 12, 2571.	12.8	12
23	Post-translational flavinylation is associated with diverse extracytosolic redox functionalities throughout bacterial life. <i>ELife</i> , 2021, 10, .	6.0	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.	11.1	11
25	Genome-resolved metagenomics reveals role of iron metabolism in drought-induced rhizosphere microbiome dynamics. <i>Nature Communications</i> , 2021, 12, 3209.	12.8	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.	11.1	14
27	Protein Family Content Uncovers Lineage Relationships and Bacterial Pathway Maintenance Mechanisms in DPANN Archaea. <i>Frontiers in Microbiology</i> , 2021, 12, 660052.	3.5	20
28	Diverse ATPase Proteins in Mobilomes Constitute a Large Potential Sink for Prokaryotic Host ATP. <i>Frontiers in Microbiology</i> , 2021, 12, 691847.	3.5	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.	4.1	30
30	DNA interference states of the hypercompact CRISPR-Cas effector. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 652-661.	8.2	50
31	Closely related Lak megaphages replicate in the microbiomes of diverse animals. <i>IScience</i> , 2021, 24, 102875.	4.1	20
32	Atomic Perspective on the Serpentine-Chlorite Solid-State Transformation. <i>Chemistry of Materials</i> , 2021, 33, 6338-6345.	6.7	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.	3.8	24
34	Stable-Isotope-Informed, Genome-Resolved Metagenomics Uncovers Potential Cross-Kingdom Interactions in Rhizosphere Soil. <i>MSphere</i> , 2021, 6, e0008521.	2.9	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.	6.5	39
36	inStrain profiles population microdiversity from metagenomic data and sensitively detects shared microbial strains. <i>Nature Biotechnology</i> , 2021, 39, 727-736.	17.5	238

#	ARTICLE	IF	CITATIONS
37	Transporter genes in biosynthetic gene clusters predict metabolite characteristics and siderophore activity. <i>Genome Research</i> , 2021, 31, 239-250.	5.5	24
38	CRISPR-Cas $\phi$ from huge phages is a hypercompact genome editor. <i>Science</i> , 2020, 369, 333-337.	12.6	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.	9.8	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.	3.5	9
41	Novel bacterial clade reveals origin of form I Rubisco. <i>Nature Plants</i> , 2020, 6, 1158-1166.	9.3	46
42	Large freshwater phages with the potential to augment aerobic methane oxidation. <i>Nature Microbiology</i> , 2020, 5, 1504-1515.	13.3	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, .	3.1	19
44	Consistent Metagenome-Derived Metrics Verify and Delineate Bacterial Species Boundaries. <i>MSystems</i> , 2020, 5, .	3.8	135
45	Bacterial Secondary Metabolite Biosynthetic Potential in Soil Varies with Phylum, Depth, and Vegetation Type. <i>MBio</i> , 2020, 11, .	4.1	116
46	Accurate and complete genomes from metagenomes. <i>Genome Research</i> , 2020, 30, 315-333.	5.5	263
47	Lipid analysis of CO <sub>2</sub> -rich subsurface aquifers suggests an autotrophy-based deep biosphere with lysolipids enriched in CPR bacteria. <i>ISME Journal</i> , 2020, 14, 1547-1560.	9.8	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.	2.5	8
49	The rise of diversity in metabolic platforms across the Candidate Phyla Radiation. <i>BMC Biology</i> , 2020, 18, 69.	3.8	54
50	A scoutRNA Is Required for Some Type V CRISPR-Cas Systems. <i>Molecular Cell</i> , 2020, 79, 416-424.e5.	9.7	49
51	Subsurface carbon monoxide oxidation capacity revealed through genome-resolved metagenomics of a carboxydrotroph. <i>Environmental Microbiology Reports</i> , 2020, 12, 525-533.	2.4	3
52	Clades of huge phages from across Earth's ecosystems. <i>Nature</i> , 2020, 578, 425-431.	27.8	331
53	Niche differentiation is spatially and temporally regulated in the rhizosphere. <i>ISME Journal</i> , 2020, 14, 999-1014.	9.8	135
54	Increased replication of dissimilatory nitrate-reducing bacteria leads to decreased anammox bioreactor performance. <i>Microbiome</i> , 2020, 8, 7.	11.1	42

#	ARTICLE	IF	CITATIONS
55	Layer size polydispersity in hydrated montmorillonite creates multiscale porosity networks. Applied Clay Science, 2020, 190, 105548.	5.2	9
56	Soil bacterial populations are shaped by recombination and gene-specific selection across a grassland meadow. ISME Journal, 2020, 14, 1834-1846.	9.8	43
57	Structure of the bacterial ribosome at 2 Å... resolution. ELife, 2020, 9, .	6.0	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. ACS Earth and Space Chemistry, 2019, 3, 2250-2258.	2.7	1
67	Ion exchange selectivity in clay is controlled by nanoscale chemicalâ€mechanical coupling. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22052-22057.	7.1	54
68	Putative Mixotrophic Nitrifying-Denitrifying Gammaproteobacteria Implicated in Nitrogen Cycling Within the Ammonia/Oxygen Transition Zone of an Oil Sands Pit Lake. Frontiers in Microbiology, 2019, 10, 2435.	3.5	42
69	The distinction of CPR bacteria from other bacteria based on protein family content. Nature Communications, 2019, 10, 4173.	12.8	112
70	Megaphages infect Prevotella and variants are widespread in gut microbiomes. Nature Microbiology, 2019, 4, 693-700.	13.3	141
71	A Functional Mini-Integrase in a Two-Protein Type V-C CRISPR System. Molecular Cell, 2019, 73, 727-737.e3.	9.7	22
72	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. Nature Communications, 2019, 10, 463.	12.8	87

#	ARTICLE	IF	CITATIONS
73	Revealing the ductility of nanoceramic MgAl <sub>2</sub> O <sub>4</sub> . Journal of Materials Research, 2019, 34, 1489-1498.	2.6	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.	1.9	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.	13.3	170
76	Metagenomic recovery of two distinct comammox <i>Nitrospira</i> from the terrestrial subsurface. Environmental Microbiology, 2019, 21, 3627-3637.	3.8	69
77	Candidate Phyla Radiation Roizmanbacteria From Hot Springs Have Novel and Unexpectedly Abundant CRISPR-Cas Systems. Frontiers in Microbiology, 2019, 10, 928.	3.5	36
78	An archaeal symbiont-host association from the deep terrestrial subsurface. ISME Journal, 2019, 13, 2135-2139.	9.8	39
79	Wide diversity of methane and short-chain alkane metabolisms in uncultured archaea. Nature Microbiology, 2019, 4, 603-613.	13.3	187
80	Genome-resolved metagenomics of an autotrophic thiocyanate-remediating microbial bioreactor consortium. Water Research, 2019, 158, 106-117.	11.3	11
81	Genome-resolved metagenomics of eukaryotic populations during early colonization of premature infants and in hospital rooms. Microbiome, 2019, 7, 26.	11.1	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.	9.8	60
83	Wide Distribution of Phage That Infect Freshwater SAR11 Bacteria. MSystems, 2019, 4, .	3.8	11
84	Unusual Metabolism and Hypervariation in the Genome of a Gracilibacterium (BD1-5) from an Oil-Degrading Community. MBio, 2019, 10, .	4.1	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.	7.1	68
86	Genome-Resolved Proteomic Stable Isotope Probing of Soil Microbial Communities Using <sup>13</sup> CO <sub>2</sub> and <sup>13</sup> C-Methanol. Frontiers in Microbiology, 2019, 10, 2706.	3.5	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.	7.1	165
88	Necrotizing enterocolitis is preceded by increased gut bacterial replication, <i>Klebsiella</i> , and fimbriae-encoding bacteria. Science Advances, 2019, 5, eaax5727.	10.3	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.	8.9	54
90	Correlative Cryogenic Spectromicroscopy to Investigate Selenium Bioreduction Products. Environmental Science & Technology, 2018, 52, 503-512.	10.0	24

#	ARTICLE	IF	CITATIONS
91	Expanded diversity of microbial groups that shape the dissimilatory sulfur cycle. ISME Journal, 2018, 12, 1715-1728.	9.8	347
92	Major New Microbial Groups Expand Diversity and Alter our Understanding of the Tree of Life. Cell, 2018, 172, 1181-1197.	28.9	498
93	Genome-reconstruction for eukaryotes from complex natural microbial communities. Genome Research, 2018, 28, 569-580.	5.5	163
94	Hospitalized Premature Infants Are Colonized by Related Bacterial Strains with Distinct Proteomic Profiles. MBio, 2018, 9, .	4.1	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.	13.3	227
96	Machine Learning Leveraging Genomes from Metagenomes Identifies Influential Antibiotic Resistance Genes in the Infant Gut Microbiome. MSystems, 2018, 3, .	3.8	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.	2.5	24
98	Ecological and genomic profiling of anaerobic methane-oxidizing archaea in a deep granitic environment. ISME Journal, 2018, 12, 31-47.	9.8	59
99	A novel Chromatiales bacterium is a potential sulfide oxidizer in multiple orders of marine sponges. Environmental Microbiology, 2018, 20, 800-814.	3.8	27
100	Atomic Structure, Defects, and Stacking of Clay Particles by Low-Dose, High Resolution (Cryo)-TEM. Microscopy and Microanalysis, 2018, 24, 1958-1959.	0.4	3
101	Programmed DNA destruction by miniature CRISPR-Cas14 enzymes. Science, 2018, 362, 839-842.	12.6	757
102	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome. Genome Research, 2018, 28, 1467-1480.	5.5	117
103	Biosynthetic capacity, metabolic variety and unusual biology in the CPR and DPANN radiations. Nature Reviews Microbiology, 2018, 16, 629-645.	28.6	314
104	Recovery of genomes from metagenomes via a dereplication, aggregation and scoring strategy. Nature Microbiology, 2018, 3, 836-843.	13.3	906
105	Insights into the ecology, evolution, and metabolism of the widespread Woese archaeal lineages. Microbiome, 2018, 6, 102.	11.1	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.	11.1	65
107	Stable isotope informed genome-resolved metagenomics reveals that Saccharibacteria utilize microbially-processed plant-derived carbon. Microbiome, 2018, 6, 122.	11.1	156
108	Novel soil bacteria possess diverse genes for secondary metabolite biosynthesis. Nature, 2018, 558, 440-444.	27.8	321

#	ARTICLE	IF	CITATIONS
109	Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO <sub>2</sub> concentrations. <i>Environmental Microbiology</i> , 2017, 19, 459-474.	3.8	212
110	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.	10.0	51
111	Asgard archaea illuminate the origin of eukaryotic cellular complexity. <i>Nature</i> , 2017, 541, 353-358.	27.8	882
112	The Source and Evolutionary History of a Microbial Contaminant Identified Through Soil Metagenomic Analysis. <i>MBio</i> , 2017, 8, .	4.1	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.	3.0	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.	5.5	99
115	Disturbances of the Perioperative Microbiome Across Multiple Body Sites in Patients Undergoing Pancreaticoduodenectomy. <i>Pancreas</i> , 2017, 46, 260-267.	1.1	56
116	Unusual respiratory capacity and nitrogen metabolism in a <i>Parcubacterium</i> (OD1) of the Candidate Phyla Radiation. <i>Scientific Reports</i> , 2017, 7, 40101.	3.3	119
117	<i>Candidatus 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.	3.3	17
118	Mechanism of Ferric Oxalate Photolysis. <i>ACS Earth and Space Chemistry</i> , 2017, 1, 270-276.	2.7	59
119	Potential for microbial H <sub>2</sub> and metal transformations associated with novel bacteria and archaea in deep terrestrial subsurface sediments. <i>ISME Journal</i> , 2017, 11, 1915-1929.	9.8	137
120	Retroelement-guided protein diversification abounds in vast lineages of Bacteria and Archaea. <i>Nature Microbiology</i> , 2017, 2, 17045.	13.3	62
121	New CRISPR-Cas systems from uncultivated microbes. <i>Nature</i> , 2017, 542, 237-241.	27.8	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.	7.1	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.	9.8	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.	17.5	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.	12.8	162



#	ARTICLE	IF	CITATIONS
127	Novel Microbial Diversity and Functional Potential in the Marine Mammal Oral Microbiome. <i>Current Biology</i> , 2017, 27, 3752-3762.e6.	3.9	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.	7.1	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.	3.5	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.	11.1	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.	3.5	66
133	Functional metagenomic selection of ribulose 1, 5-bisphosphate carboxylase/oxygenase from uncultivated bacteria. <i>Environmental Microbiology</i> , 2016, 18, 1187-1199.	3.8	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.	4.1	151
135	Microbial Metagenomics Reveals Climate-Relevant Subsurface Biogeochemical Processes. <i>Trends in Microbiology</i> , 2016, 24, 600-610.	7.7	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.	9.8	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.	6.9	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.	3.0	19
139	Short- and Long-Range Attractive Forces That Influence the Structure of Montmorillonite Osmotic Hydrates. <i>Langmuir</i> , 2016, 32, 12039-12046.	3.5	38
140	Measurement of bacterial replication rates in microbial communities. <i>Nature Biotechnology</i> , 2016, 34, 1256-1263.	17.5	342
141	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. <i>Nature Communications</i> , 2016, 7, 13219.	12.8	994
142	A new view of the tree of life. <i>Nature Microbiology</i> , 2016, 1, 16048.	13.3	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.	9.8	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.	3.8	78

#	ARTICLE	IF	CITATIONS
145	Precipitation pathways for ferrihydrite formation in acidic solutions. <i>Geochimica Et Cosmochimica Acta</i> , 2016, 172, 247-264.	3.9	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.	3.8	164
147	Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. <i>Nature Communications</i> , 2016, 7, 10613.	12.8	224
148	Metagenomic reconstructions of bacterial CRISPR loci constrain population histories. <i>ISME Journal</i> , 2016, 10, 858-870.	9.8	80
149	Concentrations and Sources of Airborne Particles in a Neonatal Intensive Care Unit. <i>PLoS ONE</i> , 2016, 11, e0154991.	2.5	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.	2.0	57
151	Proteogenomic analyses indicate bacterial methylotrophy and archaeal heterotrophy are prevalent below the grass root zone. <i>PeerJ</i> , 2016, 4, e2687.	2.0	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.	2.2	54
153	Bioreactor microbial ecosystems for thiocyanate and cyanide degradation unravelled with genome-resolved metagenomics. <i>Environmental Microbiology</i> , 2015, 17, 4929-4941.	3.8	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.	3.5	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, .	4.1	151
157	Formation and Restacking of Disordered Smectite Osmotic Hydrates. <i>Clays and Clay Minerals</i> , 2015, 63, 432-442.	1.3	26
158	Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. <i>Genome Research</i> , 2015, 25, 534-543.	5.5	121
159	Aquifer environment selects for microbial species cohorts in sediment and groundwater. <i>ISME Journal</i> , 2015, 9, 1846-1856.	9.8	88
160	Diverse uncultivated ultra-small bacterial cells in groundwater. <i>Nature Communications</i> , 2015, 6, 6372.	12.8	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.	3.9	522
162	Crystallization by particle attachment in synthetic, biogenic, and geologic environments. <i>Science</i> , 2015, 349, aaa6760.	12.6	1,467

#	ARTICLE	IF	CITATIONS
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.	2.6	36
164	Formation and transformation of a short range ordered iron carbonate precursor. <i>Geochimica Et Cosmochimica Acta</i> , 2015, 164, 94-109.	3.9	39
165	Unusual biology across a group comprising more than 15% of domain Bacteria. <i>Nature</i> , 2015, 523, 208-211.	27.8	1,050
166	Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. <i>ISME Journal</i> , 2015, 9, 2697-2711.	9.8	35
167	Bicarbonate impact on U(VI) bioreduction in a shallow alluvial aquifer. <i>Geochimica Et Cosmochimica Acta</i> , 2015, 150, 106-124.	3.9	58
168	Development of an Enhanced Metaproteomic Approach for Deepening the Microbiome Characterization of the Human Infant Gut. <i>Journal of Proteome Research</i> , 2015, 14, 133-141.	3.7	77
169	Disturbed subsurface microbial communities follow equivalent trajectories despite different structural starting points. <i>Environmental Microbiology</i> , 2015, 17, 622-636.	3.8	32
170	Community transcriptomics reveals unexpected high microbial diversity in acidophilic biofilm communities. <i>ISME Journal</i> , 2015, 9, 1014-1023.	9.8	59
171	Elevated temperature alters proteomic responses of individual organisms within a biofilm community. <i>ISME Journal</i> , 2015, 9, 180-194.	9.8	57
172	Gut bacteria are rarely shared by co-hospitalized premature infants, regardless of necrotizing enterocolitis development. <i>ELife</i> , 2015, 4, .	6.0	111
173	Recoding of the stop codon UGA to glycine by a BD1-5/SN-2 bacterium and niche partitioning between Alpha- and Gammaproteobacteria in a tidal sediment microbial community naturally selected in a laboratory chemostat. <i>Frontiers in Microbiology</i> , 2014, 5, 231.	3.5	38
174	Diverse and divergent protein post-translational modifications in two growth stages of a natural microbial community. <i>Nature Communications</i> , 2014, 5, 4405.	12.8	51
175	Quantitative Metaproteomics: Functional Insights into Microbial Communities. <i>Methods in Molecular Biology</i> , 2014, 1096, 231-240.	0.9	16
176	Biology of a widespread uncultivated archaeon that contributes to carbon fixation in the subsurface. <i>Nature Communications</i> , 2014, 5, 5497.	12.8	119
177	Impacts of Ionic Strength on Three-Dimensional Nanoparticle Aggregate Structure and Consequences for Environmental Transport and Deposition. <i>Environmental Science &amp; Technology</i> , 2014, 48, 13703-13710.	10.0	50
178	Comparison of environmental and isolate <i>Sulfobacillus</i> genomes reveals diverse carbon, sulfur, nitrogen, and hydrogen metabolisms. <i>BMC Genomics</i> , 2014, 15, 1107.	2.8	65
179	Microbes in the neonatal intensive care unit resemble those found in the gut of premature infants. <i>Microbiome</i> , 2014, 2, 1.	11.1	437
180	Interatomic Coulombic interactions as the driving force for oriented attachment. <i>CrystEngComm</i> , 2014, 16, 1568-1578.	2.6	97

#	ARTICLE	IF	CITATIONS
181	<sup>15</sup> N- and <sup>2</sup> H- proteomic stable isotope probing links nitrogen flow to archaeal heterotrophic activity. <i>Environmental Microbiology</i> , 2014, 16, 3224-3237.	3.8	48
182	Aggregation-induced growth and transformation of <sup>56</sup> Fe-FeOOH nanorods to micron-sized <sup>56</sup> Fe-Fe <sub>2</sub> O <sub>3</sub> spindles. <i>CrystEngComm</i> , 2014, 16, 1451-1458.	2.6	93
183	Kinetics of crystal growth of nanogoethite in aqueous solutions containing nitrate and sulfate anions. <i>CrystEngComm</i> , 2014, 16, 1466-1471.	2.6	18
184	Determination of the Three-Dimensional Structure of Ferrihydrite Nanoparticle Aggregates. <i>Langmuir</i> , 2014, 30, 9931-9940.	3.5	34
185	Investigating Processes of Nanocrystal Formation and Transformation via Liquid Cell TEM. <i>Microscopy and Microanalysis</i> , 2014, 20, 425-436.	0.4	94
186	A Unified Description of Attachment-Based Crystal Growth. <i>ACS Nano</i> , 2014, 8, 6526-6530.	14.6	121
187	Structural Characteristics and Mechanical and Thermodynamic Properties of Nanocrystalline TiO <sub>2</sub> . <i>Chemical Reviews</i> , 2014, 114, 9613-9644.	47.7	285
188	Metabolic interdependencies between phylogenetically novel fermenters and respiratory organisms in an unconfined aquifer. <i>ISME Journal</i> , 2014, 8, 1452-1463.	9.8	170
189	Seasonal fluctuations in ionic concentrations drive microbial succession in a hypersaline lake community. <i>ISME Journal</i> , 2014, 8, 979-990.	9.8	91
190	Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. <i>Nature Communications</i> , 2013, 4, 2120.	12.8	201
191	Titania nanorods curve to lower their energy. <i>Nanoscale</i> , 2013, 5, 6742.	5.6	8
192	Genomes from Metagenomics. <i>Science</i> , 2013, 342, 1057-1058.	12.6	149
193	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
194	Comparative genomics in acid mine drainage biofilm communities reveals metabolic and structural differentiation of co-occurring archaea. <i>BMC Genomics</i> , 2013, 14, 485.	2.8	96
195	Genome resolved analysis of a premature infant gut microbial community reveals a <i>Varibaculum</i> cambriense genome and a shift towards fermentation-based metabolism during the third week of life. <i>Microbiome</i> , 2013, 1, 30.	11.1	50
196	Biostimulation induces syntrophic interactions that impact C, S and N cycling in a sediment microbial community. <i>ISME Journal</i> , 2013, 7, 800-816.	9.8	98
197	Strong bias in the bacterial CRISPR elements that confer immunity to phage. <i>Nature Communications</i> , 2013, 4, 1430.	12.8	180
198	Gene Transfer from Bacteria and Archaea Facilitated Evolution of an Extremophilic Eukaryote. <i>Science</i> , 2013, 339, 1207-1210.	12.6	439

#	ARTICLE	IF	CITATIONS
199	Phage mutations in response to <scp>CRISPR</scp> diversification in a bacterial population. Environmental Microbiology, 2013, 15, 463-470.	3.8	97
200	Vanadate and Acetate Biostimulation of Contaminated Sediments Decreases Diversity, Selects for Specific Taxa, and Decreases Aqueous V<sup>5+</sup> Concentration. Environmental Science & Technology, 2013, 47, 6500-6509.	10.0	80
201	Iron-reducing bacteria accumulate ferric oxyhydroxide nanoparticle aggregates that may support planktonic growth. ISME Journal, 2013, 7, 338-350.	9.8	72
202	Stable-Isotope Probing Reveals That Hydrogen Isotope Fractionation in Proteins and Lipids in a Microbial Community Are Different and Species-Specific. ACS Chemical Biology, 2013, 8, 1755-1763.	3.4	30
203	Microscopic Evidence for Liquid-Liquid Separation in Supersaturated CaCO<sub>3</sub> Solutions. Science, 2013, 341, 885-889.	12.6	433
204	Time series community genomics analysis reveals rapid shifts in bacterial species, strains, and phage during infant gut colonization. Genome Research, 2013, 23, 111-120.	5.5	409
205	Metabolites Associated with Adaptation of Microorganisms to an Acidophilic, Metal-Rich Environment Identified by Stable-Isotope-Enabled Metabolomics. MBio, 2013, 4, e00484-12.	4.1	87
206	Small Genomes and Sparse Metabolisms of Sediment-Associated Bacteria from Four Candidate Phyla. MBio, 2013, 4, e00708-13.	4.1	298
207	New Group in the Leptospirillum Clade: Cultivation-Independent Community Genomics, Proteomics, and Transcriptomics of the New Species "Leptospirillum Group IV UBA BS". Applied and Environmental Microbiology, 2013, 79, 5384-5393.	3.1	49
208	New Approaches Indicate Constant Viral Diversity despite Shifts in Assemblage Structure in an Australian Hypersaline Lake. Applied and Environmental Microbiology, 2013, 79, 6755-6764.	3.1	37
209	Prokaryotic Super Program Advisory Committee DOE Joint Genome Institute, Walnut Creek, CA, March 27, 2013. Standards in Genomic Sciences, 2013, 8, 561-570.	1.5	5
210	Assembly-Driven Community Genomics of a Hypersaline Microbial Ecosystem. PLoS ONE, 2013, 8, e61692.	2.5	101
211	Quantifying Heavy Metals Sequestration by Sulfate-Reducing Bacteria in an Acid Mine Drainage-Contaminated Natural Wetland. Frontiers in Microbiology, 2013, 4, 43.	3.5	43
212	Virus-Host and CRISPR Dynamics in Archaea-Dominated Hypersaline Lake Tyrrell, Victoria, Australia. Archaea, 2013, 2013, 1-12.	2.3	82
213	Short-Read Assembly of Full-Length 16S Amplicons Reveals Bacterial Diversity in Subsurface Sediments. PLoS ONE, 2013, 8, e56018.	2.5	153
214	Fluctuations in Species-Level Protein Expression Occur during Element and Nutrient Cycling in the Subsurface. PLoS ONE, 2013, 8, e57819.	2.5	21
215	Architecture and Gene Repertoire of the Flexible Genome of the Extreme Acidophile Acidithiobacillus caldus. PLoS ONE, 2013, 8, e78237.	2.5	68
216	The human gut and groundwater harbor non-photosynthetic bacteria belonging to a new candidate phylum sibling to Cyanobacteria. ELife, 2013, 2, e01102.	6.0	355

#	ARTICLE	IF	CITATIONS
217	CRISPRs in the Microbial Community Context. , 2013, , 287-291.		1
218	X-ray structure of the fourth type of archaeal tRNA splicing endonuclease: insights into the evolution of a novel three-unit composition and a unique loop involved in broad substrate specificity. Nucleic Acids Research, 2012, 40, 10554-10566.	14.5	25
219	Persisting Viral Sequences Shape Microbial CRISPR-based Immunity. PLoS Computational Biology, 2012, 8, e1002475.	3.2	136
220	Dynamic Viral Populations in Hypersaline Systems as Revealed by Metagenomic Assembly. Applied and Environmental Microbiology, 2012, 78, 6309-6320.	3.1	83
221	Heterotrophic Archaea Contribute to Carbon Cycling in Low-pH, Suboxic Biofilm Communities. Applied and Environmental Microbiology, 2012, 78, 8321-8330.	3.1	52
222	Effect of Rainfall-Induced Soil Geochemistry Dynamics on Grassland Soil Microbial Communities. Applied and Environmental Microbiology, 2012, 78, 7587-7595.	3.1	55
223	U(VI) Sorption and Reduction Kinetics on the Magnetite (111) Surface. Environmental Science & Technology, 2012, 46, 3821-3830.	10.0	84
224	Compressibility and structural stability of nanoparticulate goethite. RSC Advances, 2012, 2, 6768.	3.6	6
225	Fermentation, Hydrogen, and Sulfur Metabolism in Multiple Uncultivated Bacterial Phyla. Science, 2012, 337, 1661-1665.	12.6	637
226	Identification of Simultaneous U(VI) Sorption Complexes and U(IV) Nanoprecipitates on the Magnetite (111) Surface. Environmental Science & Technology, 2012, 46, 3811-3820.	10.0	59
227	Early Stage Formation of Iron Oxyhydroxides during Neutralization of Simulated Acid Mine Drainage Solutions. Environmental Science & Technology, 2012, 46, 8140-8147.	10.0	74
228	Energy Calculations Predict Nanoparticle Attachment Orientations and Asymmetric Crystal Formation. Journal of Physical Chemistry Letters, 2012, 3, 2882-2886.	4.6	93
229	Contingency in the direction and mechanics of soil organic matter responses to increased rainfall. Plant and Soil, 2012, 358, 371-383.	3.7	53
230	<i>De novo</i> metagenomic assembly reveals abundant novel major lineage of Archaea in hypersaline microbial communities. ISME Journal, 2012, 6, 81-93.	9.8	347
231	NIBBS-Search for Fast and Accurate Prediction of Phenotype-Biased Metabolic Systems. PLoS Computational Biology, 2012, 8, e1002490.	3.2	5
232	Phage-Induced Expression of CRISPR-Associated Proteins Is Revealed by Shotgun Proteomics in Streptococcus thermophilus. PLoS ONE, 2012, 7, e38077.	2.5	88
233	Direction-Specific Interactions Control Crystal Growth by Oriented Attachment. Science, 2012, 336, 1014-1018.	12.6	958
234	In Situ Evolutionary Rate Measurements Show Ecological Success of Recently Emerged Bacterial Hybrids. Science, 2012, 336, 462-466.	12.6	103

#	ARTICLE	IF	CITATIONS
235	Deuterium-exchange metabolomics identifies N-methyl lyso phosphatidylethanolamines as abundant lipids in acidophilic mixed microbial communities. <i>Metabolomics</i> , 2012, 8, 566-578.	3.0	16
236	Correlative microscopy for phylogenetic and ultrastructural characterization of microbial communities. <i>Environmental Microbiology Reports</i> , 2012, 4, 36-41.	2.4	19
237	High-density PhyloChip profiling of stimulated aquifer microbial communities reveals a complex response to acetate amendment. <i>FEMS Microbiology Ecology</i> , 2012, 81, 188-204.	2.7	43
238	A portable cryo-plunger for on-site intact cryogenic microscopy sample preparation in natural environments. <i>Microscopy Research and Technique</i> , 2012, 75, 829-836.	2.2	31
239	Analysis of streptococcal CRISPRs from human saliva reveals substantial sequence diversity within and between subjects over time. <i>Genome Research</i> , 2011, 21, 126-136.	5.5	104
240	Size-Dependent Bandgap of Nanogoethite. <i>Journal of Physical Chemistry C</i> , 2011, 115, 17704-17710.	3.1	66
241	Improved genome annotation through untargeted detection of pathway-specific metabolites. <i>BMC Genomics</i> , 2011, 12, S6.	2.8	14
242	EMIRGE: reconstruction of full-length ribosomal genes from microbial community short read sequencing data. <i>Genome Biology</i> , 2011, 12, R44.	8.8	326
243	Micron-scale Fe <sup>2+</sup> /Fe <sup>3+</sup> , intermediate sulfur species and O <sub>2</sub> gradients across the biofilm-solution-sediment interface control biofilm organization. <i>Geochimica Et Cosmochimica Acta</i> , 2011, 75, 3568-3580.	3.9	19
244	Quantitative Tracking of Isotope Flows in Proteomes of Microbial Communities. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006049.	3.8	77
245	Proteome changes in the initial bacterial colonist during ecological succession in an acid mine drainage biofilm community. <i>Environmental Microbiology</i> , 2011, 13, 2279-2292.	3.8	49
246	Quantitative proteomic analyses of the response of acidophilic microbial communities to different pH conditions. <i>ISME Journal</i> , 2011, 5, 1152-1161.	9.8	53
247	A novel three-unit tRNA splicing endonuclease found in ultrasmall Archaea possesses broad substrate specificity. <i>Nucleic Acids Research</i> , 2011, 39, 9695-9704.	14.5	32
248	Identification of Biofilm Matrix-Associated Proteins from an Acid Mine Drainage Microbial Community. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5230-5237.	3.1	70
249	Strain-resolved community genomic analysis of gut microbial colonization in a premature infant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1128-1133.	7.1	224
250	A Semi-Quantitative, Synteny-Based Method to Improve Functional Predictions for Hypothetical and Poorly Annotated Bacterial and Archaeal Genes. <i>PLoS Computational Biology</i> , 2011, 7, e1002230.	3.2	32
251	Response of nanoparticle structure to different types of surface environments: Wide-angle x-ray scattering and molecular dynamics simulations. <i>Physical Review B</i> , 2010, 81, .	3.2	29
252	A high-throughput de novo sequencing approach for shotgun proteomics using high-resolution tandem mass spectrometry. <i>BMC Bioinformatics</i> , 2010, 11, 118.	2.6	52



#	ARTICLE	IF	CITATIONS
253	Cultivation and quantitative proteomic analyses of acidophilic microbial communities. ISME Journal, 2010, 4, 520-530.	9.8	65
254	AMD biofilms: using model communities to study microbial evolution and ecological complexity in nature. ISME Journal, 2010, 4, 599-610.	9.8	187
255	Posttranslational modification and sequence variation of redox-active proteins correlate with biofilm life cycle in natural microbial communities. ISME Journal, 2010, 4, 1398-1409.	9.8	26
256	Metabolome-Proteome Differentiation Coupled to Microbial Divergence. MBio, 2010, 1, .	4.1	28
257	Enigmatic, ultrasmall, uncultivated Archaea. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8806-8811.	7.1	306
258	Diversity of Dissimilatory Sulfite Reductase Genes ( <i>dsrAB</i> ) in a Salt Marsh Impacted by Long-Term Acid Mine Drainage. Applied and Environmental Microbiology, 2010, 76, 4819-4828.	3.1	48
259	Proteogenomic basis for ecological divergence of closely related bacteria in natural acidophilic microbial communities. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2383-2390.	7.1	171
260	Ecological distribution and population physiology defined by proteomics in a natural microbial community. Molecular Systems Biology, 2010, 6, 374.	7.2	63
261	Electrode voltages accompanying stimulated bioremediation of a uranium-contaminated aquifer. Journal of Geophysical Research, 2010, 115, .	3.3	7
262	Characterization of Extracellular Polymeric Substances from Acidophilic Microbial Biofilms. Applied and Environmental Microbiology, 2010, 76, 2916-2922.	3.1	239
263	Analysis of Biostimulated Microbial Communities from Two Field Experiments Reveals Temporal and Spatial Differences in Proteome Profiles. Environmental Science & Technology, 2010, 44, 8897-8903.	10.0	54
264	Computational Prediction and Experimental Validation of Signal Peptide Cleavages in the Extracellular Proteome of a Natural Microbial Community. Journal of Proteome Research, 2010, 9, 2148-2159.	3.7	17
265	Particle Size and pH Effects on Nanoparticle Dissolution. Journal of Physical Chemistry C, 2010, 114, 14876-14884.	3.1	111
266	Variety—the Splice of Life—in Microbial Communities. Science, 2009, 326, 1198-1199.	12.6	25
267	Insights into the Diversity of Eukaryotes in Acid Mine Drainage Biofilm Communities. Applied and Environmental Microbiology, 2009, 75, 2192-2199.	3.1	103
268	Natural acidophilic biofilm communities reflect distinct organismal and functional organization. ISME Journal, 2009, 3, 266-270.	9.8	79
269	Three-dimensional analysis of the structure and ecology of a novel, ultra-small archaeon. ISME Journal, 2009, 3, 159-167.	9.8	110
270	Despite strong seasonal responses, soil microbial consortia are more resilient to long-term changes in rainfall than overlying grassland. ISME Journal, 2009, 3, 738-744.	9.8	228



#	ARTICLE	IF	CITATIONS
271	Functional analysis of natural microbial consortia using community proteomics. <i>Nature Reviews Microbiology</i> , 2009, 7, 196-205.	28.6	245
272	The dynamic genetic repertoire of microbial communities. <i>FEMS Microbiology Reviews</i> , 2009, 33, 109-132.	8.6	89
273	Proteomicsâ€inferred genome typing (PIGT) demonstrates interâ€population recombination as a strategy for environmental adaptation. <i>Environmental Microbiology</i> , 2009, 11, 313-325.	3.8	59
274	The size dependence of the surface free energy of titania nanocrystals. <i>Physical Chemistry Chemical Physics</i> , 2009, 11, 2553.	2.8	109
275	Geophysical Monitoring of Coupled Microbial and Geochemical Processes During Stimulated Subsurface Bioremediation. <i>Environmental Science &amp; Technology</i> , 2009, 43, 6717-6723.	10.0	127
276	Identification and Growth Mechanism of ZnS Nanoparticles with Mixed Cubic and Hexagonal Stacking. <i>Journal of Physical Chemistry C</i> , 2009, 113, 9681-9687.	3.1	31
277	Iron oxyhydroxide mineralization on microbial extracellular polysaccharides. <i>Geochimica Et Cosmochimica Acta</i> , 2009, 73, 3807-3818.	3.9	338
278	Prediction of the effects of size and morphology on the structure of water around hematite nanoparticles. <i>Geochimica Et Cosmochimica Acta</i> , 2009, 73, 4023-4033.	3.9	64
279	Community Genomic and Proteomic Analyses of Chemoautotrophic Iron-Oxidizing â€œ <i>Leptospirillum rubrum</i> â€ (Group II) and â€œ <i>Leptospirillum ferrodiazotrophum</i> â€ (Group III) Bacteria in Acid Mine Drainage Biofilms. <i>Applied and Environmental Microbiology</i> , 2009, 75, 4599-4615.	3.1	168
280	Size-dependent elasticity of nanocrystalline titania. <i>Physical Review B</i> , 2009, 79, .	3.2	53
281	Community-wide analysis of microbial genome sequence signatures. <i>Genome Biology</i> , 2009, 10, R85.	9.6	479
282	Proteogenomic Monitoring of <i>Geobacter</i> Physiology during Stimulated Uranium Bioremediation. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6591-6599.	3.1	136
283	Rapidly evolving CRISPRs implicated in acquired resistance of microorganisms to viruses. <i>Environmental Microbiology</i> , 2008, 10, 200-207.	3.8	289
284	Virus Population Dynamics and Acquired Virus Resistance in Natural Microbial Communities. <i>Science</i> , 2008, 320, 1047-1050.	12.6	469
285	Cytochrome 572 is a conspicuous membrane protein with iron oxidation activity purified directly from a natural acidophilic microbial community. <i>ISME Journal</i> , 2008, 2, 542-550.	9.8	102
286	Community proteogenomics highlights microbial strain-variant protein expression within activated sludge performing enhanced biological phosphorus removal. <i>ISME Journal</i> , 2008, 2, 853-864.	9.8	156
287	Anatase Coarsening Kinetics under Hydrothermal Conditions As a Function of Ph and Temperature. <i>Chemistry of Materials</i> , 2008, 20, 3443-3449.	6.7	63
288	Atomic structure of nanometer-sized amorphous $\text{TiO}_2$ <i>Physical Review B</i> , 2008, 78, .	3.2	164

#	ARTICLE	IF	CITATIONS
289	Kinetics of Water Adsorption-Driven Structural Transformation of ZnS Nanoparticles. Journal of Physical Chemistry C, 2008, 112, 4791-4796.	3.1	20
290	Free Energy Change of Aggregation of Nanoparticles. Journal of Physical Chemistry C, 2008, 112, 14731-14736.	3.1	42
291	Characterization of Cytochrome 579, an Unusual Cytochrome Isolated from an Iron-Oxidizing Microbial Community. Applied and Environmental Microbiology, 2008, 74, 4454-4462.	3.1	66
292	Population Genomic Analysis of Strain Variation in Leptospirillum Group II Bacteria Involved in Acid Mine Drainage Formation. PLoS Biology, 2008, 6, e177.	5.6	125
293	Genome dynamics in a natural archaeal population. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1883-1888.	7.1	123
294	Genetic Exchange Across a Species Boundary in the Archaeal Genus Ferroplasma. Genetics, 2007, 177, 407-416.	2.9	67
295	Interaction between Water Molecules and Zinc Sulfide Nanoparticles Studied by Temperature-Programmed Desorption and Molecular Dynamics Simulations. Journal of Physical Chemistry A, 2007, 111, 5008-5014.	2.5	34
296	Extracellular Proteins Limit the Dispersal of Biogenic Nanoparticles. Science, 2007, 316, 1600-1603.	12.6	254
297	Implications of Strain- and Species-Level Sequence Divergence for Community and Isolate Shotgun Proteomic Analysis. Journal of Proteome Research, 2007, 6, 3152-3161.	3.7	32
298	Polymorphic Transformations and Particle Coarsening in Nanocrystalline Titania Ceramic Powders and Membranes. Journal of Physical Chemistry C, 2007, 111, 6621-6629.	3.1	43
299	Galvanic interpretation of self-potential signals associated with microbial sulfate reduction. Journal of Geophysical Research, 2007, 112, .	3.3	15
300	Phase Stability and Transformation in Titania Nanoparticles in Aqueous Solutions Dominated by Surface Energy. Journal of Physical Chemistry C, 2007, 111, 1962-1968.	3.1	141
301	Mechanism of Inhibition of Nanoparticle Growth and Phase Transformation by Surface Impurities. Physical Review Letters, 2007, 98, 106103.	7.8	30
302	Strain-resolved community proteomics reveals recombining genomes of acidophilic bacteria. Nature, 2007, 446, 537-541.	27.8	205
303	Strainer: software for analysis of population variation in community genomic datasets. BMC Bioinformatics, 2007, 8, 398.	2.6	30
304	Environmental Risks of Nanotechnology: A National Nanotechnology Initiative Funding, 2000-2004. Environmental Science & Technology, 2006, 40, 1401-1407.	10.0	263
305	Surface Chemistry Controls Crystallinity of ZnS Nanoparticles. Nano Letters, 2006, 6, 605-610.	9.1	80
306	Influence of Surface Potential on Aggregation and Transport of Titania Nanoparticles. Environmental Science & Technology, 2006, 40, 7688-7693.	10.0	489

#	ARTICLE	IF	CITATIONS
307	Kinetically controlled formation of a novel nanoparticulate ZnS with mixed cubic and hexagonal stacking. <i>Journal of Materials Chemistry</i> , 2006, 16, 249-254.	6.7	44
308	Lineages of Acidophilic Archaea Revealed by Community Genomic Analysis. <i>Science</i> , 2006, 314, 1933-1935.	12.6	217
309	Quantification of chemical weathering rates across an actively eroding hillslope. <i>Earth and Planetary Science Letters</i> , 2006, 242, 155-169.	4.4	90
310	Population genomics in natural microbial communities. <i>Trends in Ecology and Evolution</i> , 2006, 21, 508-516.	8.7	94
311	WAXS and PDF-Based Analyses of Chromium Doping in Nanocrystalline Titania (Anatase and Brookite). <i>Materials Research Society Symposia Proceedings</i> , 2006, 915, 1.	0.1	0
312	Community genomics in microbial ecology and evolution. <i>Nature Reviews Microbiology</i> , 2005, 3, 489-498.	28.6	218
313	Nanoparticulate Iron Oxide Minerals in Soils and Sediments: Unique Properties and Contaminant Scavenging Mechanisms. <i>Journal of Nanoparticle Research</i> , 2005, 7, 409-433.	1.9	555
314	6. Molecular-Scale Processes Involving Nanoparticulate Minerals in Biogeochemical Systems. , 2005, , 109-156.		12
315	1. The Search for a Molecular-Level Understanding of the Processes that Underpin the Earth's Biogeochemical Cycles. , 2005, , 1-8.		2
316	11. Population Dynamics Through the Lens of Extreme Environments. , 2005, , 259-278.		1
317	Genome-Directed Isolation of the Key Nitrogen Fixer <i>Leptospirillum ferro-diazotrophum</i> sp. nov. from an Acidophilic Microbial Community. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6319-6324.	3.1	225
318	Direct Microbial Reduction and Subsequent Preservation of Uranium in Natural Near-Surface Sediment. <i>Applied and Environmental Microbiology</i> , 2005, 71, 1790-1797.	3.1	111
319	Proteogenomic Approaches for the Molecular Characterization of Natural Microbial Communities. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 301-333.	2.0	65
320	Geophysical Imaging of Stimulated Microbial Biomineralization. <i>Environmental Science &amp; Technology</i> , 2005, 39, 7592-7600.	10.0	122
321	Cultivating the uncultivated: a community genomics perspective. <i>Trends in Microbiology</i> , 2005, 13, 411-415.	7.7	89
322	Sulfate requirement for heterotrophic growth of <i>Ferroplasma acidarmanus</i> strain fer1. <i>Research in Microbiology</i> , 2005, 156, 492-498.	2.1	14
323	Size-Dependent Phase Transformation Kinetics in Nanocrystalline ZnS. <i>Journal of the American Chemical Society</i> , 2005, 127, 4523-4529.	13.7	172
324	Characterization of Titanium Dioxide Nanoparticles Using Molecular Dynamics Simulations. <i>Journal of Physical Chemistry B</i> , 2005, 109, 15243-15249.	2.6	197

#	ARTICLE	IF	CITATIONS
325	Size Dependence of the Kinetic Rate Constant for Phase Transformation in TiO <sub>2</sub> Nanoparticles. Chemistry of Materials, 2005, 17, 3421-3425.	6.7	127
326	Community proteomics of a natural microbial biofilm. Science, 2005, 308, 1915-20.	12.6	509
327	Community Proteomics of a Natural Microbial Biofilm. Science, 2005, 308, 1915-1920.	12.6	134
328	Ultrastructure, aggregation-state, and crystal growth of biogenic nanocrystalline sphalerite and wurtzite. American Mineralogist, 2004, 89, 950-960.	1.9	102
329	Reversible, Surface-Controlled Structure Transformation in Nanoparticles Induced by an Aggregation State. Physical Review Letters, 2004, 92, 155501.	7.8	69
330	Analysis and simulation of the structure of nanoparticles that undergo a surface-driven structural transformation. Journal of Chemical Physics, 2004, 120, 11785-11795.	3.0	40
331	Spectral identification of hydrated sulfates on Mars and comparison with acidic environments on Earth. International Journal of Astrobiology, 2004, 3, 275-285.	1.6	73
332	Enzymatic U(VI) reduction by Desulfosporosinus species. Radiochimica Acta, 2004, 92, 11-16.	1.2	65
333	Metabolically Active Eukaryotic Communities in Extremely Acidic Mine Drainage. Applied and Environmental Microbiology, 2004, 70, 6264-6271.	3.1	159
334	Microbial Polysaccharides Template Assembly of Nanocrystal Fibers. Science, 2004, 303, 1656-1658.	12.6	399
335	Tetraether-linked membrane monolayers in Ferroplasma spp: a key to survival in acid. Extremophiles, 2004, 8, 411-419.	2.3	150
336	Acid mine drainage biogeochemistry at Iron Mountain, California. Geochemical Transactions, 2004, 5, 1.	0.7	211
337	Aggregation, Coarsening, and Phase Transformation in ZnS Nanoparticles Studied by Molecular Dynamics Simulations. Nano Letters, 2004, 4, 713-718.	9.1	89
338	Resistance to, and Accumulation of, Uranium by Bacteria from a Uranium-Contaminated Site. Geomicrobiology Journal, 2004, 21, 113-121.	2.0	179
339	Community structure and metabolism through reconstruction of microbial genomes from the environment. Nature, 2004, 428, 37-43.	27.8	2,045
340	Nanoparticles: Strained and Stiff. Science, 2004, 305, 651-654.	12.6	420
341	Kinetics and Mechanism of Trithionate and Tetrathionate Oxidation at Low pH by Hydroxyl Radicals. Aquatic Geochemistry, 2003, 9, 145-164.	1.3	31
342	Arsenic resistance in the archaeon "Ferroplasma acidarmanus": new insights into the structure and evolution of the ars genes. Extremophiles, 2003, 7, 123-130.	2.3	56

#	ARTICLE	IF	CITATIONS
343	Microbial communities in acid mine drainage. <i>FEMS Microbiology Ecology</i> , 2003, 44, 139-152.	2.7	916
344	Special phase transformation and crystal growth pathways observed in nanoparticles. <i>Geochemical Transactions</i> , 2003, 4, 1.	0.7	136
345	Water-driven structure transformation in nanoparticles at room temperature. <i>Nature</i> , 2003, 424, 1025-1029.	27.8	427
346	The Role of Oriented Attachment Crystal Growth in Hydrothermal Coarsening of Nanocrystalline ZnS. <i>Journal of Physical Chemistry B</i> , 2003, 107, 10470-10475.	2.6	161
347	Molecular Dynamics Simulations, Thermodynamic Analysis, and Experimental Study of Phase Stability of Zinc Sulfide Nanoparticles. <i>Journal of Physical Chemistry B</i> , 2003, 107, 13051-13060.	2.6	180
348	Model biomimetic studies of templated growth and assembly of nanocrystalline FeOOH. <i>Geochimica Et Cosmochimica Acta</i> , 2003, 67, 1185-1195.	3.9	50
349	Kinetics and mechanism of polythionate oxidation to sulfate at low pH by O <sub>2</sub> and Fe <sup>3+</sup> . <i>Geochimica Et Cosmochimica Acta</i> , 2003, 67, 4457-4469.	3.9	83
350	Molecular geomicrobiology: genes and geochemical cycling. <i>Earth and Planetary Science Letters</i> , 2003, 209, 1-17.	4.4	46
351	Two-Stage Crystal-Growth Kinetics Observed during Hydrothermal Coarsening of Nanocrystalline ZnS. <i>Nano Letters</i> , 2003, 3, 373-378.	9.1	370
352	Extremely Acidophilic Protists from Acid Mine Drainage Host Rickettsiales-Lineage Endosymbionts That Have Intervening Sequences in Their 16S rRNA Genes. <i>Applied and Environmental Microbiology</i> , 2003, 69, 5512-5518.	3.1	101
353	Microbial Populations Stimulated for Hexavalent Uranium Reduction in Uranium Mine Sediment. <i>Applied and Environmental Microbiology</i> , 2003, 69, 1337-1346.	3.1	170
354	Glycogen-accumulating organisms in laboratory-scale and full-scale wastewater treatment processes b bThe GenBank accession numbers for the sequences reported in this paper are given in Methods.. <i>Microbiology (United Kingdom)</i> , 2002, 148, 3353-3364.	1.8	377
355	Nanogeoscience: From the movement of electrons to lithosphere plates. <i>Eos</i> , 2002, 83, 53.	0.1	9
356	Modification of olivine surface morphology and reactivity by microbial activity during chemical weathering. <i>Geochimica Et Cosmochimica Acta</i> , 2002, 66, 213-221.	3.9	71
357	Direct determinations of the rates of rhyolite dissolution and clay formation over 52,000 years and comparison with laboratory measurements. <i>Geochimica Et Cosmochimica Acta</i> , 2002, 66, 2665-2681.	3.9	45
358	Kinetics of Crystallization and Crystal Growth of Nanocrystalline Anatase in Nanometer-Sized Amorphous Titania. <i>Chemistry of Materials</i> , 2002, 14, 4145-4154.	6.7	238
359	Nanometre-size products of uranium bioreduction. <i>Nature</i> , 2002, 419, 134-134.	27.8	360
360	Geomicrobiology: How Molecular-Scale Interactions Underpin Biogeochemical Systems. <i>Science</i> , 2002, 296, 1071-1077.	12.6	225

#	ARTICLE	IF	CITATIONS
361	Kinetics, surface chemistry, and structural evolution of microbially mediated sulfide mineral dissolution. <i>Geochimica Et Cosmochimica Acta</i> , 2001, 65, 1243-1258.	3.9	105
362	The effect of Fe-oxidizing bacteria on Fe-silicate mineral dissolution. <i>Chemical Geology</i> , 2001, 180, 99-115.	3.3	123
363	Rapid Arsenite Oxidation by <i>Thermus aquaticus</i> and <i>Thermus thermophilus</i> : A Field and Laboratory Investigations. <i>Environmental Science &amp; Technology</i> , 2001, 35, 3857-3862.	10.0	223
364	1. Nanoparticles in the Environment. , 2001, , 1-58.		11
365	Quantitative determination of elemental sulfur at the arsenopyrite surface after oxidation by ferric iron: mechanistic implications. <i>Geochemical Transactions</i> , 2001, 2, 1.	0.7	21
366	Preparing Single-Phase Nanocrystalline Anatase from Amorphous Titania with Particle Sizes Tailored by Temperature. <i>Nano Letters</i> , 2001, 1, 81-85.	9.1	194
367	Arsenite oxidation and arsenate respiration by a new <i>Thermus</i> isolate. <i>FEMS Microbiology Letters</i> , 2001, 204, 335-340.	1.8	178
368	A new look at microbial leaching patterns on sulfide minerals. <i>FEMS Microbiology Ecology</i> , 2001, 34, 197-206.	2.7	73
369	Mineralogical Biosignatures and the Search for Life on Mars. <i>Astrobiology</i> , 2001, 1, 447-465.	3.0	139
370	A new look at microbial leaching patterns on sulfide minerals. <i>FEMS Microbiology Ecology</i> , 2001, 34, 197-206.	2.7	5
371	Arsenite oxidation and arsenate respiration by a new <i>Thermus</i> isolate. <i>FEMS Microbiology Letters</i> , 2001, 204, 335-340.	1.8	3
372	Quantitative determination of elemental sulfur at the arsenopyrite surface after oxidation by ferric iron: mechanistic implications. <i>Geochemical Transactions</i> , 2001, 2, 25.	0.7	3
373	Nanoparticles and the Environment. , 2001, , .		118
374	Microstructural characterization of metamorphic magnetite crystals with implications for oxygen isotope distribution. <i>American Mineralogist</i> , 2000, 85, 14-21.	1.9	15
375	New insights into the mechanism for chloritization of biotite using polytype analysis. <i>American Mineralogist</i> , 2000, 85, 1202-1208.	1.9	24
376	Characteristics of attachment and growth of <i>Thiobacillus caldus</i> on sulphide minerals: a chemotactic response to sulphur minerals?. <i>Environmental Microbiology</i> , 2000, 2, 324-332.	3.8	86
377	Understanding Polymorphic Phase Transformation Behavior during Growth of Nanocrystalline Aggregates: A Insights from TiO <sub>2</sub> . <i>Journal of Physical Chemistry B</i> , 2000, 104, 3481-3487.	2.6	1,383
378	Phase transformation of nanocrystalline anatase-to-rutile via combined interface and surface nucleation. <i>Journal of Materials Research</i> , 2000, 15, 437-448.	2.6	331

#	ARTICLE	IF	CITATIONS
379	Phylogeny of Microorganisms Populating a Thick, Subaerial, Predominantly Lithotrophic Biofilm at an Extreme Acid Mine Drainage Site. <i>Applied and Environmental Microbiology</i> , 2000, 66, 3842-3849.	3.1	325
380	Comparison of Acid Mine Drainage Microbial Communities in Physically and Geochemically Distinct Ecosystems. <i>Applied and Environmental Microbiology</i> , 2000, 66, 4962-4971.	3.1	282
381	Geomicrobiological controls on light rare earth element, Y and Ba distributions during granite weathering and soil formation. <i>Journal of Alloys and Compounds</i> , 2000, 303-304, 30-36.	5.5	56
382	Microbial controls on phosphate and lanthanide distributions during granite weathering and soil formation. <i>Chemical Geology</i> , 2000, 169, 371-382.	3.3	141
383	Geochemical and biological aspects of sulfide mineral dissolution: lessons from Iron Mountain, California. <i>Chemical Geology</i> , 2000, 169, 383-397.	3.3	129
384	An Archaeal Iron-Oxidizing Extreme Acidophile Important in Acid Mine Drainage. <i>Science</i> , 2000, 287, 1796-1799.	12.6	510
385	Formation of Sphalerite (ZnS) Deposits in Natural Biofilms of Sulfate-Reducing Bacteria. , 2000, 290, 1744-1747.		554
386	Seasonal Variations in Microbial Populations and Environmental Conditions in an Extreme Acid Mine Drainage Environment. <i>Applied and Environmental Microbiology</i> , 1999, 65, 3627-3632.	3.1	212
387	Theoretical studies on the formation of mercury complexes in solution and the dissolution and reactions of cinnabar. <i>American Mineralogist</i> , 1999, 84, 877-883.	1.9	19
388	New kinetic model for the nanocrystalline anatase-to-rutile transformation revealing rate dependence on number of particles. <i>American Mineralogist</i> , 1999, 84, 528-535.	1.9	249
389	Enhanced Adsorption of Molecules on Surfaces of Nanocrystalline Particles. <i>Journal of Physical Chemistry B</i> , 1999, 103, 4656-4662.	2.6	238
390	Morphology development and crystal growth in nanocrystalline aggregates under hydrothermal conditions: insights from titania. <i>Geochimica Et Cosmochimica Acta</i> , 1999, 63, 1549-1557.	3.9	979
391	Formation of rutile nuclei at anatase (112) twin interfaces and the phase transformation mechanism in nanocrystalline titania. <i>American Mineralogist</i> , 1999, 84, 871-876.	1.9	238
392	8. Geomicrobiology of Uranium. , 1999, , 393-432.		50
393	TEM investigation of Lewiston, Idaho, fibrolite; microstructure and grain boundary energetics. <i>American Mineralogist</i> , 1999, 84, 152-159.	1.9	13
394	Thermodynamic analysis of phase stability of nanocrystalline titania. <i>Journal of Materials Chemistry</i> , 1998, 8, 2073-2076.	6.7	1,173
395	A model for exploring particle size and temperature dependence of excess heat capacities of nanocrystalline substances. <i>Scripta Materialia</i> , 1998, 10, 185-194.	0.5	22
396	Imperfect Oriented Attachment: Dislocation Generation in Defect-Free Nanocrystals. , 1998, 281, 969-971.		2,230



#	ARTICLE	IF	CITATIONS
397	Distribution of <i>Thiobacillus ferrooxidans</i> and <i>Leptospirillum ferrooxidans</i> : Implications for Generation of Acid Mine Drainage. <i>Science</i> , 1998, 279, 1519-1522.	12.6	315
398	Oriented attachment and growth, twinning, polytypism, and formation of metastable phases; insights from nanocrystalline $\text{TiO}_2$ . <i>American Mineralogist</i> , 1998, 83, 1077-1082.	1.9	478
399	Atomic-resolution transmission electron microscope evidence for the mechanism by which chlorite weathers to 1:1 semi-regular chlorite-vermiculite. <i>American Mineralogist</i> , 1998, 83, 348-357.	1.9	73
400	Distribution of cations and vacancies and the structure of defects in oxidized intermediate olivine by atomic-resolution TEM and image simulation. <i>American Mineralogist</i> , 1998, 83, 799-810.	1.9	25
401	Direct identification of the six polytypes of chlorite characterized by semi-random stacking. <i>American Mineralogist</i> , 1998, 83, 925-930.	1.9	35
402	Microbial oxidation of pyrite; experiments using microorganisms from an extreme acidic environment. <i>American Mineralogist</i> , 1998, 83, 1444-1453.	1.9	97
403	Low-Temperature Alteration in Tuffs from Yucca Mountain, Nevada. <i>Clays and Clay Minerals</i> , 1998, 46, 27-37.	1.3	12
404	Particle size effects on transformation kinetics and phase stability in nanocrystalline $\text{TiO}_2$ . <i>American Mineralogist</i> , 1997, 82, 717-728.	1.9	653
405	Phase Stability in the Nanocrystalline $\text{TiO}_2$ System. <i>Materials Research Society Symposia Proceedings</i> , 1997, 481, 619.	0.1	6
406	Chapter 3. PROCESSES AT MINERALS AND SURFACES WITH RELEVANCE TO MICROORGANISMS AND PREBIOTIC SYNTHESIS. , 1997, , 81-122.		22
407	Chapter 12. BIOGEOCHEMICAL WEATHERING OF SILICATE MINERALS. , 1997, , 391-428.		81
408	Formation of regularly interstratified serpentine-chlorite minerals by tetrahedral inversion in long-period serpentine polytypes. <i>American Mineralogist</i> , 1996, 81, 79-91.	1.9	45
409	Dozyite, a 1:1 regular interstratification of serpentine and chlorite. <i>American Mineralogist</i> , 1995, 80, 65-77.	1.9	31
410	HRTEM study comparing naturally and experimentally weathered pyroxenoids. <i>Geochimica Et Cosmochimica Acta</i> , 1995, 59, 19-31.	3.9	51
411	Derivation and identification of nonstandard serpentine polytypes. <i>American Mineralogist</i> , 1995, 80, 1104-1115.	1.9	19
412	Complex polytypism; relationships between serpentine structural characteristics and deformation. <i>American Mineralogist</i> , 1995, 80, 1116-1131.	1.9	32
413	Polysomatism, polytypism, defect microstructures, and reaction mechanisms in regularly and randomly interstratified serpentine and chlorite. <i>Contributions To Mineralogy and Petrology</i> , 1994, 117, 137-150.	3.1	27
414	Direct observation of reactant-product interfaces formed in natural weathering of exsolved, defective amphibole to smectite: Evidence for episodic, isovolumetric reactions involving structural inheritance. <i>Geochimica Et Cosmochimica Acta</i> , 1994, 58, 1419-1429.	3.9	51



#	ARTICLE	IF	CITATIONS
415	Leaching and reconstruction at the surfaces of dissolving chain-silicate minerals. <i>Nature</i> , 1993, 366, 253-256.	27.8	226
416	What do dissolution experiments tell us about natural weathering?. <i>Chemical Geology</i> , 1993, 105, 1-15.	3.3	126
417	TiO <sub>2</sub> accessory minerals: coarsening, and transformation kinetics in pure and doped synthetic nanocrystalline materials. <i>Chemical Geology</i> , 1993, 110, 211-231.	3.3	109
418	An aem-tem study of weathering and diagenesis, Abert Lake, Oregon: I. Weathering reactions in the volcanics. <i>Geochimica Et Cosmochimica Acta</i> , 1991, 55, 2781-2793.	3.9	97
419	An AEM-TEM study of weathering and diagenesis, Abert Lake, Oregon: II. Diagenetic modification of the sedimentary assemblage. <i>Geochimica Et Cosmochimica Acta</i> , 1991, 55, 2795-2810.	3.9	59
420	Transmission electron microscopy of subsolidus oxidation and weathering of olivine. <i>Contributions To Mineralogy and Petrology</i> , 1990, 106, 110-123.	3.1	94
421	Analytical Transmission Electron Microscope Studies of Plagioclase, Muscovite, and K-Feldspar Weathering. <i>Clays and Clay Minerals</i> , 1990, 38, 77-89.	1.3	157
422	Apatite Replacement and Rare Earth Mobilization, Fractionation, and Fixation During Weathering. <i>Clays and Clay Minerals</i> , 1989, 37, 113-127.	1.3	227
423	The surface chemistry of dissolving labradorite feldspar. <i>Geochimica Et Cosmochimica Acta</i> , 1989, 53, 821-832.	3.9	165
424	The surface of labradorite feldspar after acid hydrolysis. <i>Chemical Geology</i> , 1989, 78, 205-218.	3.3	96
425	Transmission Electron Microscope Study of Biotite Weathering. <i>Clays and Clay Minerals</i> , 1988, 36, 47-60.	1.3	164
426	A weathering-related origin of widespread monazite in S-type granites. <i>Geochimica Et Cosmochimica Acta</i> , 1986, 50, 171-175.	3.9	74
427	Microbial controls on the mineralogy of the environment. , 0, , 177-212.		4