

Konstantinos T Konstantinidis

List of Publications by Year in descending order

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Version: 2024-02-01

183
papers

27,791
citations

20759

60
h-index

7136

153
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214
all docs

214
docs citations

214
times ranked

23887
citing authors

#	ARTICLE	IF	CITATIONS
1	Solar salterns as model systems to study the units of bacterial diversity that matter for ecosystem functioning. <i>Current Opinion in Biotechnology</i> , 2022, 73, 151-157.	3.3	8
2	Microbial diversity in a military impacted lagoon (Vieques, Puerto Rico) and description of <i>Candidatus Biekeibacterium resiliens</i> gen. nov., sp. nov. comprising a new bacterial family. <i>Systematic and Applied Microbiology</i> , 2022, 45, 126288.	1.2	1
3	Toward shotgun metagenomic approaches for microbial source tracking sewage spills based on laboratory mesocosms. <i>Water Research</i> , 2022, 210, 117993.	5.3	12
4	RecruitPlotEasy: An Advanced Read Recruitment Plot Tool for Assessing Metagenomic Population Abundance and Genetic Diversity. <i>Frontiers in Bioinformatics</i> , 2022, 1, .	1.0	2
5	Judicial Opinions 103–111. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2022, 72, .	0.8	8
6	Metagenomics indicate that public health risk may be higher from flooding following dry versus rainy periods. <i>Environmental Microbiology Reports</i> , 2022, , .	1.0	2
7	Toward quantifying the adaptive role of bacterial pangenomes during environmental perturbations. <i>ISME Journal</i> , 2022, 16, 1222-1234.	4.4	13
8	How to Maintain a Healthy Gut Microbiome in Children with Cancer? Gut Microbiome Association with Diet in Children with Solid Tumors Postchemotherapy. <i>OMICS A Journal of Integrative Biology</i> , 2022, , .	1.0	3
9	MetaPop: a pipeline for macro- and microdiversity analyses and visualization of microbial and viral metagenome-derived populations. <i>Microbiome</i> , 2022, 10, 49.	4.9	24
10	<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.	1.2	13
11	Defining Virus-Carrier Networks that Shape the Composition of the Mosquito Core Virome of a Local Ecosystem. <i>Virus Evolution</i> , 2022, 8, veac036.	2.2	10
12	ROCKER Models for Reliable Detection and Typing of Short-Read Sequences Carrying β -Lactamase Genes. <i>MSystems</i> , 2022, 7, .	1.7	1
13	Quinone Moieties Link the Microbial Respiration of Natural Organic Matter to the Chemical Reduction of Diverse Nitroaromatic Compounds. <i>Environmental Science & Technology</i> , 2022, 56, 9387-9397.	4.6	7
14	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	9.4	457
15	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.	4.4	14
16	Time series metagenomic sampling of the Thermopyles, Greece, geothermal springs reveals stable microbial communities dominated by novel sulfur-oxidizing chemoautotrophs. <i>Environmental Microbiology</i> , 2021, 23, 3710-3726.	1.8	10
17	Environmental stability impacts the differential sensitivity of marine microbiomes to increases in temperature and acidity. <i>ISME Journal</i> , 2021, 15, 19-28.	4.4	35
18	MicrobeAnnotator: a user-friendly, comprehensive functional annotation pipeline for microbial genomes. <i>BMC Bioinformatics</i> , 2021, 22, 11.	1.2	61

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19	Hidden Diversity within Common Protozoan Parasites as Revealed by a Novel Genomotyping Scheme. Applied and Environmental Microbiology, 2021, 87, .	1.4	23
20	The Reliability of Metagenome-Assembled Genomes (MAGs) in Representing Natural Populations: Insights from Comparing MAGs against Isolate Genomes Derived from the Same Fecal Sample. Applied and Environmental Microbiology, 2021, 87, .	1.4	82
21	Metagenomic insights into the effect of sulfate on enhanced biological phosphorus removal. Applied Microbiology and Biotechnology, 2021, 105, 2181-2193.	1.7	21
22	Beyond denitrification: The role of microbial diversity in controlling nitrous oxide reduction and soil nitrous oxide emissions. Global Change Biology, 2021, 27, 2669-2683.	4.2	57
23	Description of Candidatus Mesopelagibacter carboxydoxydans and Candidatus Anoxipelagibacter denitrificans: Nitrate-reducing SAR11 genera that dominate mesopelagic and anoxic marine zones. Systematic and Applied Microbiology, 2021, 44, 126185.	1.2	14
24	Bacteria Make a Living Breathing the Nitroheterocyclic Insensitive Munitions Compound 3-Nitro-1,2,4-triazol-5-one (NTO). Environmental Science & Technology, 2021, 55, 5806-5814.	4.6	12
25	Metagenomic Characterization of Soil Microbial Communities in the Luquillo Experimental Forest (Puerto Rico) and Implications for Nitrogen Cycling. Applied and Environmental Microbiology, 2021, 87, e0054621.	1.4	8
26	Microbial Taxonomy Run Amok. Trends in Microbiology, 2021, 29, 394-404.	3.5	38
27	Gut Microbiome Changes with Acute Diarrheal Disease in Urban Versus Rural Settings in Northern Ecuador. American Journal of Tropical Medicine and Hygiene, 2021, 104, 2275-2285.	0.6	7
28	Beach sand oil spills select for generalist microbial populations. ISME Journal, 2021, 15, 3418-3422.	4.4	3
29	Impact of an Urban Sanitation Intervention on Enteric Pathogen Detection in Soils. Environmental Science & Technology, 2021, 55, 9989-10000.	4.6	16
30	Reply to: "Re-evaluating the evidence for a universal genetic boundary among microbial species" Nature Communications, 2021, 12, 4060.	5.8	36
31	High Arsenic Levels Increase Activity Rather than Diversity or Abundance of Arsenic Metabolism Genes in Paddy Soils. Applied and Environmental Microbiology, 2021, 87, e0138321.	1.4	9
32	The influence of alfalfa-switchgrass intercropping on microbial community structure and function. Environmental Microbiology, 2021, 23, 6828-6843.	1.8	5
33	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. Science of the Total Environment, 2021, 788, 147693.	3.9	12
34	A novel, divergent alkane monooxygenase (<sc><i>alkB</i></sc>) clade involved in crude oil biodegradation. Environmental Microbiology Reports, 2021, 13, 830-840.	1.0	9
35	Gut microbiome, enteric infections and child growth across a rural-urban gradient: protocol for the ECoMiD prospective cohort study. BMJ Open, 2021, 11, e046241.	0.8	7
36	Transcriptomic and rRNA:rDNA Signatures of Environmental versus Enteric Enterococcus faecalis Isolates under Oligotrophic Freshwater Conditions. Microbiology Spectrum, 2021, 9, e0081721.	1.2	0

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37	Changes in the Vaginal Microbiome and Associated Toxicities Following Radiation Therapy for Gynecologic Cancers. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 680038.	1.8	5
38	Genomics Tools and Microbiota: Applications to Response in Coastal Ecosystems. <i>International Oil Spill Conference Proceedings</i> , 2021, 2021, .	0.1	0
39	A novel droplet digital PCR human mtDNA assay for fecal source tracking. <i>Water Research</i> , 2020, 183, 116085.	5.3	28
40	Gene-informed decomposition model predicts lower soil carbon loss due to persistent microbial adaptation to warming. <i>Nature Communications</i> , 2020, 11, 4897.	5.8	67
41	Integrated Omics Elucidate the Mechanisms Driving the Rapid Biodegradation of Deepwater Horizon Oil in Intertidal Sediments Undergoing Oxidic-Anoxic Cycles. <i>Environmental Science & Technology</i> , 2020, 54, 10088-10099.	4.6	11
42	Non-denitrifier nitrous oxide reductases dominate marine biomes. <i>Environmental Microbiology Reports</i> , 2020, 12, 681-692.	1.0	26
43	Iterative subtractive binning of freshwater chronoserics metagenomes identifies over 400 novel species and their ecologic preferences. <i>Environmental Microbiology</i> , 2020, 22, 3394-3412.	1.8	69
44	Winter warming in Alaska accelerates lignin decomposition contributed by Proteobacteria. <i>Microbiome</i> , 2020, 8, 84.	4.9	47
45	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	5.9	115
46	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.	1.8	21
47	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
48	Model-based Comparisons of the Abundance Dynamics of Bacterial Communities in Two Lakes. <i>Scientific Reports</i> , 2020, 10, 2423.	1.6	14
49	Opinion: Response to concerns about the use of DNA sequences as types in the nomenclature of prokaryotes. <i>Systematic and Applied Microbiology</i> , 2020, 43, 126070.	1.2	8
50	Giant virus diversity and host interactions through global metagenomics. <i>Nature</i> , 2020, 578, 432-436.	13.7	207
51	Warming-induced permafrost thaw exacerbates tundra soil carbon decomposition mediated by microbial community. <i>Microbiome</i> , 2020, 8, 3.	4.9	75
52	Advantages outweigh concerns about using genome sequence as type material for prokaryotic taxonomy. <i>Environmental Microbiology</i> , 2020, 22, 819-822.	1.8	12
53	Metagenomics as a Public Health Risk Assessment Tool in a Study of Natural Creek Sediments Influenced by Agricultural and Livestock Runoff: Potential and Limitations. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	27
54	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.	3.3	96

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55	Comparison of vaginal microbiota in gynecologic cancer patients pre- and post-radiation therapy and healthy women. <i>Cancer Medicine</i> , 2020, 9, 3714-3724.	1.3	23
56	Using flow cytometry and light-induced fluorescence to characterize the variability and characteristics of bioaerosols in springtime in Metro Atlanta, Georgia. <i>Atmospheric Chemistry and Physics</i> , 2020, 20, 1817-1838.	1.9	10
57	Abstract LB-362: Vaginal microbiome associated with patient-reported sexual dysfunction and physician-reported vaginal adverse events in gynecologic cancer women across radiotherapy. , 2020, , .		0
58	Tundra microbial community taxa and traits predict decomposition parameters of stable, old soil organic carbon. <i>ISME Journal</i> , 2019, 13, 2901-2915.	4.4	24
59	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.	3.3	83
60	Decomposition of sediment-oil-agglomerates in a Gulf of Mexico sandy beach. <i>Scientific Reports</i> , 2019, 9, 10071.	1.6	35
61	Prevalence of viral photosynthesis genes along a freshwater to saltwater transect in Southeast USA. <i>Environmental Microbiology Reports</i> , 2019, 11, 672-689.	1.0	24
62	Niche differentiation among annually recurrent coastal Marine Group II Euryarchaeota. <i>ISME Journal</i> , 2019, 13, 3024-3036.	4.4	41
63	Predominance of deterministic microbial community dynamics in salterns exposed to different light intensities. <i>Environmental Microbiology</i> , 2019, 21, 4300-4315.	1.8	20
64	Comparative Genomics and Phylogenomic Analysis of the Genus <i>Salinivibrio</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2104.	1.5	23
65	Metagenomic Signatures of Gut Infections Caused by Different <i>Escherichia coli</i> Pathotypes. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	33
66	Toward unrestricted use of public genomic data. <i>Science</i> , 2019, 363, 350-352.	6.0	45
67	Ecogenomic characterization of widespread, closely-related SAR11 clades of the freshwater genus <i>Candidatus Fonsibacter</i> and proposal of <i>Ca. Fonsibacter lacus</i> sp. nov. <i>Systematic and Applied Microbiology</i> , 2019, 42, 495-505.	1.2	33
68	Consent insufficient for data release—Response. <i>Science</i> , 2019, 364, 446-446.	6.0	5
69	Drinking Water Microbiome Project: Is it Time?. <i>Trends in Microbiology</i> , 2019, 27, 670-677.	3.5	50
70	Long-Term Warming in Alaska Enlarges the Diazotrophic Community in Deep Soils. <i>MBio</i> , 2019, 10, .	1.8	22
71	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. <i>Systematic and Applied Microbiology</i> , 2019, 42, 457-467.	1.2	22
72	<i>Candidatus</i> <i>Macondimonas diazotrophica</i> , a novel gammaproteobacterial genus dominating crude-oil-contaminated coastal sediments. <i>ISME Journal</i> , 2019, 13, 2129-2134.	4.4	46

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73	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.	1.6	31
74	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.	1.5	21
75	Genomic Variations Underlying Speciation and Niche Specialization of <i>Shewanella baltica</i> . <i>MSystems</i> , 2019, 4, .	1.7	10
76	Comparing DNA, RNA and protein levels for measuring microbial dynamics in soil microcosms amended with nitrogen fertilizer. <i>Scientific Reports</i> , 2019, 9, 17630.	1.6	18
77	Moving the cataloguing of the "uncultivated majority" forward. <i>Systematic and Applied Microbiology</i> , 2019, 42, 3-4.	1.2	3
78	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.	4.4	40
79	Intensive allochthonous inputs along the Ganges River and their effect on microbial community composition and dynamics. <i>Environmental Microbiology</i> , 2019, 21, 182-196.	1.8	40
80	Glucose addition increases the magnitude and decreases the age of soil respired carbon in a long-term permafrost incubation study. <i>Soil Biology and Biochemistry</i> , 2019, 129, 201-211.	4.2	26
81	Phosphate addition increases tropical forest soil respiration primarily by deconstraining microbial population growth. <i>Soil Biology and Biochemistry</i> , 2019, 130, 43-54.	4.2	26
82	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.	1.6	17
83	Genomic and Transcriptomic Insights into How Bacteria Withstand High Concentrations of Benzalkonium Chloride Biocides. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	43
84	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.	1.8	33
85	Genomic comparison between members of the Salinibacteraceae 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.	1.2	29
86	Reply to the commentary "Uncultivated microbes" in need of their own nomenclature?. <i>ISME Journal</i> , 2018, 12, 653-654.	4.4	8
87	How Much Do rRNA Gene Surveys Underestimate Extant Bacterial Diversity?. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	47
88	Microbial functional diversity covaries with permafrost thaw-induced environmental heterogeneity in tundra soil. <i>Global Change Biology</i> , 2018, 24, 297-307.	4.2	22
89	Divergence in Gene Regulation Contributes to Sympatric Speciation of <i>Shewanella baltica</i> Strains. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	5
90	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, .	1.4	121

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91	Single cell genomic and transcriptomic evidence for the use of alternative nitrogen substrates by anammox bacteria. ISME Journal, 2018, 12, 2706-2722.	4.4	45
92	High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. Nature Communications, 2018, 9, 5114.	5.8	2,816
93	Nonpareil 3: Fast Estimation of Metagenomic Coverage and Sequence Diversity. MSystems, 2018, 3, .	1.7	152
94	Genomic Characterization and Copy Number Variation of <i>Bacillus anthracis</i> Plasmids pXO1 and pXO2 in a Historical Collection of 412 Strains. MSystems, 2018, 3, .	1.7	32
95	Biotic responses buffer warming-induced soil organic carbon loss in Arctic tundra. Global Change Biology, 2018, 24, 4946-4959.	4.2	21
96	Widely Used Benzalkonium Chloride Disinfectants Can Promote Antibiotic Resistance. Applied and Environmental Microbiology, 2018, 84, .	1.4	134
97	More replenishment than priming loss of soil organic carbon with additional carbon input. Nature Communications, 2018, 9, 3175.	5.8	69
98	The Microbial Genomes Atlas (MiGA) webserver: taxonomic and gene diversity analysis of Archaea and Bacteria at the whole genome level. Nucleic Acids Research, 2018, 46, W282-W288.	6.5	458
99	imGLAD: accurate detection and quantification of target organisms in metagenomes. PeerJ, 2018, 6, e5882.	0.9	24
100	ROcker: accurate detection and quantification of target genes in short-read metagenomic data sets by modeling sliding-window bitscores. Nucleic Acids Research, 2017, 45, gkw900.	6.5	37
101	Quantifying the Importance of the Rare Biosphere for Microbial Community Response to Organic Pollutants in a Freshwater Ecosystem. Applied and Environmental Microbiology, 2017, 83, .	1.4	60
102	Warming enhances old organic carbon decomposition through altering functional microbial communities. ISME Journal, 2017, 11, 1825-1835.	4.4	136
103	Draft Genome Sequence of <i>Bacillus cereus</i> LA2007, a Human-Pathogenic Isolate Harboring Anthrax-Like Plasmids. Genome Announcements, 2017, 5, .	0.8	18
104	The low diverse gastric microbiome of the jellyfish <i>Cotylorhiza tuberculata</i> is dominated by four novel taxa. Environmental Microbiology, 2017, 19, 3039-3058.	1.8	62
105	â€ˆ Candidatus <i>Dichloromethanomonas elyunquensis</i> gen. nov., sp. nov., a dichloromethane-degrading anaerobe of the Peptococcaceae family. Systematic and Applied Microbiology, 2017, 40, 150-159.	1.2	50
106	Experimental warming reveals positive feedbacks to climate change in the Eurasian Steppe. ISME Journal, 2017, 11, 885-895.	4.4	47
107	Uncultivated microbes in need of their own taxonomy. ISME Journal, 2017, 11, 2399-2406.	4.4	572
108	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. Nature Biotechnology, 2017, 35, 725-731.	9.4	1,512

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109	A Rieske-Type Oxygenase of <i>Pseudomonas</i> sp. BIOMIG1 Converts Benzalkonium Chlorides to Benzyldimethyl Amine. <i>Environmental Science & Technology</i> , 2017, 51, 175-181.	4.6	21
110	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, .	1.4	54
111	Metagenomics Reveals Pervasive Bacterial Populations and Reduced Community Diversity across the Alaska Tundra Ecosystem. <i>Frontiers in Microbiology</i> , 2016, 7, 579.	1.5	66
112	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.	1.8	58
113	Temperature sensitivity of organic matter decomposition of permafrost-region soils during laboratory incubations. <i>Soil Biology and Biochemistry</i> , 2016, 97, 1-14.	4.2	73
114	SAR11 bacteria linked to ocean anoxia and nitrogen loss. <i>Nature</i> , 2016, 536, 179-183.	13.7	160
115	Dynamic models of the complex microbial metapopulation of lake mendota. <i>Npj Systems Biology and Applications</i> , 2016, 2, 16007.	1.4	43
116	Meeting report: GenBank microbial genomic taxonomy workshop (12-13 May, 2015). <i>Standards in Genomic Sciences</i> , 2016, 11, .	1.5	81
117	Similar Microbial Consortia and Genes Are Involved in the Biodegradation of Benzalkonium Chlorides in Different Environments. <i>Environmental Science & Technology</i> , 2016, 50, 4304-4313.	4.6	47
118	Tundra soil carbon is vulnerable to rapid microbial decomposition under climate warming. <i>Nature Climate Change</i> , 2016, 6, 595-600.	8.1	260
119	Detection and Diversity of Fungal Nitric Oxide Reductase Genes (<i>p45nor</i>) in Agricultural Soils. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2919-2928.	1.4	55
120	Biofilms on Hospital Shower Hoses: Characterization and Implications for Nosocomial Infections. <i>Applied and Environmental Microbiology</i> , 2016, 82, 2872-2883.	1.4	102
121	Draft Genome Sequence of a Strictly Anaerobic Dichloromethane-Degrading Bacterium. <i>Genome Announcements</i> , 2016, 4, .	0.8	13
122	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.	4.4	63
123	Microbial community successional patterns in beach sands impacted by the Deepwater Horizon oil spill. <i>ISME Journal</i> , 2015, 9, 1928-1940.	4.4	155
124	Classifying the uncultivated microbial majority: A place for metagenomic data in the Candidatus proposal. <i>Systematic and Applied Microbiology</i> , 2015, 38, 223-230.	1.2	61
125	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.	1.4	57
126	Microbial species delineation using whole genome sequences. <i>Nucleic Acids Research</i> , 2015, 43, 6761-6771.	6.5	609

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127	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.	4.2	61
128	Inter-phylum HGT has shaped the metabolism of many mesophilic and anaerobic bacteria. <i>ISME Journal</i> , 2015, 9, 958-967.	4.4	50
129	Strengths and Limitations of 16S rRNA Gene Amplicon Sequencing in Revealing Temporal Microbial Community Dynamics. <i>PLoS ONE</i> , 2014, 9, e93827.	1.1	508
130	Detecting Nitrous Oxide Reductase (<i>nosZ</i>) Genes in Soil Metagenomes: Method Development and Implications for the Nitrogen Cycle. <i>MBio</i> , 2014, 5, e01193-14.	1.8	142
131	MyTaxa: an advanced taxonomic classifier for genomic and metagenomic sequences. <i>Nucleic Acids Research</i> , 2014, 42, e73-e73.	6.5	445
132	Soil Microbial Community Responses to a Decade of Warming as Revealed by Comparative Metagenomics. <i>Applied and Environmental Microbiology</i> , 2014, 80, 1777-1786.	1.4	131
133	Microbial Community Degradation of Widely Used Quaternary Ammonium Disinfectants. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5892-5900.	1.4	60
134	Genome Sequencing Reveals the Environmental Origin of Enterococci and Potential Biomarkers for Water Quality Monitoring. <i>Environmental Science & Technology</i> , 2014, 48, 3707-3714.	4.6	14
135	Nonpareil: a redundancy-based approach to assess the level of coverage in metagenomic datasets. <i>Bioinformatics</i> , 2014, 30, 629-635.	1.8	186
136	Evaluation of metatranscriptomic protocols and application to the study of freshwater microbial communities. <i>Environmental Microbiology Reports</i> , 2014, 6, 640-655.	1.0	36
137	Estimating coverage in metagenomic data sets and why it matters. <i>ISME Journal</i> , 2014, 8, 2349-2351.	4.4	142
138	Do airborne microbes matter for atmospheric chemistry and cloud formation?. <i>Environmental Microbiology</i> , 2014, 16, 1482-1484.	1.8	14
139	Stability, genotypic and phenotypic diversity of <i>Sphaerobacter</i> in the redox transition zone of the Baltic Sea. <i>Environmental Microbiology</i> , 2014, 16, 1854-1866.	1.8	26
140	Bypassing Cultivation To Identify Bacterial Species. <i>Microbe Magazine</i> , 2014, 9, 111-118.	0.4	581
141	Sequencing platform and library preparation choices impact viral metagenomes. <i>BMC Genomics</i> , 2013, 14, 320.	1.2	90
142	Long-Term Exposure to Benzalkonium Chloride Disinfectants Results in Change of Microbial Community Structure and Increased Antimicrobial Resistance. <i>Environmental Science & Technology</i> , 2013, 47, 9730-9738.	4.6	170
143	A User's Guide to Quantitative and Comparative Analysis of Metagenomic Datasets. <i>Methods in Enzymology</i> , 2013, 531, 525-547.	0.4	28
144	Defining Taxonomic Ranks. , 2013, , 229-254.		14

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145	<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 classis</i> 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.	0.8	502
146	Microbial community adaptation to quaternary ammonium biocides as revealed by metagenomics. <i>Environmental Microbiology</i> , 2013, 15, 2850-2864.	1.8	82
147	Microbiome of the upper troposphere: Species composition and prevalence, effects of tropical storms, and atmospheric implications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2575-2580.	3.3	377
148	Reply to Smith and Griffin: Methods, air flows, and conclusions are robust in the DeLeon-Rodriguez et al. study. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2085.	3.3	2
149	Draft Genome Sequence of <i>Catelicoccus marimammalium</i> , a Novel Species Commonly Found in Gull Feces. <i>Genome Announcements</i> , 2013, 1, .	0.8	9
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