

# Konstantinos T Konstantinidis

## List of Publications by Year in descending order

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183  
papers

27,791  
citations

20817

60  
h-index

7160

153  
g-index

214  
all docs

214  
docs citations

214  
times ranked

23887  
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA-DNA hybridization values and their relationship to whole-genome sequence similarities. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2007, 57, 81-91.	1.7	3,968
2	High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. <i>Nature Communications</i> , 2018, 9, 5114.	12.8	2,816
3	Genomic insights that advance the species definition for prokaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2567-2572.	7.1	1,869
4	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	17.5	1,512
5	Towards a Genome-Based Taxonomy for Prokaryotes. <i>Journal of Bacteriology</i> , 2005, 187, 6258-6264.	2.2	966
6	Microbial species delineation using whole genome sequences. <i>Nucleic Acids Research</i> , 2015, 43, 6761-6771.	14.5	609
7	Bypassing Cultivation To Identify Bacterial Species. <i>Microbe Magazine</i> , 2014, 9, 111-118.	0.4	581
8	Uncultivated microbes in need of their own taxonomy. <i>ISME Journal</i> , 2017, 11, 2399-2406.	9.8	572
9	The bacterial species definition in the genomic era. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 1929-1940.	4.0	550
10	Strengths and Limitations of 16S rRNA Gene Amplicon Sequencing in Revealing Temporal Microbial Community Dynamics. <i>PLoS ONE</i> , 2014, 9, e93827.	2.5	508
11	Unexpected nondenitrifier nitrous oxide reductase gene diversity and abundance in soils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19709-19714.	7.1	502
12	<i>Dehalococcoides mccartyi</i> gen. nov., sp. nov., obligately organohalide-respiring anaerobic bacteria relevant to halogen cycling and bioremediation, belong to a novel bacterial class, <i>Dehalococcoidia</i> classis nov., order <i>Dehalococcoidales</i> ord. nov. and family <i>Dehalococcoidaceae</i> fam. nov., within the phylum <i>Chloroflexi</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 625-635.	1.7	502
13	Trends between gene content and genome size in prokaryotic species with larger genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 3160-3165.	7.1	464
14	The Microbial Genomes Atlas (MiGA) webserver: taxonomic and gene diversity analysis of Archaea and Bacteria at the whole genome level. <i>Nucleic Acids Research</i> , 2018, 46, W282-W288.	14.5	458
15	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
16	MyTaxa: an advanced taxonomic classifier for genomic and metagenomic sequences. <i>Nucleic Acids Research</i> , 2014, 42, e73-e73.	14.5	445
17	Genomic analysis of the uncultivated marine crenarchaeote <i>Cenarchaeum symbiosum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18296-18301.	7.1	420
18	Prokaryotic taxonomy and phylogeny in the genomic era: advancements and challenges ahead. <i>Current Opinion in Microbiology</i> , 2007, 10, 504-509.	5.1	403

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19	Microbiome of the upper troposphere: Species composition and prevalence, effects of tropical storms, and atmospheric implications. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 2575-2580.	7.1	377
20	Direct Comparisons of Illumina vs. Roche 454 Sequencing Technologies on the Same Microbial Community DNA Sample. PLoS ONE, 2012, 7, e30087.	2.5	360
21	<i>Burkholderia xenovorans</i> LB400 harbors a multi-replicon, 9.73-Mbp genome shaped for versatility. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 15280-15287.	7.1	339
22	Genome sequencing of environmental <i>Escherichia coli</i> expands understanding of the ecology and speciation of the model bacterial species. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7200-7205.	7.1	279
23	Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. Nature Climate Change, 2016, 6, 595-600.	18.8	260
24	Bacterial species may exist, metagenomics reveal. Environmental Microbiology, 2012, 14, 347-355.	3.8	210
25	Giant virus diversity and host interactions through global metagenomics. Nature, 2020, 578, 432-436.	27.8	207
26	Comparative Metagenomic Analysis of a Microbial Community Residing at a Depth of 4,000 Meters at Station ALOHA in the North Pacific Subtropical Gyre. Applied and Environmental Microbiology, 2009, 75, 5345-5355.	3.1	203
27	Toward a More Robust Assessment of Intraspecies Diversity, Using Fewer Genetic Markers— <i>z</i> . Applied and Environmental Microbiology, 2006, 72, 7286-7293.	3.1	196
28	Nonpareil: a redundancy-based approach to assess the level of coverage in metagenomic datasets. Bioinformatics, 2014, 30, 629-635.	4.1	186
29	Long-Term Exposure to Benzalkonium Chloride Disinfectants Results in Change of Microbial Community Structure and Increased Antimicrobial Resistance. Environmental Science & Technology, 2013, 47, 9730-9738.	10.0	170
30	SAR11 bacteria linked to ocean anoxia and nitrogen loss. Nature, 2016, 536, 179-183.	27.8	160
31	Microbial community successional patterns in beach sands impacted by the Deepwater Horizon oil spill. ISME Journal, 2015, 9, 1928-1940.	9.8	155
32	Nonpareil 3: Fast Estimation of Metagenomic Coverage and Sequence Diversity. MSystems, 2018, 3, .	3.8	152
33	Metagenomic Insights into the Evolution, Function, and Complexity of the Planktonic Microbial Community of Lake Lanier, a Temperate Freshwater Ecosystem. Applied and Environmental Microbiology, 2011, 77, 6000-6011.	3.1	151
34	Microbial Community Structure and Activity Linked to Contrasting Biogeochemical Gradients in Bog and Fen Environments of the Glacial Lake Agassiz Peatland. Applied and Environmental Microbiology, 2012, 78, 7023-7031.	3.1	149
35	Detecting Nitrous Oxide Reductase ( <i>nosZ</i> ) Genes in Soil Metagenomes: Method Development and Implications for the Nitrogen Cycle. MBio, 2014, 5, e01193-14.	4.1	142
36	Estimating coverage in metagenomic data sets and why it matters. ISME Journal, 2014, 8, 2349-2351.	9.8	142

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37	Warming enhances old organic carbon decomposition through altering functional microbial communities. <i>ISME Journal</i> , 2017, 11, 1825-1835.	9.8	136
38	New insights from the biogas microbiome by comprehensive genome-resolved metagenomics of nearly 1600 species originating from multiple anaerobic digesters. <i>Biotechnology for Biofuels</i> , 2020, 13, 25.	6.2	136
39	Widely Used Benzalkonium Chloride Disinfectants Can Promote Antibiotic Resistance. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	134
40	Soil Microbial Community Responses to a Decade of Warming as Revealed by Comparative Metagenomics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1777-1786.	3.1	131
41	Genomic patterns of recombination, clonal divergence and environment in marine microbial populations. <i>ISME Journal</i> , 2008, 2, 1052-1065.	9.8	121
42	Year-Round Shotgun Metagenomes Reveal Stable Microbial Communities in Agricultural Soils and Novel Ammonia Oxidizers Responding to Fertilization. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	121
43	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	13.3	115
44	Global profiling of <i>Shewanella oneidensis</i> MR-1: Expression of hypothetical genes and improved functional annotations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2099-2104.	7.1	113
45	Individual genome assembly from complex community short-read metagenomic datasets. <i>ISME Journal</i> , 2012, 6, 898-901.	9.8	106
46	Phylogenetic analyses of ribosomal DNA-containing bacterioplankton genome fragments from a 4000m vertical profile in the North Pacific Subtropical Gyre. <i>Environmental Microbiology</i> , 2008, 10, 2313-2330.	3.8	104
47	Biofilms on Hospital Shower Hoses: Characterization and Implications for Nosocomial Infections. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2872-2883.	3.1	102
48	Comparative systems biology across an evolutionary gradient within the <i>Shewanella</i> genus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15909-15914.	7.1	96
49	The Great Oxidation Event expanded the genetic repertoire of arsenic metabolism and cycling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10414-10421.	7.1	96
50	Sequencing platform and library preparation choices impact viral metagenomes. <i>BMC Genomics</i> , 2013, 14, 320.	2.8	90
51	Microbial Diversity and Resistance to Copper in Metal-Contaminated Lake Sediment. <i>Microbial Ecology</i> , 2003, 45, 191-202.	2.8	85
52	Responses of tundra soil microbial communities to half a decade of experimental warming at two critical depths. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15096-15105.	7.1	83
53	Microbial community adaptation to quaternary ammonium biocides as revealed by metagenomics. <i>Environmental Microbiology</i> , 2013, 15, 2850-2864.	3.8	82
54	The Reliability of Metagenome-Assembled Genomes (MAGs) in Representing Natural Populations: Insights from Comparing MAGs against Isolate Genomes Derived from the Same Fecal Sample. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	82

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55	Meeting report: GenBank microbial genomic taxonomy workshop (12–13 May, 2015). <i>Standards in Genomic Sciences</i> , 2016, 11, .	1.5	81
56	Genomic determinants of organohalide-respiration in <i>Geobacter lovleyi</i> , an unusual member of the Geobacteraceae. <i>BMC Genomics</i> , 2012, 13, 200.	2.8	76
57	Warming-induced permafrost thaw exacerbates tundra soil carbon decomposition mediated by microbial community. <i>Microbiome</i> , 2020, 8, 3.	11.1	75
58	Temperature sensitivity of organic matter decomposition of permafrost-region soils during laboratory incubations. <i>Soil Biology and Biochemistry</i> , 2016, 97, 1-14.	8.8	73
59	More replenishment than priming loss of soil organic carbon with additional carbon input. <i>Nature Communications</i> , 2018, 9, 3175.	12.8	69
60	Iterative subtractive binning of freshwater chronoserics metagenomes identifies over 400 novel species and their ecologic preferences. <i>Environmental Microbiology</i> , 2020, 22, 3394-3412.	3.8	69
61	Gene-informed decomposition model predicts lower soil carbon loss due to persistent microbial adaptation to warming. <i>Nature Communications</i> , 2020, 11, 4897.	12.8	67
62	Metagenomics Reveals Pervasive Bacterial Populations and Reduced Community Diversity across the Alaska Tundra Ecosystem. <i>Frontiers in Microbiology</i> , 2016, 7, 579.	3.5	66
63	Unprecedented levels of horizontal gene transfer among spatially co-occurring <i>Shewanella</i> bacteria from the Baltic Sea. <i>ISME Journal</i> , 2011, 5, 131-140.	9.8	64
64	Gene expression analysis of <i>E. coli</i> strains provides insights into the role of gene regulation in diversification. <i>ISME Journal</i> , 2015, 9, 1130-1140.	9.8	63
65	The low diverse gastric microbiome of the jellyfish <i>Cotylorhiza tuberculata</i> is dominated by four novel taxa. <i>Environmental Microbiology</i> , 2017, 19, 3039-3058.	3.8	62
66	Classifying the uncultivated microbial majority: A place for metagenomic data in the Candidatus proposal. <i>Systematic and Applied Microbiology</i> , 2015, 38, 223-230.	2.8	61
67	Methods for estimating temperature sensitivity of soil organic matter based on incubation data: A comparative evaluation. <i>Soil Biology and Biochemistry</i> , 2015, 80, 127-135.	8.8	61
68	MicrobeAnnotator: a user-friendly, comprehensive functional annotation pipeline for microbial genomes. <i>BMC Bioinformatics</i> , 2021, 22, 11.	2.6	61
69	Microbial Community Degradation of Widely Used Quaternary Ammonium Disinfectants. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5892-5900.	3.1	60
70	Quantifying the Importance of the Rare Biosphere for Microbial Community Response to Organic Pollutants in a Freshwater Ecosystem. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	60
71	Anthropogenic effects on bacterial diversity and function along a river–estuary gradient in Northwest Greece revealed by metagenomics. <i>Environmental Microbiology</i> , 2016, 18, 4640-4652.	3.8	58
72	Implications of Genome-Based Discrimination between <i>Clostridium botulinum</i> Group I and <i>Clostridium sporogenes</i> Strains for Bacterial Taxonomy. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5420-5429.	3.1	57

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73	Beyond denitrification: The role of microbial diversity in controlling nitrous oxide reduction and soil nitrous oxide emissions. <i>Global Change Biology</i> , 2021, 27, 2669-2683.	9.5	57
74	Detection and Diversity of Fungal Nitric Oxide Reductase Genes ( <i>nor</i> ) in Agricultural Soils. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2919-2928.	3.1	55
75	Metagenomics of Two Severe Foodborne Outbreaks Provides Diagnostic Signatures and Signs of Coinfection Not Attainable by Traditional Methods. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	54
76	Inter-phylum HGT has shaped the metabolism of many mesophilic and anaerobic bacteria. <i>ISME Journal</i> , 2015, 9, 958-967.	9.8	50
77	â€ˆ Candidatus <i>Dichloromethanomonas elyunquensis</i> â€™ gen. nov., sp. nov., a dichloromethane-degrading anaerobe of the Peptococcaceae family. <i>Systematic and Applied Microbiology</i> , 2017, 40, 150-159.	2.8	50
78	Drinking Water Microbiome Project: Is it Time?. <i>Trends in Microbiology</i> , 2019, 27, 670-677.	7.7	50
79	Similar Microbial Consortia and Genes Are Involved in the Biodegradation of Benzalkonium Chlorides in Different Environments. <i>Environmental Science &amp; Technology</i> , 2016, 50, 4304-4313.	10.0	47
80	Experimental warming reveals positive feedbacks to climate change in the Eurasian Steppe. <i>ISME Journal</i> , 2017, 11, 885-895.	9.8	47
81	How Much Do rRNA Gene Surveys Underestimate Extant Bacterial Diversity?. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	47
82	Winter warming in Alaska accelerates lignin decomposition contributed by Proteobacteria. <i>Microbiome</i> , 2020, 8, 84.	11.1	47
83	â€ˆ Candidatus <i>Macondimonas diazotrophica</i> â€™, a novel gammaproteobacterial genus dominating crude-oil-contaminated coastal sediments. <i>ISME Journal</i> , 2019, 13, 2129-2134.	9.8	46
84	Single cell genomic and transcriptomic evidence for the use of alternative nitrogen substrates by anammox bacteria. <i>ISME Journal</i> , 2018, 12, 2706-2722.	9.8	45
85	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	12.6	45
86	Identification of Potential Therapeutic Targets for <i>Burkholderia cenocepacia</i> by Comparative Transcriptomics. <i>PLoS ONE</i> , 2010, 5, e8724.	2.5	45
87	Dynamic models of the complex microbial metapopulation of lake mendota. <i>Npj Systems Biology and Applications</i> , 2016, 2, 16007.	3.0	43
88	Genomic and Transcriptomic Insights into How Bacteria Withstand High Concentrations of Benzalkonium Chloride Biocides. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	43
89	Niche differentiation among annually recurrent coastal Marine Group II Euryarchaeota. <i>ISME Journal</i> , 2019, 13, 3024-3036.	9.8	41
90	Quantifying the changes in genetic diversity within sequence-discrete bacterial populations across a spatial and temporal riverine gradient. <i>ISME Journal</i> , 2019, 13, 767-779.	9.8	40

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91	Intensive allochthonous inputs along the Ganges River and their effect on microbial community composition and dynamics. <i>Environmental Microbiology</i> , 2019, 21, 182-196.	3.8	40
92	Genomic Insights into the Convergence and Pathogenicity Factors of <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> Species. <i>Journal of Bacteriology</i> , 2009, 191, 5824-5831.	2.2	39
93	Design and testing of "genome-proxy" microarrays to profile marine microbial communities. <i>Environmental Microbiology</i> , 2008, 10, 506-521.	3.8	38
94	Genomic Diversity of <i>Escherichia</i> Isolates from Diverse Habitats. <i>PLoS ONE</i> , 2012, 7, e47005.	2.5	38
95	Microbial Taxonomy Run Amok. <i>Trends in Microbiology</i> , 2021, 29, 394-404.	7.7	38
96	ROCKER: accurate detection and quantification of target genes in short-read metagenomic data sets by modeling sliding-window bitscores. <i>Nucleic Acids Research</i> , 2017, 45, gkw900.	14.5	37
97	Evaluation of metatranscriptomic protocols and application to the study of freshwater microbial communities. <i>Environmental Microbiology Reports</i> , 2014, 6, 640-655.	2.4	36
98	Reply to: "Re-evaluating the evidence for a universal genetic boundary among microbial species". <i>Nature Communications</i> , 2021, 12, 4060.	12.8	36
99	Decomposition of sediment-oil-agglomerates in a Gulf of Mexico sandy beach. <i>Scientific Reports</i> , 2019, 9, 10071.	3.3	35
100	Environmental stability impacts the differential sensitivity of marine microbiomes to increases in temperature and acidity. <i>ISME Journal</i> , 2021, 15, 19-28.	9.8	35
101	Comparison of closely related, uncultivated <i>Coxiella</i> tick endosymbiont population genomes reveals clues about the mechanisms of symbiosis. <i>Environmental Microbiology</i> , 2018, 20, 1751-1764.	3.8	33
102	Metagenomic Signatures of Gut Infections Caused by Different <i>Escherichia coli</i> Pathotypes. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	33
103	Ecogenomic characterization of widespread, closely-related SAR11 clades of the freshwater genus "Candidatus Fonsibacter" and proposal of <i>Ca. Fonsibacter lacus</i> sp. nov. <i>Systematic and Applied Microbiology</i> , 2019, 42, 495-505.	2.8	33
104	Genomic Characterization and Copy Number Variation of <i>Bacillus anthracis</i> Plasmids pXO1 and pXO2 in a Historical Collection of 412 Strains. <i>MSystems</i> , 2018, 3, .	3.8	32
105	Anaerobic degradation of hexadecane and phenanthrene coupled to sulfate reduction by enriched consortia from northern Gulf of Mexico seafloor sediment. <i>Scientific Reports</i> , 2019, 9, 1239.	3.3	31
106	Genomic comparison between members of the <i>Salinibacteraceae</i> family, and description of a new species of <i>Salinibacter</i> ( <i>Salinibacter altiplanensis</i> sp. nov.) isolated from high altitude hypersaline environments of the Argentinian Altiplano. <i>Systematic and Applied Microbiology</i> , 2018, 41, 198-212.	2.8	29
107	A User's Guide to Quantitative and Comparative Analysis of Metagenomic Datasets. <i>Methods in Enzymology</i> , 2013, 531, 525-547.	1.0	28
108	A novel droplet digital PCR human mtDNA assay for fecal source tracking. <i>Water Research</i> , 2020, 183, 116085.	11.3	28

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109	Phosphorus-related gene content is similar in <i>Prochlorococcus</i> populations from the North Pacific and North Atlantic Oceans. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E62-3; author reply E64-6.	7.1	27
110	Metagenomics as a Public Health Risk Assessment Tool in a Study of Natural Creek Sediments Influenced by Agricultural and Livestock Runoff: Potential and Limitations. Applied and Environmental Microbiology, 2020, 86, .	3.1	27
111	Stability, genotypic and phenotypic diversity of <i>Sewanella baltica</i> in the redox transition zone of the Baltic Sea. Environmental Microbiology, 2014, 16, 1854-1866.	3.8	26
112	Glucose addition increases the magnitude and decreases the age of soil respired carbon in a long-term permafrost incubation study. Soil Biology and Biochemistry, 2019, 129, 201-211.	8.8	26
113	Phosphate addition increases tropical forest soil respiration primarily by deconstraining microbial population growth. Soil Biology and Biochemistry, 2019, 130, 43-54.	8.8	26
114	Non-denitrifier nitrous oxide reductases dominate marine biomes. Environmental Microbiology Reports, 2020, 12, 681-692.	2.4	26
115	Tundra microbial community taxa and traits predict decomposition parameters of stable, old soil organic carbon. ISME Journal, 2019, 13, 2901-2915.	9.8	24
116	Prevalence of viral photosynthesis genes along a freshwater to saltwater transect in Southeast USA. Environmental Microbiology Reports, 2019, 11, 672-689.	2.4	24
117	imGLAD: accurate detection and quantification of target organisms in metagenomes. PeerJ, 2018, 6, e5882.	2.0	24
118	MetaPop: a pipeline for macro- and microdiversity analyses and visualization of microbial and viral metagenome-derived populations. Microbiome, 2022, 10, 49.	11.1	24
119	Comparative Genomics and Phylogenomic Analysis of the Genus <i>Salinivibrio</i> . Frontiers in Microbiology, 2019, 10, 2104.	3.5	23
120	Comparison of vaginal microbiota in gynecologic cancer patients pre- and post-radiation therapy and healthy women. Cancer Medicine, 2020, 9, 3714-3724.	2.8	23
121	Hidden Diversity within Common Protozoan Parasites as Revealed by a Novel Genotyping Scheme. Applied and Environmental Microbiology, 2021, 87, .	3.1	23
122	Microbial functional diversity covaries with permafrost thaw-induced environmental heterogeneity in tundra soil. Global Change Biology, 2018, 24, 297-307.	9.5	22
123	Long-Term Warming in Alaska Enlarges the Diazotrophic Community in Deep Soils. MBio, 2019, 10, .	4.1	22
124	First description of two moderately halophilic and psychrotolerant <i>Mycoplasma</i> species isolated from cephalopods and proposal of <i>Mycoplasma marinum</i> sp. nov. and <i>Mycoplasma todarodis</i> sp. nov. Systematic and Applied Microbiology, 2019, 42, 457-467.	2.8	22
125	A Rieske-Type Oxygenase of <i>Pseudomonas</i> sp. BIOMIG1 Converts Benzalkonium Chlorides to Benzyltrimethyl Amine. Environmental Science & Technology, 2017, 51, 175-181.	10.0	21
126	Biotic responses buffer warming-induced soil organic carbon loss in Arctic tundra. Global Change Biology, 2018, 24, 4946-4959.	9.5	21



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127	The Bacterial Symbionts of Closely Related Hydrothermal Vent Snails With Distinct Geochemical Habitats Show Broad Similarity in Chemoautotrophic Gene Content. <i>Frontiers in Microbiology</i> , 2019, 10, 1818.	3.5	21
128	Genome repository of oil systems: An interactive and searchable database that expands the catalogued diversity of crude oil-associated microbes. <i>Environmental Microbiology</i> , 2020, 22, 2094-2106.	3.8	21
129	Metagenomic insights into the effect of sulfate on enhanced biological phosphorus removal. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 2181-2193.	3.6	21
130	Predominance of deterministic microbial community dynamics in salterns exposed to different light intensities. <i>Environmental Microbiology</i> , 2019, 21, 4300-4315.	3.8	20
131	Genome Sequencing of Five <i>Shewanella baltica</i> Strains Recovered from the Oxidic-Anoxic Interface of the Baltic Sea. <i>Journal of Bacteriology</i> , 2012, 194, 1236-1236.	2.2	19
132	Draft Genome Sequence of <i>Bacillus cereus</i> LA2007, a Human-Pathogenic Isolate Harboring Anthrax-Like Plasmids. <i>Genome Announcements</i> , 2017, 5, .	0.8	18
133	Comparing DNA, RNA and protein levels for measuring microbial dynamics in soil microcosms amended with nitrogen fertilizer. <i>Scientific Reports</i> , 2019, 9, 17630.	3.3	18
134	Effects of timber harvesting on the genetic potential for carbon and nitrogen cycling in five North American forest ecozones. <i>Scientific Reports</i> , 2018, 8, 3142.	3.3	17
135	Impact of an Urban Sanitation Intervention on Enteric Pathogen Detection in Soils. <i>Environmental Science &amp; Technology</i> , 2021, 55, 9989-10000.	10.0	16
136	Defining Taxonomic Ranks. , 2013, , 229-254.		14
137	Genome Sequencing Reveals the Environmental Origin of Enterococci and Potential Biomarkers for Water Quality Monitoring. <i>Environmental Science &amp; Technology</i> , 2014, 48, 3707-3714.	10.0	14
138	Do airborne microbes matter for atmospheric chemistry and cloud formation?. <i>Environmental Microbiology</i> , 2014, 16, 1482-1484.	3.8	14
139	Model-based Comparisons of the Abundance Dynamics of Bacterial Communities in Two Lakes. <i>Scientific Reports</i> , 2020, 10, 2423.	3.3	14
140	Distinct ecotypes within a natural haloarchaeal population enable adaptation to changing environmental conditions without causing population sweeps. <i>ISME Journal</i> , 2021, 15, 1178-1191.	9.8	14
141	Description of <i>Candidatus Mesopelagibacter carboxydoxydans</i> and <i>Candidatus Anoxipelagibacter denitrificans</i> : Nitrate-reducing SAR11 genera that dominate mesopelagic and anoxic marine zones. <i>Systematic and Applied Microbiology</i> , 2021, 44, 126185.	2.8	14
142	Draft Genome Sequence of a Strictly Anaerobic Dichloromethane-Degrading Bacterium. <i>Genome Announcements</i> , 2016, 4, .	0.8	13
143	Toward quantifying the adaptive role of bacterial pangenomes during environmental perturbations. <i>ISME Journal</i> , 2022, 16, 1222-1234.	9.8	13
144	<i>Candidatus ferrigenium straubiae</i> sp. nov., <i>Candidatus ferrigenium bremense</i> sp. nov., <i>Candidatus ferrigenium altingense</i> sp. nov., are autotrophic Fe(II)-oxidizing bacteria of the family Gallionellaceae. <i>Systematic and Applied Microbiology</i> , 2022, 45, 126306.	2.8	13

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145	Advantages outweigh concerns about using genome sequence as type material for prokaryotic taxonomy. <i>Environmental Microbiology</i> , 2020, 22, 819-822.	3.8	12
146	Bacteria Make a Living Breathing the Nitroheterocyclic Insensitive Munitions Compound 3-Nitro-1,2,4-triazol-5-one (NTO). <i>Environmental Science &amp; Technology</i> , 2021, 55, 5806-5814.	10.0	12
147	Diversity of microbial communities and genes involved in nitrous oxide emissions in Antarctic soils impacted by marine animals as revealed by metagenomics and 100 metagenome-assembled genomes. <i>Science of the Total Environment</i> , 2021, 788, 147693.	8.0	12
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