Jillian F Banfield

List of Publications by Citations

470 papers	48,578 citations	112 h-index	209 g-index
511 ext. papers	59,316 ext. citations	11 avg, IF	7.82 L-index

#	Paper	IF	Citations
470	Imperfect oriented attachment: dislocation generation in defect-free nanocrystals. *Science*, **1998**, 281, 969-71	33.3	2024
469	Community structure and metabolism through reconstruction of microbial genomes from the environment. *Nature*, **2004**, 428, 37-43	50.4	1710
468	Understanding Polymorphic Phase Transformation Behavior during Growth of Nanocrystalline Aggregates: Insights from TiO2. *Journal of Physical Chemistry B*, **2000**, 104, 3481-3487	3.4	1254
467	A new view of the tree of life. *Nature Microbiology*, **2016**, 1, 16048	26.6	1128
466	Thermodynamic analysis of phase stability of nanocrystalline titania. *Journal of Materials Chemistry*, **1998**, 8, 2073-2076		1079
465	CRYSTAL GROWTH. Crystallization by particle attachment in synthetic, biogenic, and geologic environments. *Science*, **2015**, 349, aaa6760	33.3	1035
464	Morphology development and crystal growth in nanocrystalline aggregates under hydrothermal conditions: insights from titania. *Geochimica Et Cosmochimica Acta*, **1999**, 63, 1549-1557	5.5	898
463	Direction-specific interactions control crystal growth by oriented attachment. *Science*, **2012**, 336, 1014-8	33.3	812
462	Microbial communities in acid mine drainage. *FEMS Microbiology Ecology*, **2003**, 44, 139-52	4.3	766
461	Unusual biology across a group comprising more than 15% of domain Bacteria. *Nature*, **2015**, 523, 208-11	50.4	688
460	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. *Nature Biotechnology*, **2017**, 35, 725-731	44.5	648
459	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. *Nature Communications*, **2016**, 7, 13219	17.4	589
458	Particle size effects on transformation kinetics and phase stability in nanocrystalline TiO2. *American Mineralogist*, **1997**, 82, 717-728	2.9	581
457	Asgard archaea illuminate the origin of eukaryotic cellular complexity. *Nature*, **2017**, 541, 353-358	50.4	579
456	. *Science*,	33.3	
455	Nanoparticulate Iron Oxide Minerals in Soils and Sediments: Unique Properties and Contaminant Scavenging Mechanisms. *Journal of Nanoparticle Research*, **2005**, 7, 409-433	2.3	487
454	Fermentation, hydrogen, and sulfur metabolism in multiple uncultivated bacterial phyla. *Science*, **2012**, 337, 1661-5	33.3	464

453	Formation of sphalerite (ZnS) deposits in natural biofilms of sulfate-reducing bacteria. *Science*, **2000**, 290, 1744-7	33.3	460
452	Influence of surface potential on aggregation and transport of titania nanoparticles. *Environmental Science & Technology*, **2006**, 40, 7688-93	10.3	451
451	An archaeal iron-oxidizing extreme acidophile important in acid mine drainage. *Science*, **2000**, 287, 1796-9	33.3	442
450	Oriented attachment and growth, twinning, polytypism, and formation of metastable phases; insights from nanocrystalline TiO2. *American Mineralogist*, **1998**, 83, 1077-1082	2.9	421
449	dRep: a tool for fast and accurate genomic comparisons that enables improved genome recovery from metagenomes through de-replication. *ISME Journal*, **2017**, 11, 2864-2868	11.9	419
448	Community-wide analysis of microbial genome sequence signatures. *Genome Biology*, **2009**, 10, R85	18.3	396
447	Programmed DNA destruction by miniature CRISPR-Cas14 enzymes. *Science*, **2018**, 362, 839-842	33.3	394
446	Virus population dynamics and acquired virus resistance in natural microbial communities. *Science*, **2008**, 320, 1047-50	33.3	392
445	Water-driven structure transformation in nanoparticles at room temperature. *Nature*, **2003**, 424, 1025-9	50.4	392
444	Nanoparticles: strained and stiff. *Science*, **2004**, 305, 651-4	33.3	370
443	Microbial polysaccharides template assembly of nanocrystal fibers. *Science*, **2004**, 303, 1656-8	33.3	362
442	Genomic expansion of domain archaea highlights roles for organisms from new phyla in anaerobic carbon cycling. *Current Biology*, **2015**, 25, 690-701	6.3	354
441	Recovery of genomes from metagenomes via a dereplication, aggregation and scoring strategy. *Nature Microbiology*, **2018**, 3, 836-843	26.6	354
440	Microscopic evidence for liquid-liquid separation in supersaturated CaCO3 solutions. *Science*, **2013**, 341, 885-9	33.3	346
439	Two-Stage Crystal-Growth Kinetics Observed during Hydrothermal Coarsening of Nanocrystalline ZnS. *Nano Letters*, **2003**, 3, 373-378	11.5	343
438	Glycogen-accumulating organisms in laboratory-scale and full-scale wastewater treatment processes. *Microbiology (United Kingdom)*, **2002**, 148, 3353-3364	2.9	336
437	Gene transfer from bacteria and archaea facilitated evolution of an extremophilic eukaryote. *Science*, **2013**, 339, 1207-10	33.3	324
436	Time series community genomics analysis reveals rapid shifts in bacterial species, strains, and phage during infant gut colonization. *Genome Research*, **2013**, 23, 111-20	9.7	324

435	New CRISPR-Cas systems from uncultivated microbes. *Nature*, **2017**, 542, 237-241	50.4	320
434	Community genomic analyses constrain the distribution of metabolic traits across the Chloroflexi phylum and indicate roles in sediment carbon cycling. *Microbiome*, **2013**, 1, 22	16.6	305
433	Nanometre-size products of uranium bioreduction. *Nature*, **2002**, 419, 134	50.4	304
432	Phase transformation of nanocrystalline anatase-to-rutile via combined interface and surface nucleation. *Journal of Materials Research*, **2000**, 15, 437-448	2.5	300
431	Phylogeny of microorganisms populating a thick, subaerial, predominantly lithotrophic biofilm at an extreme acid mine drainage site. *Applied and Environmental Microbiology*, **2000**, 66, 3842-9	4.8	294
430	Major New Microbial Groups Expand Diversity and Alter our Understanding of the Tree of Life. *Cell*, **2018**, 172, 1181-1197	56.2	272
429	Distribution of thiobacillus ferrooxidans and leptospirillum ferrooxidans: implications for generation of acid mine drainage. *Science*, **1998**, 279, 1519-22	33.3	265
428	EMIRGE: reconstruction of full-length ribosomal genes from microbial community short read sequencing data. *Genome Biology*, **2011**, 12, R44	18.3	256
427	De novo metagenomic assembly reveals abundant novel major lineage of Archaea in hypersaline microbial communities. *ISME Journal*, **2012**, 6, 81-93	11.9	254
426	Microbes in the neonatal intensive care unit resemble those found in the gut of premature infants. *Microbiome*, **2014**, 2, 1	16.6	251
425	The human gut and groundwater harbor non-photosynthetic bacteria belonging to a new candidate phylum sibling to Cyanobacteria. *ELife*, **2013**, 2, e01102	8.9	247
424	Iron oxyhydroxide mineralization on microbial extracellular polysaccharides. *Geochimica Et Cosmochimica Acta*, **2009**, 73, 3807-3818	5.5	245
423	Rapidly evolving CRISPRs implicated in acquired resistance of microorganisms to viruses. *Environmental Microbiology*, **2008**, 10, 200-7	5.2	242
422	Comparison of acid mine drainage microbial communities in physically and geochemically distinct ecosystems. *Applied and Environmental Microbiology*, **2000**, 66, 4962-71	4.8	233
421	Diverse uncultivated ultra-small bacterial cells in groundwater. *Nature Communications*, **2015**, 6, 6372	17.4	232
420	Enigmatic, ultrasmall, uncultivated Archaea. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 8806-11	11.5	231
419	Structural characteristics and mechanical and thermodynamic properties of nanocrystalline TiO2. *Chemical Reviews*, **2014**, 114, 9613-44	68.1	226
418	Kinetics of Crystallization and Crystal Growth of Nanocrystalline Anatase in Nanometer-Sized Amorphous Titania. *Chemistry of Materials*, **2002**, 14, 4145-4154	9.6	222

417	Extracellular proteins limit the dispersal of biogenic nanoparticles. *Science*, **2007**, 316, 1600-3	33.3	221
416	Environmental risks of nanotechnology: National Nanotechnology Initiative funding, 2000-2004. *Environmental Science & Technology*, **2006**, 40, 1401-7	10.3	219
415	New kinetic model for the nanocrystalline anatase-to-rutile transformation revealing rate dependence on number of particles. *American Mineralogist*, **1999**, 84, 528-535	2.9	218
414	Enhanced Adsorption of Molecules on Surfaces of Nanocrystalline Particles. *Journal of Physical Chemistry B*, **1999**, 103, 4656-4662	3.4	217
413	Measurement of bacterial replication rates in microbial communities. *Nature Biotechnology*, **2016**, 34, 1256-1263	44.5	207
412	Small genomes and sparse metabolisms of sediment-associated bacteria from four candidate phyla. *MBio*, **2013**, 4, e00708-13	7.8	204
411	Formation of rutile nuclei at anatase (112) twin interfaces and the phase transformation mechanism in nanocrystalline titania. *American Mineralogist*, **1999**, 84, 871-876	2.9	204
410	Systems biology: Functional analysis of natural microbial consortia using community proteomics. *Nature Reviews Microbiology*, **2009**, 7, 196-205	22.2	203
409	Strain-resolved community genomic analysis of gut microbial colonization in a premature infant. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 1128-33	11.5	201
408	Leaching and reconstruction at the surfaces of dissolving chain-silicate minerals. *Nature*, **1993**, 366, 253-256	3.4	199
407	Genome-directed isolation of the key nitrogen fixer Leptospirillum ferrodiazotrophum sp. nov. from an acidophilic microbial community. *Applied and Environmental Microbiology*, **2005**, 71, 6319-24	4.8	195
406	Despite strong seasonal responses, soil microbial consortia are more resilient to long-term changes in rainfall than overlying grassland. *ISME Journal*, **2009**, 3, 738-44	11.9	194
405	Strain-resolved community proteomics reveals recombining genomes of acidophilic bacteria. *Nature*, **2007**, 446, 537-41	50.4	193
404	Apatite Replacement and Rare Earth Mobilization, Fractionation, and Fixation During Weathering. *Clays and Clay Minerals*, **1989**, 37, 113-127	2.1	193
403	Lineages of acidophilic archaea revealed by community genomic analysis. *Science*, **2006**, 314, 1933-5	33.3	190
402	Characterization of extracellular polymeric substances from acidophilic microbial biofilms. *Applied and Environmental Microbiology*, **2010**, 76, 2916-22	4.8	189
401	Preparing Single-Phase Nanocrystalline Anatase from Amorphous Titania with Particle Sizes Tailored by Temperature. *Nano Letters*, **2001**, 1, 81-85	11.5	188
400	Rapid arsenite oxidation by Thermus aquaticus and Thermus thermophilus: field and laboratory investigations. *Environmental Science & Technology*, **2001**, 35, 3857-62	10.3	188

399	Geomicrobiology: how molecular-scale interactions underpin biogeochemical systems. *Science*, **2002**, 296, 1071-7	33.3	183
398	Community genomics in microbial ecology and evolution. *Nature Reviews Microbiology*, **2005**, 3, 489-98	22.2	182
397	Acid mine drainage biogeochemistry at Iron Mountain, California. *Geochemical Transactions*, **2004**, 5, 1	3	181
396	Characterization of titanium dioxide nanoparticles using molecular dynamics simulations. *Journal of Physical Chemistry B*, **2005**, 109, 15243-9	3.4	179
395	Seasonal variations in microbial populations and environmental conditions in an extreme acid mine drainage environment. *Applied and Environmental Microbiology*, **1999**, 65, 3627-32	4.8	173
394	Expanded diversity of microbial groups that shape the dissimilatory sulfur cycle. *ISME Journal*, **2018**, 12, 1715-1728	11.9	165
393	Novel soil bacteria possess diverse genes for secondary metabolite biosynthesis. *Nature*, **2018**, 558, 440-444	50.4	165
392	Molecular Dynamics Simulations, Thermodynamic Analysis, and Experimental Study of Phase Stability of Zinc Sulfide Nanoparticles. *Journal of Physical Chemistry B*, **2003**, 107, 13051-13060	3.4	165
391	AMD biofilms: using model communities to study microbial evolution and ecological complexity in nature. *ISME Journal*, **2010**, 4, 599-610	11.9	164
390	CRISPR-Cas from huge phages is a hypercompact genome editor. *Science*, **2020**, 369, 333-337	33.3	158
389	Size-dependent phase transformation kinetics in nanocrystalline ZnS. *Journal of the American Chemical Society*, **2005**, 127, 4523-9	16.4	157
388	Resistance to, and Accumulation of, Uranium by Bacteria from a Uranium-Contaminated Site. *Geomicrobiology Journal*, **2004**, 21, 113-121	2.5	157
387	Arsenite oxidation and arsenate respiration by a new Thermus isolate. *FEMS Microbiology Letters*, **2001**, 204, 335-40	2.9	155
386	Clades of huge phages from across Earth's ecosystems. *Nature*, **2020**, 578, 425-431	50.4	154
385	The Role of Oriented Attachment Crystal Growth in Hydrothermal Coarsening of Nanocrystalline ZnS. *Journal of Physical Chemistry B*, **2003**, 107, 10470-10475	3.4	153
384	Biosynthetic capacity, metabolic variety and unusual biology in the CPR and DPANN radiations. *Nature Reviews Microbiology*, **2018**, 16, 629-645	22.2	153
383	Community genomic and proteomic analyses of chemoautotrophic iron-oxidizing "Leptospirillum rubarum" (Group II) and "Leptospirillum ferrodiazotrophum" (Group III) bacteria in acid mine drainage biofilms. *Applied and Environmental Microbiology*, **2009**, 75, 4599-615	4.8	149
382	The surface chemistry of dissolving labradorite feldspar. *Geochimica Et Cosmochimica Acta*, **1989**, 53, 821-832	5.5	149

381	Microbial populations stimulated for hexavalent uranium reduction in uranium mine sediment. *Applied and Environmental Microbiology*, **2003**, 69, 1337-46	4.8	148
380	Extraordinary phylogenetic diversity and metabolic versatility in aquifer sediment. *Nature Communications*, **2013**, 4, 2120	17.4	145
379	Metabolically active eukaryotic communities in extremely acidic mine drainage. *Applied and Environmental Microbiology*, **2004**, 70, 6264-71	4.8	144
378	Strong bias in the bacterial CRISPR elements that confer immunity to phage. *Nature Communications*, **2013**, 4, 1430	17.4	143
377	Atomic structure of nanometer-sized amorphous TiO2. *Physical Review B*, **2008**, 78,	3.3	141
376	Community proteogenomics highlights microbial strain-variant protein expression within activated sludge performing enhanced biological phosphorus removal. *ISME Journal*, **2008**, 2, 853-64	11.9	137
375	Transmission Electron Microscope Study of Biotite Weathering. *Clays and Clay Minerals*, **1988**, 36, 47-60	2.1	135
374	Differential depth distribution of microbial function and putative symbionts through sediment-hosted aquifers in the deep terrestrial subsurface. *Nature Microbiology*, **2018**, 3, 328-336	26.6	133
373	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, 2383-90	11.5	133
372	Metabolic interdependencies between phylogenetically novel fermenters and respiratory organisms in an unconfined aquifer. *ISME Journal*, **2014**, 8, 1452-63	11.9	131
371	Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. *Nature Communications*, **2016**, 7, 10613	17.4	129
370	Special phase transformation and crystal growth pathways observed in nanoparticles *Geochemical Transactions*, **2003**, 4, 1	3	127
369	Phase Stability and Transformation in Titania Nanoparticles in Aqueous Solutions Dominated by Surface Energy. *Journal of Physical Chemistry C*, **2007**, 111, 1962-1968	3.8	125
368	Tetraether-linked membrane monolayers in Ferroplasma spp: a key to survival in acid. *Extremophiles*, **2004**, 8, 411-9	3	124
367	Analytical Transmission Electron Microscope Studies of Plagioclase, Muscovite, and K-Feldspar Weathering. *Clays and Clay Minerals*, **1990**, 38, 77-89	2.1	124
366	CRISPR immunity drives rapid phage genome evolution in Streptococcus thermophilus. *MBio*, **2015**, 6,	7.8	119
365	What do dissolution experiments tell us about natural weathering?. *Chemical Geology*, **1993**, 105, 1-15	4.2	117
364	Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO concentrations. *Environmental Microbiology*, **2017**, 19, 459-474	5.2	116

363	Proteogenomic monitoring of Geobacter physiology during stimulated uranium bioremediation. *Applied and Environmental Microbiology*, **2009**, 75, 6591-9	4.8	116
362	Genome dynamics in a natural archaeal population. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 1883-8	11.5	115
361	Microbial controls on phosphate and lanthanide distributions during granite weathering and soil formation. *Chemical Geology*, **2000**, 169, 371-382	4.2	114
360	Persisting viral sequences shape microbial CRISPR-based immunity. *PLoS Computational Biology*, **2012**, 8, e1002475	5	113
359	Accurate and complete genomes from metagenomes. *Genome Research*, **2020**, 30, 315-333	9.7	112
358	Microbiology. Genomes from metagenomics. *Science*, **2013**, 342, 1057-8	33.3	112
357	Mineralogical biosignatures and the search for life on Mars. *Astrobiology*, **2001**, 1, 447-65	3.7	112
356	Critical biogeochemical functions in the subsurface are associated with bacteria from new phyla and little studied lineages. *Environmental Microbiology*, **2016**, 18, 159-73	5.2	111
355	Geomicrobiology **1997**,		109
354	Geophysical imaging of stimulated microbial biomineralization. *Environmental Science & Technology*, **2005**, 39, 7592-600	10.3	108
353	Geophysical monitoring of coupled microbial and geochemical processes during stimulated subsurface bioremediation. *Environmental Science & Technology*, **2009**, 43, 6717-23	10.3	107
352	Population genomic analysis of strain variation in Leptospirillum group II bacteria involved in acid mine drainage formation. *PLoS Biology*, **2008**, 6, e177	9.7	106
351	Size Dependence of the Kinetic Rate Constant for Phase Transformation in TiO2 Nanoparticles. *Chemistry of Materials*, **2005**, 17, 3421-3425	9.6	106
350	Geochemical and biological aspects of sulfide mineral dissolution: lessons from Iron Mountain, California. *Chemical Geology*, **2000**, 169, 383-397	4.2	105
349	Strain-resolved analysis of hospital rooms and infants reveals overlap between the human and room microbiome. *Nature Communications*, **2017**, 8, 1814	17.4	102
348	Three-dimensional analysis of the structure and ecology of a novel, ultra-small archaeon. *ISME Journal*, **2009**, 3, 159-67	11.9	101
347	The effect of Fe-oxidizing bacteria on Fe-silicate mineral dissolution. *Chemical Geology*, **2001**, 180, 99-115	4.2	101
346	Genome-Resolved Metagenomic Analysis Reveals Roles for Candidate Phyla and Other Microbial Community Members in Biogeochemical Transformations in Oil Reservoirs. *MBio*, **2016**, 7, e01669-15	7.8	100

345	A unified description of attachment-based crystal growth. *ACS Nano*, **2014**, 8, 6526-30	16.7	99
344	Insights into the ecology, evolution, and metabolism of the widespread Woesearchaeotal lineages. *Microbiome*, **2018**, 6, 102	16.6	98
343	Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. *Genome Research*, **2015**, 25, 534-43	9.7	96
342	The size dependence of the surface free energy of titania nanocrystals. *Physical Chemistry Chemical Physics*, **2009**, 11, 2553-8	3.6	96
341	TiO2 accessory minerals: coarsening, and transformation kinetics in pure and doped synthetic nanocrystalline materials. *Chemical Geology*, **1993**, 110, 211-231	4.2	96
340	Gut bacteria are rarely shared by co-hospitalized premature infants, regardless of necrotizing enterocolitis development. *ELife*, **2015**, 4,	8.9	96
339	The surface of labradorite feldspar after acid hydrolysis. *Chemical Geology*, **1989**, 78, 205-218	4.2	93
338	Particle Size and pH Effects on Nanoparticle Dissolution. *Journal of Physical Chemistry C*, **2010**, 114, 14876-14884	5.1	92
337	Direct microbial reduction and subsequent preservation of uranium in natural near-surface sediment. *Applied and Environmental Microbiology*, **2005**, 71, 1790-7	4.8	92
336	Kinetics, surface chemistry, and structural evolution of microbially mediated sulfide mineral dissolution. *Geochimica Et Cosmochimica Acta*, **2001**, 65, 1243-1258	5.5	92
335	Analysis of streptococcal CRISPRs from human saliva reveals substantial sequence diversity within and between subjects over time. *Genome Research*, **2011**, 21, 126-36	9.7	90
334	Insights into the diversity of eukaryotes in acid mine drainage biofilm communities. *Applied and Environmental Microbiology*, **2009**, 75, 2192-9	4.8	90
333	Megaphages infect Prevotella and variants are widespread in gut microbiomes. *Nature Microbiology* , **2019**, 4, 693-700	26.6	89
332	Biology of a widespread uncultivated archaeon that contributes to carbon fixation in the subsurface. *Nature Communications*, **2014**, 5, 5497	17.4	86
331	Ultrastructure, aggregation-state, and crystal growth of biogenic nanocrystalline sphalerite and wurtzite. *American Mineralogist*, **2004**, 89, 950-960	2.9	86
330	The dynamic genetic repertoire of microbial communities. *FEMS Microbiology Reviews*, **2009**, 33, 109-32	15.1	85
329	Aggregation, Coarsening, and Phase Transformation in ZnS Nanoparticles Studied by Molecular Dynamics Simulations. *Nano Letters*, **2004**, 4, 713-718	11.5	85
328	Wide diversity of methane and short-chain alkane metabolisms in uncultured archaea. *Nature Microbiology*, **2019**, 4, 603-613	26.6	84

327	Interatomic Coulombic interactions as the driving force for oriented attachment. *CrystEngComm*, **2014**, 16, 1568-1578	3.3	84
326	Energy Calculations Predict Nanoparticle Attachment Orientations and Asymmetric Crystal Formation. *Journal of Physical Chemistry Letters*, **2012**, 3, 2882-2886	6.4	84
325	Population genomics in natural microbial communities. *Trends in Ecology and Evolution*, **2006**, 21, 508-16	10.9	84
324	Transmission electron microscopy of subsolidus oxidation and weathering of olivine. *Contributions To Mineralogy and Petrology*, **1990**, 106, 110-123	3.5	84
323	Simulation of oil plume reveals substrate specialization within a complex community of hydrocarbon degraders. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 7432-7437	11.5	82
322	In situ evolutionary rate measurements show ecological success of recently emerged bacterial hybrids. *Science*, **2012**, 336, 462-6	33.3	82
321	Aggregation-induced growth and transformation of ╫FeOOH nanorods to micron-sized ╪Fe2O3 spindles. *CrystEngComm*, **2014**, 16, 1451-1458	3.3	81
320	Quantification of chemical weathering rates across an actively eroding hillslope. *Earth and Planetary Science Letters*, **2006**, 242, 155-169	5.3	81
319	Microbial oxidation of pyrite; experiments using microorganisms from an extreme acidic environment. *American Mineralogist*, **1998**, 83, 1444-1453	2.9	81
318	An aem-tem study of weathering and diagenesis, Abert Lake, Oregon: I. Weathering reactions in the volcanics. *Geochimica Et Cosmochimica Acta*, **1991**, 55, 2781-2793	5.5	81
317	Short-read assembly of full-length 16S amplicons reveals bacterial diversity in subsurface sediments. *PLoS ONE*, **2013**, 8, e56018	3.7	81
316	Phage mutations in response to CRISPR diversification in a bacterial population. *Environmental Microbiology*, **2013**, 15, 463-70	5.2	80
315	Potential for microbial H and metal transformations associated with novel bacteria and archaea in deep terrestrial subsurface sediments. *ISME Journal*, **2017**, 11, 1915-1929	11.9	79
314	Biostimulation induces syntrophic interactions that impact C, S and N cycling in a sediment microbial community. *ISME Journal*, **2013**, 7, 800-16	11.9	78
313	Stable isotope informed genome-resolved metagenomics reveals that Saccharibacteria utilize microbially-processed plant-derived carbon. *Microbiome*, **2018**, 6, 122	16.6	77
312	Investigating processes of nanocrystal formation and transformation via liquid cell TEM. *Microscopy and Microanalysis*, **2014**, 20, 425-36	0.5	76
311	Cultivating the uncultivated: a community genomics perspective. *Trends in Microbiology*, **2005**, 13, 411-5	12.4	76
310	Comparative genomics in acid mine drainage biofilm communities reveals metabolic and structural differentiation of co-occurring archaea. *BMC Genomics*, **2013**, 14, 485	4.5	75

309	Natural acidophilic biofilm communities reflect distinct organismal and functional organization. *ISME Journal*, **2009**, 3, 266-70	11.9	75
308	Characteristics of attachment and growth of Thiobacillus caldus on sulphide minerals: a chemotactic response to sulphur minerals?. *Environmental Microbiology*, **2000**, 2, 324-32	5.2	74
307	Surface chemistry controls crystallinity of ZnS nanoparticles. *Nano Letters*, **2006**, 6, 605-10	11.5	73
306	Extremely acidophilic protists from acid mine drainage host Rickettsiales-lineage endosymbionts that have intervening sequences in their 16S rRNA genes. *Applied and Environmental Microbiology*, **2003**, 69, 5512-8	4.8	73
305	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome. *Genome Research*, **2018**, 28, 1467-1480	9.7	73
304	Proteogenomic analyses indicate bacterial methylotrophy and archaeal heterotrophy are prevalent below the grass root zone. *PeerJ*, **2016**, 4, e2687	3.1	72
303	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	11.5	72
302	Genome-reconstruction for eukaryotes from complex natural microbial communities. *Genome Research*, **2018**, 28, 569-580	9.7	71
301	U(VI) sorption and reduction kinetics on the magnetite (111) surface. *Environmental Science & Technology*, **2012**, 46, 3821-30	10.3	71
300	Assembly-driven community genomics of a hypersaline microbial ecosystem. *PLoS ONE*, **2013**, 8, e61692	3.7	71
299	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	26.6	70
298	Cytochrome 572 is a conspicuous membrane protein with iron oxidation activity purified directly from a natural acidophilic microbial community. *ISME Journal*, **2008**, 2, 542-50	11.9	70
297	A weathering-related origin of widespread monazite in S-type granites. *Geochimica Et Cosmochimica Acta*, **1986**, 50, 171-175	5.5	69
296	Community Proteomics of a Natural Microbial Biofilm. *Science*, **2005**, 308, 1915-1920	33.3	68
295	Kinetics and mechanism of polythionate oxidation to sulfate at low pH by O2 and Fe3+. *Geochimica Et Cosmochimica Acta*, **2003**, 67, 4457-4469	5.5	67
294	Bioreactor microbial ecosystems for thiocyanate and cyanide degradation unravelled with genome-resolved metagenomics. *Environmental Microbiology*, **2015**, 17, 4929-41	5.2	66
293	Quantitative tracking of isotope flows in proteomes of microbial communities. *Molecular and Cellular Proteomics*, **2011**, 10, M110.006049	7.6	66
292	RubisCO of a nucleoside pathway known from Archaea is found in diverse uncultivated phyla in bacteria. *ISME Journal*, **2016**, 10, 2702-2714	11.9	65

291	Identical bacterial populations colonize premature infant gut, skin, and oral microbiomes and exhibit different in situ growth rates. *Genome Research*, **2017**, 27, 601-612	9.7	63
290	Aquifer environment selects for microbial species cohorts in sediment and groundwater. *ISME Journal*, **2015**, 9, 1846-56	11.9	63
289	Phage-induced expression of CRISPR-associated proteins is revealed by shotgun proteomics in Streptococcus thermophilus. *PLoS ONE*, **2012**, 7, e38077	3.7	63
288	Metabolites associated with adaptation of microorganisms to an acidophilic, metal-rich environment identified by stable-isotope-enabled metabolomics. *MBio*, **2013**, 4, e00484-12	7.8	63
287	Dynamic viral populations in hypersaline systems as revealed by metagenomic assembly. *Applied and Environmental Microbiology*, **2012**, 78, 6309-20	4.8	63
286	Early stage formation of iron oxyhydroxides during neutralization of simulated acid mine drainage solutions. *Environmental Science & Technology*, **2012**, 46, 8140-7	10.3	62
285	Genetic exchange across a species boundary in the archaeal genus ferroplasma. *Genetics*, **2007**, 177, 407-416	4	62
284	A new look at microbial leaching patterns on sulfide minerals. *FEMS Microbiology Ecology*, **2001**, 34, 197-206	4.6	62
283	Development of an enhanced metaproteomic approach for deepening the microbiome characterization of the human infant gut. *Journal of Proteome Research*, **2015**, 14, 133-41	5.6	61
282	Chapter 12. BIOGEOCHEMICAL WEATHERING OF SILICATE MINERALS **1997**, 391-428		60
281	Metagenomic analysis of a high carbon dioxide subsurface microbial community populated by chemolithoautotrophs and bacteria and archaea from candidate phyla. *Environmental Microbiology*, **2016**, 18, 1686-703	5.2	59
280	Cultivation and quantitative proteomic analyses of acidophilic microbial communities. *ISME Journal*, **2010**, 4, 520-30	11.9	59
279	Spectral identification of hydrated sulfates on Mars and comparison with acidic environments on Earth. *International Journal of Astrobiology*, **2004**, 3, 275-285	1.4	59
278	Modification of olivine surface morphology and reactivity by microbial activity during chemical weathering. *Geochimica Et Cosmochimica Acta*, **2002**, 66, 213-221	5.5	59
277	inStrain profiles population microdiversity from metagenomic data and sensitively detects shared microbial strains. *Nature Biotechnology*, **2021**, 39, 727-736	44.5	59
276	Consistent Metagenome-Derived Metrics Verify and Delineate Bacterial Species Boundaries. *MSystems*, **2020**, 5,	7.6	58
275	Seasonal fluctuations in ionic concentrations drive microbial succession in a hypersaline lake community. *ISME Journal*, **2014**, 8, 979-90	11.9	58
274	Vanadate and acetate biostimulation of contaminated sediments decreases diversity, selects for specific taxa, and decreases aqueous V5+ concentration. *Environmental Science & Technology*, **2013**, 47, 6500-9	10.3	58

273	Anatase Coarsening Kinetics under Hydrothermal Conditions As a Function of Ph and Temperature. *Chemistry of Materials*, **2008**, 20, 3443-3449	9.6	58
272	Reversible, surface-controlled structure transformation in nanoparticles induced by an aggregation state. *Physical Review Letters*, **2004**, 92, 155501	7.4	58
271	Virus-host and CRISPR dynamics in Archaea-dominated hypersaline Lake Tyrrell, Victoria, Australia. *Archaea*, **2013**, 2013, 370871	2	57
270	Prediction of the effects of size and morphology on the structure of water around hematite nanoparticles. *Geochimica Et Cosmochimica Acta*, **2009**, 73, 4023-4033	5.5	57
269	Proteogenomic approaches for the molecular characterization of natural microbial communities. *OMICS A Journal of Integrative Biology*, **2005**, 9, 301-33	3.8	57
268	Enzymatic U(VI) reduction by Desulfosporosinus species. *Radiochimica Acta*, **2004**, 92, 11-16	1.9	57
267	Unusual respiratory capacity and nitrogen metabolism in a Parcubacterium (OD1) of the Candidate Phyla Radiation. *Scientific Reports*, **2017**, 7, 40101	4.9	56
266	The distinction of CPR bacteria from other bacteria based on protein family content. *Nature Communications*, **2019**, 10, 4173	17.4	56
265	Iron-reducing bacteria accumulate ferric oxyhydroxide nanoparticle aggregates that may support planktonic growth. *ISME Journal*, **2013**, 7, 338-50	11.9	56
264	Proteomics-inferred genome typing (PIGT) demonstrates inter-population recombination as a strategy for environmental adaptation. *Environmental Microbiology*, **2009**, 11, 313-25	5.2	56
263	Comparison of environmental and isolate Sulfobacillus genomes reveals diverse carbon, sulfur, nitrogen, and hydrogen metabolisms. *BMC Genomics*, **2014**, 15, 1107	4.5	54
262	Size-Dependent Bandgap of Nanogoethite. *Journal of Physical Chemistry C*, **2011**, 115, 17704-17710	3.8	54
261	Characterization of cytochrome 579, an unusual cytochrome isolated from an iron-oxidizing microbial community. *Applied and Environmental Microbiology*, **2008**, 74, 4454-62	4.8	54
260	Niche differentiation is spatially and temporally regulated in the rhizosphere. *ISME Journal*, **2020**, 14, 999-1014	11.9	53
259	Necrotizing enterocolitis is preceded by increased gut bacterial replication, , and fimbriae-encoding bacteria. *Science Advances*, **2019**, 5, eaax5727	14.3	53
258	Bacterial Secondary Metabolite Biosynthetic Potential in Soil Varies with Phylum, Depth, and Vegetation Type. *MBio*, **2020**, 11,	7.8	52
257	Ecological distribution and population physiology defined by proteomics in a natural microbial community. *Molecular Systems Biology*, **2010**, 6, 374	12.2	52
256	Metagenomic reconstructions of bacterial CRISPR loci constrain population histories. *ISME Journal*, **2016**, 10, 858-70	11.9	51

255	Microbial Community Structure and the Persistence of Cyanobacterial Populations in Salt Crusts of the Hyperarid Atacama Desert from Genome-Resolved Metagenomics. *Frontiers in Microbiology*, **2017**, 8, 1435	5.7	51
254	Atomic-resolution transmission electron microscope evidence for the mechanism by which chlorite weathers to 1:1 semi-regular chlorite-vermiculite. *American Mineralogist*, **1998**, 83, 348-357	2.9	50
253	Precipitation pathways for ferrihydrite formation in acidic solutions. *Geochimica Et Cosmochimica Acta*, **2016**, 172, 247-264	5.5	49
252	Identification of simultaneous U(VI) sorption complexes and U(IV) nanoprecipitates on the magnetite (111) surface. *Environmental Science & Technology*, **2012**, 46, 3811-20	10.3	49
251	Analysis of biostimulated microbial communities from two field experiments reveals temporal and spatial differences in proteome profiles. *Environmental Science & Technology*, **2010**, 44, 8897-903	10.3	49
250	A high-throughput de novo sequencing approach for shotgun proteomics using high-resolution tandem mass spectrometry. *BMC Bioinformatics*, **2010**, 11, 118	3.6	49
249	Arsenic resistance in the archaeon "Ferroplasma acidarmanus": new insights into the structure and evolution of the ars genes. *Extremophiles*, **2003**, 7, 123-30	3	49
248	Heterotrophic archaea contribute to carbon cycling in low-pH, suboxic biofilm communities. *Applied and Environmental Microbiology*, **2012**, 78, 8321-30	4.8	48
247	Size-dependent elasticity of nanocrystalline titania. *Physical Review B*, **2009**, 79,	3.3	48
246	Model biomimetic studies of templated growth and assembly of nanocrystalline FeOOH. *Geochimica Et Cosmochimica Acta*, **2003**, 67, 1185-1195	5.5	48
245	An AEM-TEM study of weathering and diagenesis, Abert Lake, Oregon: II. Diagenetic modification of the sedimentary assemblage. *Geochimica Et Cosmochimica Acta*, **1991**, 55, 2795-2810	5.5	47
244	Architecture and gene repertoire of the flexible genome of the extreme acidophile Acidithiobacillus caldus. *PLoS ONE*, **2013**, 8, e78237	3.7	47
243	Community transcriptomics reveals unexpected high microbial diversity in acidophilic biofilm communities. *ISME Journal*, **2015**, 9, 1014-23	11.9	46
242	Quantitative proteomic analyses of the response of acidophilic microbial communities to different pH conditions. *ISME Journal*, **2011**, 5, 1152-61	11.9	46
241	Identification of biofilm matrix-associated proteins from an acid mine drainage microbial community. *Applied and Environmental Microbiology*, **2011**, 77, 5230-7	4.8	46
240	Bicarbonate impact on U(VI) bioreduction in a shallow alluvial aquifer. *Geochimica Et Cosmochimica Acta*, **2015**, 150, 106-124	5.5	44
239	Novel Microbial Diversity and Functional Potential in the Marine Mammal Oral Microbiome. *Current Biology*, **2017**, 27, 3752-3762.e6	6.3	44
238	Direct observation of reactant-product interfaces formed in natural weathering of exsolved, defective amphibole to smectite: Evidence for episodic, isovolumetric reactions involving structural inheritance. *Geochimica Et Cosmochimica Acta*, **1994**, 58, 1419-1429	5.5	44

237	Proteome changes in the initial bacterial colonist during ecological succession in an acid mine drainage biofilm community. *Environmental Microbiology*, **2011**, 13, 2279-92	5.2	43
236	HRTEM study comparing naturally and experimentally weathered pyroxenoids. *Geochimica Et Cosmochimica Acta*, **1995**, 59, 19-31	5.5	43
235	Nanoparticles and the Environment **2001**,		43
234	Retroelement-guided protein diversification abounds in vast lineages of Bacteria and Archaea. *Nature Microbiology*, **2017**, 2, 17045	26.6	42
233	Elevated temperature alters proteomic responses of individual organisms within a biofilm community. *ISME Journal*, **2015**, 9, 180-94	11.9	42
232	Machine Learning Leveraging Genomes from Metagenomes Identifies Influential Antibiotic Resistance Genes in the Infant Gut Microbiome. *MSystems*, **2018**, 3,	7.6	42
231	High-density PhyloChip profiling of stimulated aquifer microbial communities reveals a complex response to acetate amendment. *FEMS Microbiology Ecology*, **2012**, 81, 188-204	4.3	42
230	Direct determinations of the rates of rhyolite dissolution and clay formation over 52,000 years and comparison with laboratory measurements. *Geochimica Et Cosmochimica Acta*, **2002**, 66, 2665-2681	5.5	42
229	The developing premature infant gut microbiome is a major factor shaping the microbiome of neonatal intensive care unit rooms. *Microbiome*, **2018**, 6, 112	16.6	41
228	Metaproteomics reveals functional shifts in microbial and human proteins during a preterm infant gut colonization case. *Proteomics*, **2015**, 15, 3463-73	4.8	41
227	Impacts of ionic strength on three-dimensional nanoparticle aggregate structure and consequences for environmental transport and deposition. *Environmental Science & Technology*, **2014**, 48, 13703-10	10.3	41
226	Effect of rainfall-induced soil geochemistry dynamics on grassland soil microbial communities. *Applied and Environmental Microbiology*, **2012**, 78, 7587-95	4.8	41
225	Kinetically controlled formation of a novel nanoparticulate ZnS with mixed cubic and hexagonal stacking. *Journal of Materials Chemistry*, **2006**, 16, 249-254		41
224	Geomicrobiological controls on light rare earth element, Y and Ba distributions during granite weathering and soil formation. *Journal of Alloys and Compounds*, **2000**, 303-304, 30-36	5.7	41
223	Mechanism of Ferric Oxalate Photolysis. *ACS Earth and Space Chemistry*, **2017**, 1, 270-276	3.2	40
222	Contingency in the direction and mechanics of soil organic matter responses to increased rainfall. *Plant and Soil*, **2012**, 358, 371-383	4.2	40
221	Molecular geomicrobiology: genes and geochemical cycling. *Earth and Planetary Science Letters*, **2003**, 209, 1-17	5.3	40
220	Structure of the bacterial ribosome at 2 Å resolution. *ELife*, **2020**, 9,	8.9	40

219	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. *Frontiers in Microbiology*, **2016**, 7, 238	5.7	40
218	Genome resolved analysis of a premature infant gut microbial community reveals a Varibaculum cambriense genome and a shift towards fermentation-based metabolism during the third week of life. *Microbiome*, **2013**, 1, 30	16.6	39
217	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, 5384-93	4.8	39
216	Polymorphic Transformations and Particle Coarsening in Nanocrystalline Titania Ceramic Powders and Membranes. *Journal of Physical Chemistry C*, **2007**, 111, 6621-6629	3.8	39
215	Ecological and genomic profiling of anaerobic methane-oxidizing archaea in a deep granitic environment. *ISME Journal*, **2018**, 12, 31-47	11.9	38
214	Free Energy Change of Aggregation of Nanoparticles. *Journal of Physical Chemistry C*, **2008**, 112, 14731-14736	3.8	37
213	Metagenomic recovery of two distinct comammox Nitrospira from the terrestrial subsurface. *Environmental Microbiology*, **2019**, 21, 3627-3637	5.2	36
212	(15)N- and (2)H proteomic stable isotope probing links nitrogen flow to archaeal heterotrophic activity. *Environmental Microbiology*, **2014**, 16, 3224-37	5.2	36
211	Diverse and divergent protein post-translational modifications in two growth stages of a natural microbial community. *Nature Communications*, **2014**, 5, 4405	17.4	36
210	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	11.9	36
209	Diversity of dissimilatory sulfite reductase genes (dsrAB) in a salt marsh impacted by long-term acid mine drainage. *Applied and Environmental Microbiology*, **2010**, 76, 4819-28	4.8	35
208	Analysis and simulation of the structure of nanoparticles that undergo a surface-driven structural transformation. *Journal of Chemical Physics*, **2004**, 120, 11785-95	3.9	35
207	Genome-Resolved Meta-Omics Ties Microbial Dynamics to Process Performance in Biotechnology for Thiocyanate Degradation. *Environmental Science & Technology*, **2017**, 51, 2944-2953	10.3	34
206	Genome-resolved metagenomics of eukaryotic populations during early colonization of premature infants and in hospital rooms. *Microbiome*, **2019**, 7, 26	16.6	34
205	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**,	11.5	34
204	Disturbances of the Perioperative Microbiome Across Multiple Body Sites in Patients Undergoing Pancreaticoduodenectomy. *Pancreas*, **2017**, 46, 260-267	2.6	33
203	Lateral Gene Transfer Shapes the Distribution of RuBisCO among Candidate Phyla Radiation Bacteria and DPANN Archaea. *Molecular Biology and Evolution*, **2019**, 36, 435-446	8.3	33
202	Evidence for persistent and shared bacterial strains against a background of largely unique gut colonization in hospitalized premature infants. *ISME Journal*, **2016**, 10, 2817-2830	11.9	32

201	Implications of strain- and species-level sequence divergence for community and isolate shotgun proteomic analysis. *Journal of Proteome Research*, **2007**, 6, 3152-61	5.6	31
200	Interaction between water molecules and zinc sulfide nanoparticles studied by temperature-programmed desorption and molecular dynamics simulations. *Journal of Physical Chemistry A*, **2007**, 111, 5008-14	2.8	31
199	Analysis of five complete genome sequences for members of the class Peribacteria in the recently recognized Peregrinibacteria bacterial phylum. *PeerJ*, **2016**, 4, e1607	3.1	31
198	Identification and Growth Mechanism of ZnS Nanoparticles with Mixed Cubic and Hexagonal Stacking. *Journal of Physical Chemistry C*, **2009**, 113, 9681-9687	3.8	30
197	8. Geomicrobiology of Uranium **1999**, 393-432		30
196	Strainer: software for analysis of population variation in community genomic datasets. *BMC Bioinformatics*, **2007**, 8, 398	3.6	29
195	Disturbed subsurface microbial communities follow equivalent trajectories despite different structural starting points. *Environmental Microbiology*, **2015**, 17, 622-36	5.2	28
194	Short- and Long-Range Attractive Forces That Influence the Structure of Montmorillonite Osmotic Hydrates. *Langmuir*, **2016**, 32, 12039-12046	4	28
193	Determination of the three-dimensional structure of ferrihydrite nanoparticle aggregates. *Langmuir*, **2014**, 30, 9931-40	4	28
192	New approaches indicate constant viral diversity despite shifts in assemblage structure in an Australian hypersaline lake. *Applied and Environmental Microbiology*, **2013**, 79, 6755-64	4.8	28
191	Ion exchange selectivity in clay is controlled by nanoscale chemical-mechanical coupling. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 22052-22057	11.5	27
190	A novel three-unit tRNA splicing endonuclease found in ultrasmall Archaea possesses broad substrate specificity. *Nucleic Acids Research*, **2011**, 39, 9695-704	20.1	27
189	A semi-quantitative, synteny-based method to improve functional predictions for hypothetical and poorly annotated bacterial and archaeal genes. *PLoS Computational Biology*, **2011**, 7, e1002230	5	27
188	Response of nanoparticle structure to different types of surface environments: Wide-angle x-ray scattering and molecular dynamics simulations. *Physical Review B*, **2010**, 81,	3.3	27
187	Mechanism of inhibition of nanoparticle growth and phase transformation by surface impurities. *Physical Review Letters*, **2007**, 98, 106103	7.4	27
186	Molecular Dynamics Simulation Study of the Early Stages of Nucleation of Iron Oxyhydroxide Nanoparticles in Aqueous Solutions. *Journal of Physical Chemistry B*, **2015**, 119, 10630-42	3.4	26
185	Genome-resolved metaproteomic characterization of preterm infant gut microbiota development reveals species-specific metabolic shifts and variabilities during early life. *Microbiome*, **2017**, 5, 72	16.6	26
184	A portable cryo-plunger for on-site intact cryogenic microscopy sample preparation in natural environments. *Microscopy Research and Technique*, **2012**, 75, 829-36	2.8	26

183	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. *Frontiers in Microbiology*, **2014**, 5, 231	5.7	26
182	Metabolome-proteome differentiation coupled to microbial divergence. *MBio*, **2010**, 1,	7.8	26
181	Formation of regularly interstratified serpentine-chlorite minerals by tetrahedral inversion in long-period serpentine polytypes. *American Mineralogist*, **1996**, 81, 79-91	2.9	26
180	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. *Nature Communications*, **2019**, 10, 463	17.4	25
179	Formation and transformation of a short range ordered iron carbonate precursor. *Geochimica Et Cosmochimica Acta*, **2015**, 164, 94-109	5.5	25
178	Hospitalized Premature Infants Are Colonized by Related Bacterial Strains with Distinct Proteomic Profiles. *MBio*, **2018**, 9,	7.8	25
177	Concentrations and Sources of Airborne Particles in a Neonatal Intensive Care Unit. *PLoS ONE*, **2016** , 11, e0154991	3.7	25
176	Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. *ISME Journal*, **2015**, 9, 2697-711	11.9	24
175	A scoutRNA Is Required for Some Type V CRISPR-Cas Systems. *Molecular Cell*, **2020**, 79, 416-424.e5	17.6	24
174	Formation and Restacking of Disordered Smectite Osmotic Hydrates. *Clays and Clay Minerals*, **2015**, 63, 432-442	2.1	24
173	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, 1755-63	4.9	24
172	Kinetics and Mechanism of Trithionate and Tetrathionate Oxidation at Low pH by Hydroxyl Radicals. *Aquatic Geochemistry*, **2003**, 9, 145-164	1.7	24
171	Genome-resolved metagenomics reveals site-specific diversity of episymbiotic CPR bacteria and DPANN archaea in groundwater ecosystems. *Nature Microbiology*, **2021**, 6, 354-365	26.6	24
170	Quantifying heavy metals sequestration by sulfate-reducing bacteria in an Acid mine drainage-contaminated natural wetland. *Frontiers in Microbiology*, **2013**, 4, 43	5.7	23
169	Dozyite, a 1:1 regular interstratification of serpentine and chlorite. *American Mineralogist*, **1995**, 80, 65-72	2.9	23
168	Polysomatism, polytypism, defect microstructures, and reaction mechanisms in regularly and randomly interstratified serpentine and chlorite. *Contributions To Mineralogy and Petrology*, **1994**, 117, 137-150	3.5	23
167	Complex polytypism; relationships between serpentine structural characteristics and deformation. *American Mineralogist*, **1995**, 80, 1116-1131	2.9	23
166	Candidate Phyla Radiation Roizmanbacteria From Hot Springs Have Novel and Unexpectedly Abundant CRISPR-Cas Systems. *Frontiers in Microbiology*, **2019**, 10, 928	5.7	22

165	Increased replication of dissimilatory nitrate-reducing bacteria leads to decreased anammox bioreactor performance. *Microbiome*, **2020**, 8, 7	16.6	22
164	Strain-resolved microbial community proteomics reveals simultaneous aerobic and anaerobic function during gastrointestinal tract colonization of a preterm infant. *Frontiers in Microbiology*, **2015**, 6, 654	5.7	22
163	Microbiology. Variety--the splice of life--in microbial communities. *Science*, **2009**, 326, 1198-9	33.3	22
162	Chapter 3. PROCESSES AT MINERALS AND SURFACES WITH RELEVANCE TO MICROORGANISMS AND PREBIOTIC SYNTHESIS **1997**, 81-122		22
161	Petabase-scale sequence alignment catalyses viral discovery.. *Nature*, **2022**,	50.4	22
160	Microbial Metagenomics Reveals Climate-Relevant Subsurface Biogeochemical Processes. *Trends in Microbiology*, **2016**, 24, 600-610	12.4	22
159	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	5.7	21
158	Posttranslational modification and sequence variation of redox-active proteins correlate with biofilm life cycle in natural microbial communities. *ISME Journal*, **2010**, 4, 1398-409	11.9	21
157	Recovery of genomes from metagenomes via a dereplication, aggregation, and scoring strategy		21
156	The NIH Somatic Cell Genome Editing program. *Nature*, **2021**, 592, 195-204	50.4	21
155	Functional metagenomic selection of ribulose 1, 5-bisphosphate carboxylase/oxygenase from uncultivated bacteria. *Environmental Microbiology*, **2016**, 18, 1187-99	5.2	21
154	Soil bacterial populations are shaped by recombination and gene-specific selection across a grassland meadow. *ISME Journal*, **2020**, 14, 1834-1846	11.9	19
153	Distribution of cations and vacancies and the structure of defects in oxidized intermediate olivine by atomic-resolution TEM and image simulation. *American Mineralogist*, **1998**, 83, 799-810	2.9	19
152	Unusual Metabolism and Hypervariation in the Genome of a Gracilibacterium (BD1-5) from an Oil-Degrading Community. *MBio*, **2019**, 10,	7.8	19
151	Kinetics of crystal growth of nanogoethite in aqueous solutions containing nitrate and sulfate anions. *CrystEngComm*, **2014**, 16, 1466-1471	3.3	18
150	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, 10554-66	20.1	18
149	A model for exploring particle size and temperature dependence of excess heat capacities of nanocrystalline substances. *Scripta Materialia*, **1998**, 10, 185-194		18
148	Kinetics of Water Adsorption-Driven Structural Transformation of ZnS Nanoparticles. *Journal of Physical Chemistry C*, **2008**, 112, 4791-4796	3.8	18

147	Targeted Genome Editing of Bacteria Within Microbial Communities		18
146	Groundwater Elusimicrobia are metabolically diverse compared to gut microbiome Elusimicrobia and some have a novel nitrogenase paralog. *ISME Journal*, **2020**, 14, 2907-2922	11.9	18
145	Large freshwater phages with the potential to augment aerobic methane oxidation. *Nature Microbiology*, **2020**, 5, 1504-1515	26.6	18
144	A novel Chromatiales bacterium is a potential sulfide oxidizer in multiple orders of marine sponges. *Environmental Microbiology*, **2018**, 20, 800-814	5.2	18
143	Genome-resolved metagenomics of a bioremediation system for degradation of thiocyanate in mine water containing suspended solid tailings. *MicrobiologyOpen*, **2017**, 6, e00446	3.4	17
142	An archaeal symbiont-host association from the deep terrestrial subsurface. *ISME Journal*, **2019**, 13, 2135-2139	11.9	17
141	Correlative Cryogenic Spectromicroscopy to Investigate Selenium Bioreduction Products. *Environmental Science & Technology*, **2018**, 52, 503-512	10.3	17
140	Quantitative determination of elemental sulfur at the arsenopyrite surface after oxidation by ferric iron: mechanistic implications. *Geochemical Transactions*, **2001**, 2, 1	3	17
139	Direct identification of the six polytypes of chlorite characterized by semi-random stacking. *American Mineralogist*, **1998**, 83, 925-930	2.9	17
138	Formation of rutile nuclei at anatase {112} twin interfaces and the phase transformation mechanism in nanocrystalline titania. *American Mineralogist*, **1999**, 84, 877-883	2.9	17
137	Computational prediction and experimental validation of signal peptide cleavages in the extracellular proteome of a natural microbial community. *Journal of Proteome Research*, **2010**, 9, 2148-59	5.6	16
136	Clades of huge phage from across Earth's ecosystems		16
135	A Functional Mini-Integrase in a Two-Protein-type V-C CRISPR System. *Molecular Cell*, **2019**, 73, 727-737.e3	17.6	15
134	Correlative microscopy for phylogenetic and ultrastructural characterization of microbial communities. *Environmental Microbiology Reports*, **2012**, 4, 36-41	3.7	15
133	Quantitative metaproteomics: functional insights into microbial communities. *Methods in Molecular Biology*, **2014**, 1096, 231-40	1.4	15
132	Micron-scale Fe2+/Fe3+, intermediate sulfur species and O2 gradients across the biofilm–solution–sediment interface control biofilm organization. *Geochimica Et Cosmochimica Acta* , **2011**, 75, 3568-3580	5.5	15
131	Fluctuations in species-level protein expression occur during element and nutrient cycling in the subsurface. *PLoS ONE*, **2013**, 8, e57819	3.7	15
130	InStrain enables population genomic analysis from metagenomic data and rigorous detection of identical microbial strains		15

129	The rise of diversity in metabolic platforms across the Candidate Phyla Radiation. *BMC Biology*, **2020**, 18, 69	7.3	14
128	A Model for Nucleation When Nuclei Are Nonstoichiometric: Understanding the Precipitation of Iron Oxyhydroxide Nanoparticles. *Crystal Growth and Design*, **2016**, 16, 5726-5737	3.5	14
127	Galvanic interpretation of self-potential signals associated with microbial sulfate-reduction. *Journal of Geophysical Research*, **2007**, 112, n/a-n/a		14
126	Genome-resolved metagenomics reveals role of iron metabolism in drought-induced rhizosphere microbiome dynamics. *Nature Communications*, **2021**, 12, 3209	17.4	14
125	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	2.8	13
124	Lipid analysis of CO-rich subsurface aquifers suggests an autotrophy-based deep biosphere with lysolipids enriched in CPR bacteria. *ISME Journal*, **2020**, 14, 1547-1560	11.9	13
123	Sulfate requirement for heterotrophic growth of "Ferroplasma acidarmanus" strain fer1. *Research in Microbiology*, **2005**, 156, 492-8	4	13
122	New insights into the mechanism for chloritization of biotite using polytype analysis. *American Mineralogist*, **2000**, 85, 1202-1208	2.9	13
121	Novel bacterial clade reveals origin of form I Rubisco. *Nature Plants*, **2020**, 6, 1158-1166	11.5	13
120	Deuterium-exchange metabolomics identifies N-methyl lyso phosphatidylethanolamines as abundant lipids in acidophilic mixed microbial communities. *Metabolomics*, **2012**, 8, 566-578	4.7	12
119	Improved genome annotation through untargeted detection of pathway-specific metabolites. *BMC Genomics*, **2011**, 12 Suppl 1, S6	4.5	12
118	Microstructural characterization of metamorphic magnetite crystals with implications for oxygen isotope distribution. *American Mineralogist*, **2000**, 85, 14-21	2.9	12
117	Derivation and identification of nonstandard serpentine polytypes. *American Mineralogist*, **1995**, 80, 1104-1115	2.9	12
116	Petabase-scale sequence alignment catalyses viral discovery		12
115	Accurate and Complete Genomes from Metagenomes		12
114	Species- and site-specific genome editing in complex bacterial communities. *Nature Microbiology*, **2021**,	26.6	11
113	The Source and Evolutionary History of a Microbial Contaminant Identified Through Soil Metagenomic Analysis. *MBio*, **2017**, 8,	7.8	10
112	6. Molecular-Scale Processes Involving Nanoparticulate Minerals in Biogeochemical Systems **2005**, 109-156		10

111	Candidatus Mycoplasma girerdii replicates, diversifies, and co-occurs with Trichomonas vaginalis in the oral cavity of a premature infant. *Scientific Reports*, **2017**, 7, 3764	4.9	9
110	De novo sequences of Haloquadratum walsbyi from Lake Tyrrell, Australia, reveal a variable genomic landscape. *Archaea*, **2015**, 2015, 875784	2	9
109	1. Nanoparticles in the Environment **2001**, 1-58		9
108	Low-Temperature Alteration in Tuffs from Yucca Mountain, Nevada. *Clays and Clay Minerals*, **1998**, 46, 27-37	2.1	9
107	Genome-Resolved Metagenomics and Detailed Geochemical Speciation Analyses Yield New Insights into Microbial Mercury Cycling in Geothermal Springs. *Applied and Environmental Microbiology*, **2020**, 86,	4.8	8
106	Titania nanorods curve to lower their energy. *Nanoscale*, **2013**, 5, 6742-6	7.7	8
105	Brockarchaeota, a novel archaeal phylum with unique and versatile carbon cycling pathways. *Nature Communications*, **2021**, 12, 2404	17.4	8
104	Pilot study of sources and concentrations of size-resolved airborne particles in a neonatal intensive care unit. *Building and Environment*, **2016**, 106, 10-19	6.5	8
103	Genome-Resolved Proteomic Stable Isotope Probing of Soil Microbial Communities Using CO and C-Methanol. *Frontiers in Microbiology*, **2019**, 10, 2706	5.7	8
102	Infant gut strain persistence is associated with maternal origin, phylogeny, and traits including surface adhesion and iron acquisition. *Cell Reports Medicine*, **2021**, 2, 100393	18	8
101	Genome-resolved metagenomics of an autotrophic thiocyanate-remediating microbial bioreactor consortium. *Water Research*, **2019**, 158, 106-117	12.5	7
100	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	3.9	7
99	Nanogeoscience: From the movement of electrons to lithosphere plates. *Eos*, **2002**, 83, 53	1.5	7
98	Necrotizing enterocolitis is preceded by increased gut bacterial replication, Klebsiella, and fimbriae-encoding bacteria that may stimulate TLR4 receptors		7
97	Diverse Microorganisms in Sediment and Groundwater Are Implicated in Extracellular Redox Processes Based on Genomic Analysis of Bioanode Communities. *Frontiers in Microbiology*, **2020**, 11, 1694	5.7	7
96	Wide Distribution of Phage That Infect Freshwater SAR11 Bacteria. *MSystems*, **2019**, 4,	7.6	7
95	DNA interference states of the hypercompact CRISPR-Cas effector. *Nature Structural and Molecular Biology*, **2021**, 28, 652-661	17.6	7
94	Compressibility and structural stability of nanoparticulate goethite. *RSC Advances*, **2012**, 2, 6768	3.7	6

93	Electrodic voltages accompanying stimulated bioremediation of a uranium-contaminated aquifer. *Journal of Geophysical Research*, **2010**, 115, n/a-n/a		6
92	TEM investigation of Lewiston, Idaho, fibrolite: Microstructure and grain boundary energetics. *American Mineralogist*, **1999**, 84, 152-159	2.9	6
91	Unexpected diversity of CPR bacteria and nanoarchaea in the rare biosphere of rhizosphere-associated grassland soil		6
90	Consistent metagenome-derived metrics verify and define bacterial species boundaries		6
89	Bacterial secondary metabolite biosynthetic potential in soil varies with phylum, depth, and vegetation type		6
88	Structural coordination between active sites of a CRISPR reverse transcriptase-integrase complex. *Nature Communications*, **2021**, 12, 2571	17.4	6
87	Patterns of Gene Content and Co-occurrence Constrain the Evolutionary Path toward Animal Association in Candidate Phyla Radiation Bacteria. *MBio*, **2021**, 12, e0052121	7.8	6
86	Closely related Lak megaphages replicate in the microbiomes of diverse animals. *IScience*, **2021**, 24, 102875	6.1	6
85	Revealing the ductility of nanoceramic MgAl2O4. *Journal of Materials Research*, **2019**, 34, 1489-1498	2.5	5
84	Prokaryotic Super Program Advisory Committee DOE Joint Genome Institute, Walnut Creek, CA, March 27, 2013. *Standards in Genomic Sciences*, **2013**, 8, 561-70		5
83	Genome-reconstruction for eukaryotes from complex natural microbial communities		5
82	Transporter genes in biosynthetic gene clusters predict metabolite characteristics and siderophore activity. *Genome Research*, **2020**,	9.7	5
81	Genetic and behavioral adaptation of Candida parapsilosis to the microbiome of hospitalized infants revealed by in situ genomics, transcriptomics, and proteomics. *Microbiome*, **2021**, 9, 142	16.6	5
80	Soil Candidate Phyla Radiation Bacteria Encode Components of Aerobic Metabolism and Co-occur with Nanoarchaea in the Rare Biosphere of Rhizosphere Grassland Communities. *MSystems*, **2021**, 6, e0120520	7.6	5
79	Layer size polydispersity in hydrated montmorillonite creates multiscale porosity networks. *Applied Clay Science*, **2020**, 190, 105548	5.2	4
78	Meanders as a scaling motif for understanding of floodplain soil microbiome and biogeochemical potential at the watershed scale		4
77	Stable isotope informed genome-resolved metagenomics uncovers potential trophic interactions in rhizosphere soil		4
76	Processing of grassland soil C-N compounds into soluble and volatile molecules is depth stratified and mediated by genomically novel bacteria and archaea		4

75	Niche differentiation is spatially and temporally regulated in the rhizosphere		4
74	Groundwater Elusimicrobia are metabolically diverse compared to gut microbiome Elusimicrobia and some have a novel nitrogenase paralog		4
73	dRep: A tool for fast and accurate genome de-replication that enables tracking of microbial genotypes and improved genome recovery from metagenomes		4
72	Post-translational flavinylation is associated with diverse extracytosolic redox functionalities throughout bacterial life. *ELife*, **2021**, 10,	8.9	4
71	Unusual metabolism and hypervariation in the genome of a Gracilibacteria (BD1-5) from an oil degrading community **2019**,		4
70	Wide distribution of alternatively coded Lak megaphages in animal microbiomes		4
69	Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut. *PLoS ONE*, **2020**, 15, e0229537	3.7	3
68	NIBBS-search for fast and accurate prediction of phenotype-biased metabolic systems. *PLoS Computational Biology*, **2012**, 8, e1002490	5	3
67	Phase Stability in the Nanocrystalline Tio2 System. *Materials Research Society Symposia Proceedings*, **1997**, 481, 619		3
66	The rise of diversity in metabolic platforms across the Candidate Phyla Radiation		3
65	Large Freshwater Phages with the Potential to Augment Aerobic Methane Oxidation		3
64	Biological capacities clearly define a major subdivision in Domain Bacteria		3
63	Taxonomically and metabolically distinct microbial communities with depth and across a hillslope to riparian zone transect		3
62	Patterns of gene content and co-occurrence constrain the evolutionary path toward animal association in CPR bacteria		3
61	Thiocyanate and Organic Carbon Inputs Drive Convergent Selection for Specific Autotrophic and Strains Within Complex Microbiomes. *Frontiers in Microbiology*, **2021**, 12, 643368	5.7	3
60	Infant gut strain persistence is associated with maternal origin, phylogeny, and functional potential including surface adhesion and iron acquisition		3
59	Subsurface carbon monoxide oxidation capacity revealed through genome-resolved metagenomics of a carboxydotroph. *Environmental Microbiology Reports*, **2020**, 12, 525-533	3.7	2
58	Complete 4.55-Megabase-Pair Genome of " Fluviicola riflensis," Curated from Short-Read Metagenomic Sequences. *Genome Announcements*, **2017**, 5,		2

57	1. The Search for a Molecular-Level Understanding of the Processes that Underpin the Earth's Biogeochemical Cycles **2005**, 1-8		2
56	Microbiological, Geochemical and Hydrologic Processes Controlling Uranium Mobility: An Integrated Field Scale Subsurface Research Challenge Site at Rifle, Colorado, February 2011 to January 2012		2
55	The developing premature infant gut microbiome is a major factor shaping the microbiome of neonatal intensive care unit rooms		2
54	In Situ Replication Rates for Uncultivated Bacteria in Microbial Communities		2
53	Machine learning leveraging genomes from metagenomes identifies influential antibiotic resistance genes in the infant gut microbiome		2
52	Thiocyanate and organic carbon inputs drive convergent selection for specific autotrophic Afipia and Thiobacillus strains within complex microbiomes		2
51	Early acquisition of conserved, lineage-specific proteins currently lacking functional predictions were central to the rise and diversification of archaea		2
50	Stable isotope informed genome-resolved metagenomics reveals that Saccharibacteria utilize microbially processed plant derived carbon		2
49	Candidate Phyla Radiation Roizmanbacteria from hot springs have novel, unexpectedly abundant, and potentially alternatively functioning CRISPR-Cas systems		2
48	Lipid analysis of CO2-rich subsurface aquifers suggests an autotrophy-based deep biosphere with lysolipids enriched in CPR bacteria		2
47	Functional potential of bacterial strains in the premature infant gut microbiome is associated with gestational age		2
46	Metatranscriptomic reconstruction reveals RNA viruses with the potential to shape carbon cycling in soil		2
45	Wide distribution of phage that infect freshwater SAR11 bacteria		2
44	Protein Family Content Uncovers Lineage Relationships and Bacterial Pathway Maintenance Mechanisms in DPANN Archaea. *Frontiers in Microbiology*, **2021**, 12, 660052	5.7	2
43	Borgs are giant extrachromosomal elements with the potential to augment methane oxidation		2
42	Atomic Structure, Defects, and Stacking of Clay Particles by Low-Dose, High Resolution (Cryo)-TEM. *Microscopy and Microanalysis*, **2018**, 24, 1958-1959	0.5	2
41	Stable-Isotope-Informed, Genome-Resolved Metagenomics Uncovers Potential Cross-Kingdom Interactions in Rhizosphere Soil. *MSphere*, **2021**, 6, e0008521	5	2
40	Protein family content uncovers lineage relationships and bacterial pathway maintenance mechanisms in DPANN archaea		2

39	Widespread stop-codon recoding in bacteriophages may regulate translation of lytic genes. *Nature Microbiology*, **2022**, 7, 918-927	26.6	2
38	CRISPRs in the Microbial Community Context **2013**, 287-291		1
37	11. Population Dynamics Through the Lens of Extreme Environments **2005**, 259-278		1
36	Soils and sediments host Thermoplasmata archaea encoding novel copper membrane monooxygenases (CuMMOs).. *ISME Journal*, **2022**,	11.9	1
35	Validation that human microbiome phages use alternative genetic coding with TAG stop read as Q		1
34	Microbial controls on the mineralogy of the environment177-212		1
33	CRISPRs in the Microbial Community Context **2013**, 287-291		1
32	Microcoleus (Cyanobacteria) form watershed-wide populations without strong gradients in population structure. *Molecular Ecology*, **2021**, 31, 86	5.7	1
31	Strain-level overlap between infant and hospital fungal microbiomes revealed throughde novoassembly of eukaryotic genomes from metagenomes		1
30	Microbial communities across a hillslope-riparian transect shaped by proximity to the stream, groundwater table, and weathered bedrock		1
29	Quantitative determination of elemental sulfur at the arsenopyrite surface after oxidation by ferric iron: mechanistic implications. *Geochemical Transactions*, **2001**, 2, 25	3	1
28	Dramatic expansion of microbial groups that shape the global sulfur cycle		1
27	Structure of the Bacterial Ribosome at 2 Resolution		1
26	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome		1
25	Hydrogen-based metabolism an ancestral trait in lineages sibling to the Cyanobacteria		1
24	Meanders as a scaling motif for understanding of floodplain soil microbiome and biogeochemical potential at the watershed scale. *Microbiome*, **2021**, 9, 121	16.6	1
23	Soils and sediments host novel archaea with divergent monooxygenases implicated in ammonia oxidation		1
22	A widely distributed genus of soil Acidobacteria genomically enriched in biosynthetic gene clusters		1

21	Secondary lanthanide phosphate mineralisation in weathering profiles of I-, S- and A-type granites. *Mineralogical Magazine*, **2021**, 85, 82-93	1.7	1
20	Post-translational flavinylation is associated with diverse extracytosolic redox functionalities throughout bacterial life		1
19	Stop codon recoding is widespread in diverse phage lineages and has the potential to regulate translation of late stage and lytic genes		1
18	Polytypism in semi-disordered lizardite and amesite by low-dose HAADF- STEM		1
17	From legacy contamination to watershed systems science: a review of scientific insights and technologies developed through DOE-supported research in water and energy security. *Environmental Research Letters*, **2022**, 17, 043004	6.2	1
16	Pathways for the Photoreduction of Fumarate on ZnS. *ACS Earth and Space Chemistry*, **2019**, 3, 2250-2258	3.2	0
15	Global genomic analysis of microbial biotransformation of arsenic highlights the importance of arsenic methylation in environmental and human microbiomes. *Computational and Structural Biotechnology Journal*, **2022**, 20, 559-559	6.8	0
14	Diverse ATPase Proteins in Mobilomes Constitute a Large Potential Sink for Prokaryotic Host ATP. *Frontiers in Microbiology*, **2021**, 12, 691847	5.7	0
13	Atomic Perspective on the Serpentine□hlorite Solid-State Transformation. *Chemistry of Materials*, **2021**, 33, 6338-6345	9.6	0
12	Long-Term Incubation of Lake Water Enables Genomic Sampling of Consortia Involving and Candidate Phyla Radiation Bacteria.. *MSystems*, **2022**, e0022322	7.6	0
11	Reply to Delmont and Eren: Strain variants and population structure during the oil spill. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E8950-E8952	11.5	
10	Analysis of Microbial Communities Associated with Bioremediation Systems for Thiocyanate-Laden Mine Water Effluents. *Solid State Phenomena*, **2017**, 262, 601-604	0.4	
9	WAXS and PDF-Based Analyses of Chromium Doping in Nanocrystalline Titania (Anatase and Brookite). *Materials Research Society Symposia Proceedings*, **2006**, 915, 1		
8	Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut **2020**, 15, e0229537		
7	Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut **2020**, 15, e0229537		
6	Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut **2020**, 15, e0229537		
5	Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut **2020**, 15, e0229537		
4	Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut **2020**, 15, e0229537		

3 Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut **2020**, 15, e0229537

2 Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut **2020**, 15, e0229537

1 Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut **2020**, 15, e0229537