Jillian F Banfield

List of Publications by Year in Descending Order

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	Soils and sediments host Thermoplasmata archaea encoding novel copper membrane monooxygenases (CuMMOs).. *ISME Journal*, **2022**,	11.9	1
469	Petabase-scale sequence alignment catalyses viral discovery.. *Nature*, **2022**,	50.4	22
468	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
467	Long-Term Incubation of Lake Water Enables Genomic Sampling of Consortia Involving and Candidate Phyla Radiation Bacteria.. *MSystems*, **2022**, e0022322	7.6	0
466	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
465	Widespread stop-codon recoding in bacteriophages may regulate translation of lytic genes. *Nature Microbiology*, **2022**, 7, 918-927	26.6	2
464	Species- and site-specific genome editing in complex bacterial communities. *Nature Microbiology*, **2021**,	26.6	11
463	Microcoleus (Cyanobacteria) form watershed-wide populations without strong gradients in population structure. *Molecular Ecology*, **2021**, 31, 86	5.7	1
462	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
461	The NIH Somatic Cell Genome Editing program. *Nature*, **2021**, 592, 195-204	50.4	21
460	Brockarchaeota, a novel archaeal phylum with unique and versatile carbon cycling pathways. *Nature Communications*, **2021**, 12, 2404	17.4	8
459	Structural coordination between active sites of a CRISPR reverse transcriptase-integrase complex. *Nature Communications*, **2021**, 12, 2571	17.4	6
458	Post-translational flavinylation is associated with diverse extracytosolic redox functionalities throughout bacterial life. *ELife*, **2021**, 10,	8.9	4
457	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
456	Genome-resolved metagenomics reveals role of iron metabolism in drought-induced rhizosphere microbiome dynamics. *Nature Communications*, **2021**, 12, 3209	17.4	14
455	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
454	Protein Family Content Uncovers Lineage Relationships and Bacterial Pathway Maintenance Mechanisms in DPANN Archaea. *Frontiers in Microbiology*, **2021**, 12, 660052	5.7	2

453	Secondary lanthanide phosphate mineralisation in weathering profiles of I-, S- and A-type granites. *Mineralogical Magazine*, **2021**, 85, 82-93	1.7	1
452	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
451	Diverse ATPase Proteins in Mobilomes Constitute a Large Potential Sink for Prokaryotic Host ATP. *Frontiers in Microbiology*, **2021**, 12, 691847	5.7	0
450	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
449	DNA interference states of the hypercompact CRISPR-Cas effector. *Nature Structural and Molecular Biology*, **2021**, 28, 652-661	17.6	7
448	Closely related Lak megaphages replicate in the microbiomes of diverse animals. *IScience*, **2021**, 24, 102875	6.1	6
447	Atomic Perspective on the Serpentine Chlorite Solid-State Transformation. *Chemistry of Materials*, **2021**, 33, 6338-6345	9.6	0
446	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
445	Stable-Isotope-Informed, Genome-Resolved Metagenomics Uncovers Potential Cross-Kingdom Interactions in Rhizosphere Soil. *MSphere*, **2021**, 6, e0008521	5	2
444	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
443	inStrain profiles population microdiversity from metagenomic data and sensitively detects shared microbial strains. *Nature Biotechnology*, **2021**, 39, 727-736	44.5	59
442	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
441	Consistent Metagenome-Derived Metrics Verify and Delineate Bacterial Species Boundaries. *MSystems*, **2020**, 5,	7.6	58
440	Bacterial Secondary Metabolite Biosynthetic Potential in Soil Varies with Phylum, Depth, and Vegetation Type. *MBio*, **2020**, 11,	7.8	52
439	Accurate and complete genomes from metagenomes. *Genome Research*, **2020**, 30, 315-333	9.7	112
438	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
437	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
436	The rise of diversity in metabolic platforms across the Candidate Phyla Radiation. *BMC Biology*, **2020**, 18, 69	7.3	14

435	A scoutRNA Is Required for Some Type V CRISPR-Cas Systems. *Molecular Cell*, **2020**, 79, 416-424.e5	17.6	24
434	Subsurface carbon monoxide oxidation capacity revealed through genome-resolved metagenomics of a carboxydotroph. *Environmental Microbiology Reports*, **2020**, 12, 525-533	3.7	2
433	Clades of huge phages from across Earth's ecosystems. *Nature*, **2020**, 578, 425-431	50.4	154
432	Niche differentiation is spatially and temporally regulated in the rhizosphere. *ISME Journal*, **2020**, 14, 999-1014	11.9	53
431	Increased replication of dissimilatory nitrate-reducing bacteria leads to decreased anammox bioreactor performance. *Microbiome*, **2020**, 8, 7	16.6	22
430	Layer size polydispersity in hydrated montmorillonite creates multiscale porosity networks. *Applied Clay Science*, **2020**, 190, 105548	5.2	4
429	Soil bacterial populations are shaped by recombination and gene-specific selection across a grassland meadow. *ISME Journal*, **2020**, 14, 1834-1846	11.9	19
428	Structure of the bacterial ribosome at 2 Å resolution. *ELife*, **2020**, 9,	8.9	40
427	Transporter genes in biosynthetic gene clusters predict metabolite characteristics and siderophore activity. *Genome Research*, **2020**,	9.7	5
426	CRISPR-Cas Φ from huge phages is a hypercompact genome editor. *Science*, **2020**, 369, 333-337	33.3	158
425	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
424	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
423	Novel bacterial clade reveals origin of form I Rubisco. *Nature Plants*, **2020**, 6, 1158-1166	11.5	13
422	Large freshwater phages with the potential to augment aerobic methane oxidation. *Nature Microbiology*, **2020**, 5, 1504-1515	26.6	18
421	Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut **2020**, 15, e0229537		
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414	Combined analysis of microbial metagenomic and metatranscriptomic sequencing data to assess in situ physiological conditions in the premature infant gut **2020**, 15, e0229537		
413	The distinction of CPR bacteria from other bacteria based on protein family content. *Nature Communications*, **2019**, 10, 4173	17.4	56
412	Megaphages infect Prevotella and variants are widespread in gut microbiomes. *Nature Microbiology* , **2019**, 4, 693-700	26.6	89
411	A Functional Mini-Integrase in a Two-Protein-type V-C CRISPR System. *Molecular Cell*, **2019**, 73, 727-737.e3	17.6	15
410	Hydrogen-based metabolism as an ancestral trait in lineages sibling to the Cyanobacteria. *Nature Communications*, **2019**, 10, 463	17.4	25
409	Revealing the ductility of nanoceramic MgAl2O4. *Journal of Materials Research*, **2019**, 34, 1489-1498	2.5	5
408	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
407	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
406	Metagenomic recovery of two distinct comammox Nitrospira from the terrestrial subsurface. *Environmental Microbiology*, **2019**, 21, 3627-3637	5.2	36
405	Candidate Phyla Radiation Roizmanbacteria From Hot Springs Have Novel and Unexpectedly Abundant CRISPR-Cas Systems. *Frontiers in Microbiology*, **2019**, 10, 928	5.7	22
404	An archaeal symbiont-host association from the deep terrestrial subsurface. *ISME Journal*, **2019**, 13, 2135-2139	11.5	17
403	Wide diversity of methane and short-chain alkane metabolisms in uncultured archaea. *Nature Microbiology*, **2019**, 4, 603-613	26.6	84
402	Genome-resolved metagenomics of an autotrophic thiocyanate-remediating microbial bioreactor consortium. *Water Research*, **2019**, 158, 106-117	12.5	7
401	Pathways for the Photoreduction of Fumarate on ZnS. *ACS Earth and Space Chemistry*, **2019**, 3, 2250-2258	3.2	0
400	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

399	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
398	Genome-resolved metagenomics of eukaryotic populations during early colonization of premature infants and in hospital rooms. *Microbiome*, **2019**, 7, 26	16.6	34
397	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
396	Wide Distribution of Phage That Infect Freshwater SAR11 Bacteria. *MSystems*, **2019**, 4,	7.6	7
395	Unusual Metabolism and Hypervariation in the Genome of a Gracilibacterium (BD1-5) from an Oil-Degrading Community. *MBio*, **2019**, 10,	7.8	19
394	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
393	Unusual metabolism and hypervariation in the genome of a Gracilibacteria (BD1-5) from an oil degrading community **2019**,		4
392	Genome-Resolved Proteomic Stable Isotope Probing of Soil Microbial Communities Using CO and C-Methanol. *Frontiers in Microbiology*, **2019**, 10, 2706	5.7	8
391	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
390	Necrotizing enterocolitis is preceded by increased gut bacterial replication, , and fimbriae-encoding bacteria. *Science Advances*, **2019**, 5, eaax5727	14.3	53
389	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
388	Correlative Cryogenic Spectromicroscopy to Investigate Selenium Bioreduction Products. *Environmental Science & Technology*, **2018**, 52, 503-512	10.3	17
387	Expanded diversity of microbial groups that shape the dissimilatory sulfur cycle. *ISME Journal*, **2018** , 12, 1715-1728	11.9	165
386	Major New Microbial Groups Expand Diversity and Alter our Understanding of the Tree of Life. *Cell*, **2018**, 172, 1181-1197	56.2	272
385	Genome-reconstruction for eukaryotes from complex natural microbial communities. *Genome Research*, **2018**, 28, 569-580	9.7	71
384	Hospitalized Premature Infants Are Colonized by Related Bacterial Strains with Distinct Proteomic Profiles. *MBio*, **2018**, 9,	7.8	25
383	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
382	Machine Learning Leveraging Genomes from Metagenomes Identifies Influential Antibiotic Resistance Genes in the Infant Gut Microbiome. *MSystems*, **2018**, 3,	7.6	42

381	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
380	Ecological and genomic profiling of anaerobic methane-oxidizing archaea in a deep granitic environment. *ISME Journal*, **2018**, 12, 31-47	11.9	38
379	Insights into the ecology, evolution, and metabolism of the widespread Woesearchaeotal lineages. *Microbiome*, **2018**, 6, 102	16.6	98
378	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
377	Stable isotope informed genome-resolved metagenomics reveals that Saccharibacteria utilize microbially-processed plant-derived carbon. *Microbiome*, **2018**, 6, 122	16.6	77
376	Novel soil bacteria possess diverse genes for secondary metabolite biosynthesis. *Nature*, **2018**, 558, 440-444	38.1	165
375	A novel Chromatiales bacterium is a potential sulfide oxidizer in multiple orders of marine sponges. *Environmental Microbiology*, **2018**, 20, 800-814	5.2	18
374	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
373	Programmed DNA destruction by miniature CRISPR-Cas14 enzymes. *Science*, **2018**, 362, 839-842	33.3	394
372	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome. *Genome Research*, **2018**, 28, 1467-1480	9.7	73
371	Biosynthetic capacity, metabolic variety and unusual biology in the CPR and DPANN radiations. *Nature Reviews Microbiology*, **2018**, 16, 629-645	22.2	153
370	Recovery of genomes from metagenomes via a dereplication, aggregation and scoring strategy. *Nature Microbiology*, **2018**, 3, 836-843	26.6	354
369	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
368	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
367	Asgard archaea illuminate the origin of eukaryotic cellular complexity. *Nature*, **2017**, 541, 353-358	50.4	579
366	The Source and Evolutionary History of a Microbial Contaminant Identified Through Soil Metagenomic Analysis. *MBio*, **2017**, 8,	7.8	10
365	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
364	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

363	Disturbances of the Perioperative Microbiome Across Multiple Body Sites in Patients Undergoing Pancreaticoduodenectomy. *Pancreas*, **2017**, 46, 260-267	2.6	33
362	Unusual respiratory capacity and nitrogen metabolism in a Parcubacterium (OD1) of the Candidate Phyla Radiation. *Scientific Reports*, **2017**, 7, 40101	4.9	56
361	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
360	Mechanism of Ferric Oxalate Photolysis. *ACS Earth and Space Chemistry*, **2017**, 1, 270-276	3.2	40
359	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
358	Retroelement-guided protein diversification abounds in vast lineages of Bacteria and Archaea. *Nature Microbiology*, **2017**, 2, 17045	26.6	42
357	New CRISPR-Cas systems from uncultivated microbes. *Nature*, **2017**, 542, 237-241	50.4	320
356	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	
355	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
354	Analysis of Microbial Communities Associated with Bioremediation Systems for Thiocyanate-Laden Mine Water Effluents. *Solid State Phenomena*, **2017**, 262, 601-604	0.4	
353	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
352	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
351	Strain-resolved analysis of hospital rooms and infants reveals overlap between the human and room microbiome. *Nature Communications*, **2017**, 8, 1814	17.4	102
350	Novel Microbial Diversity and Functional Potential in the Marine Mammal Oral Microbiome. *Current Biology*, **2017**, 27, 3752-3762.e6	6.3	44
349	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
348	Complete 4.55-Megabase-Pair Genome of " Fluviicola riflensis," Curated from Short-Read Metagenomic Sequences. *Genome Announcements*, **2017**, 5,		2
347	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
346	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

345	Short- and Long-Range Attractive Forces That Influence the Structure of Montmorillonite Osmotic Hydrates. *Langmuir*, **2016**, 32, 12039-12046	4	28
344	Measurement of bacterial replication rates in microbial communities. *Nature Biotechnology*, **2016**, 34, 1256-1263	44.5	207
343	Thousands of microbial genomes shed light on interconnected biogeochemical processes in an aquifer system. *Nature Communications*, **2016**, 7, 13219	17.4	589
342	A new view of the tree of life. *Nature Microbiology*, **2016**, 1, 16048	26.6	1128
341	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
340	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
339	Precipitation pathways for ferrihydrite formation in acidic solutions. *Geochimica Et Cosmochimica Acta*, **2016**, 172, 247-264	5.5	49
338	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
337	Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. *Nature Communications*, **2016**, 7, 10613	17.4	129
336	Metagenomic reconstructions of bacterial CRISPR loci constrain population histories. *ISME Journal*, **2016**, 10, 858-70	11.9	51
335	Concentrations and Sources of Airborne Particles in a Neonatal Intensive Care Unit. *PLoS ONE*, **2016** , 11, e0154991	3.7	25
334	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
333	Proteogenomic analyses indicate bacterial methylotrophy and archaeal heterotrophy are prevalent below the grass root zone. *PeerJ*, **2016**, 4, e2687	3.1	72
332	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
331	Functional metagenomic selection of ribulose 1, 5-bisphosphate carboxylase/oxygenase from uncultivated bacteria. *Environmental Microbiology*, **2016**, 18, 1187-99	5.2	21
330	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
329	Microbial Metagenomics Reveals Climate-Relevant Subsurface Biogeochemical Processes. *Trends in Microbiology*, **2016**, 24, 600-610	12.4	22
328	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

327	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
326	Diverse uncultivated ultra-small bacterial cells in groundwater. *Nature Communications*, **2015**, 6, 6372	17.4	232
325	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
324	CRYSTAL GROWTH. Crystallization by particle attachment in synthetic, biogenic, and geologic environments. *Science*, **2015**, 349, aaa6760	33.3	1035
323	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
322	Formation and transformation of a short range ordered iron carbonate precursor. *Geochimica Et Cosmochimica Acta*, **2015**, 164, 94-109	5.5	25
321	Unusual biology across a group comprising more than 15% of domain Bacteria. *Nature*, **2015**, 523, 208-11	50.4	688
320	Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. *ISME Journal*, **2015**, 9, 2697-711	11.9	24
319	Bicarbonate impact on U(VI) bioreduction in a shallow alluvial aquifer. *Geochimica Et Cosmochimica Acta*, **2015**, 150, 106-124	5.5	44
318	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
317	Disturbed subsurface microbial communities follow equivalent trajectories despite different structural starting points. *Environmental Microbiology*, **2015**, 17, 622-36	5.2	28
316	Community transcriptomics reveals unexpected high microbial diversity in acidophilic biofilm communities. *ISME Journal*, **2015**, 9, 1014-23	11.9	46
315	Elevated temperature alters proteomic responses of individual organisms within a biofilm community. *ISME Journal*, **2015**, 9, 180-94	11.9	42
314	Metaproteomics reveals functional shifts in microbial and human proteins during a preterm infant gut colonization case. *Proteomics*, **2015**, 15, 3463-73	4.8	41
313	Bioreactor microbial ecosystems for thiocyanate and cyanide degradation unravelled with genome-resolved metagenomics. *Environmental Microbiology*, **2015**, 17, 4929-41	5.2	66
312	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
311	De novo sequences of Haloquadratum walsbyi from Lake Tyrrell, Australia, reveal a variable genomic landscape. *Archaea*, **2015**, 2015, 875784	2	9
310	CRISPR immunity drives rapid phage genome evolution in Streptococcus thermophilus. *MBio*, **2015**, 6,	7.8	119

309	Formation and Restacking of Disordered Smectite Osmotic Hydrates. *Clays and Clay Minerals*, **2015**, 63, 432-442	2.1	24
308	Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. *Genome Research*, **2015**, 25, 534-43	9.7	96
307	Aquifer environment selects for microbial species cohorts in sediment and groundwater. *ISME Journal*, **2015**, 9, 1846-56	11.9	63
306	Gut bacteria are rarely shared by co-hospitalized premature infants, regardless of necrotizing enterocolitis development. *ELife*, **2015**, 4,	8.9	96
305	Interatomic Coulombic interactions as the driving force for oriented attachment. *CrystEngComm*, **2014**, 16, 1568-1578	3.3	84
304	(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
303	Aggregation-induced growth and transformation of ╫FeOOH nanorods to micron-sized ╪Fe2O3 spindles. *CrystEngComm*, **2014**, 16, 1451-1458	3.3	81
302	Kinetics of crystal growth of nanogoethite in aqueous solutions containing nitrate and sulfate anions. *CrystEngComm*, **2014**, 16, 1466-1471	3.3	18
301	Determination of the three-dimensional structure of ferrihydrite nanoparticle aggregates. *Langmuir*, **2014**, 30, 9931-40	4	28
300	Investigating processes of nanocrystal formation and transformation via liquid cell TEM. *Microscopy and Microanalysis*, **2014**, 20, 425-36	0.5	76
299	A unified description of attachment-based crystal growth. *ACS Nano*, **2014**, 8, 6526-30	16.7	99
298	Structural characteristics and mechanical and thermodynamic properties of nanocrystalline TiO2. *Chemical Reviews*, **2014**, 114, 9613-44	68.1	226
297	Metabolic interdependencies between phylogenetically novel fermenters and respiratory organisms in an unconfined aquifer. *ISME Journal*, **2014**, 8, 1452-63	11.9	131
296	Seasonal fluctuations in ionic concentrations drive microbial succession in a hypersaline lake community. *ISME Journal*, **2014**, 8, 979-90	11.9	58
295	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
294	Diverse and divergent protein post-translational modifications in two growth stages of a natural microbial community. *Nature Communications*, **2014**, 5, 4405	17.4	36
293	Quantitative metaproteomics: functional insights into microbial communities. *Methods in Molecular Biology*, **2014**, 1096, 231-40	1.4	15
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48	Strain-level overlap between infant and hospital fungal microbiomes revealed throughde novoassembly of eukaryotic genomes from metagenomes		1
47	The developing premature infant gut microbiome is a major factor shaping the microbiome of neonatal intensive care unit rooms		2
46	Microbial communities across a hillslope-riparian transect shaped by proximity to the stream, groundwater table, and weathered bedrock		1
45	In Situ Replication Rates for Uncultivated Bacteria in Microbial Communities		2
44	Recovery of genomes from metagenomes via a dereplication, aggregation, and scoring strategy		21
43	Dramatic expansion of microbial groups that shape the global sulfur cycle		1
42	Genome-reconstruction for eukaryotes from complex natural microbial communities		5
41	Machine learning leveraging genomes from metagenomes identifies influential antibiotic resistance genes in the infant gut microbiome		2
40	The rise of diversity in metabolic platforms across the Candidate Phyla Radiation		3

39	InStrain enables population genomic analysis from metagenomic data and rigorous detection of identical microbial strains	15
38	Large Freshwater Phages with the Potential to Augment Aerobic Methane Oxidation	3
37	Thiocyanate and organic carbon inputs drive convergent selection for specific autotrophic Afipia and Thiobacillus strains within complex microbiomes	2
36	Meanders as a scaling motif for understanding of floodplain soil microbiome and biogeochemical potential at the watershed scale	4
35	Structure of the Bacterial Ribosome at 2 Resolution	1
34	Unexpected diversity of CPR bacteria and nanoarchaea in the rare biosphere of rhizosphere-associated grassland soil	6
33	Early acquisition of conserved, lineage-specific proteins currently lacking functional predictions were central to the rise and diversification of archaea	2
32	Targeted Genome Editing of Bacteria Within Microbial Communities	18
31	Petabase-scale sequence alignment catalyses viral discovery	12
30	Stable isotope informed genome-resolved metagenomics uncovers potential trophic interactions in rhizosphere soil	4
29	Stable isotope informed genome-resolved metagenomics reveals that Saccharibacteria utilize microbially processed plant derived carbon	2
28	Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome	1
27	Hydrogen-based metabolism an ancestral trait in lineages sibling to the Cyanobacteria	1
26	Biological capacities clearly define a major subdivision in Domain Bacteria	3
25	Processing of grassland soil C-N compounds into soluble and volatile molecules is depth stratified and mediated by genomically novel bacteria and archaea	4
24	Candidate Phyla Radiation Roizmanbacteria from hot springs have novel, unexpectedly abundant, and potentially alternatively functioning CRISPR-Cas systems	2
23	Lipid analysis of CO2-rich subsurface aquifers suggests an autotrophy-based deep biosphere with lysolipids enriched in CPR bacteria	2
22	Functional potential of bacterial strains in the premature infant gut microbiome is associated with gestational age	2

21	Necrotizing enterocolitis is preceded by increased gut bacterial replication, Klebsiella, and fimbriae-encoding bacteria that may stimulate TLR4 receptors	7
20	Clades of huge phage from across Earth's ecosystems	16
19	Metatranscriptomic reconstruction reveals RNA viruses with the potential to shape carbon cycling in soil	2
18	Niche differentiation is spatially and temporally regulated in the rhizosphere	4
17	Consistent metagenome-derived metrics verify and define bacterial species boundaries	6
16	Wide distribution of phage that infect freshwater SAR11 bacteria	2
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14	Taxonomically and metabolically distinct microbial communities with depth and across a hillslope to riparian zone transect	3
13	Accurate and Complete Genomes from Metagenomes	12
12	Bacterial secondary metabolite biosynthetic potential in soil varies with phylum, depth, and vegetation type	6
11	dRep: A tool for fast and accurate genome de-replication that enables tracking of microbial genotypes and improved genome recovery from metagenomes	4
10	Patterns of gene content and co-occurrence constrain the evolutionary path toward animal association in CPR bacteria	3
9	Soils and sediments host novel archaea with divergent monooxygenases implicated in ammonia oxidation	1
8	A widely distributed genus of soil Acidobacteria genomically enriched in biosynthetic gene clusters	1
7	Borgs are giant extrachromosomal elements with the potential to augment methane oxidation	2
6	Post-translational flavinylation is associated with diverse extracytosolic redox functionalities throughout bacterial life	1
5	Infant gut strain persistence is associated with maternal origin, phylogeny, and functional potential including surface adhesion and iron acquisition	3
4	Wide distribution of alternatively coded Lak megaphages in animal microbiomes	4

3	Stop codon recoding is widespread in diverse phage lineages and has the potential to regulate translation of late stage and lytic genes	1
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