

Christa Schleper

List of Publications by Year in descending order

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130
papers

18,952
citations

13068

68
h-index

14156

128
g-index

149
all docs

149
docs citations

149
times ranked

14816
citing authors

#	ARTICLE	IF	CITATIONS
1	The influence of soil pH on the diversity, abundance and transcriptional activity of ammonia oxidizing archaea and bacteria. <i>Environmental Microbiology</i> , 2008, 10, 2966-2978.	1.8	1,104
2	Complex archaea that bridge the gap between prokaryotes and eukaryotes. <i>Nature</i> , 2015, 521, 173-179.	13.7	995
3	<i>Nitrososphaera viennensis</i> , an ammonia oxidizing archaeon from soil. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 8420-8425.	3.3	810
4	Novel genes for nitrite reductase and Amo-related proteins indicate a role of uncultivated mesophilic crenarchaeota in nitrogen cycling. <i>Environmental Microbiology</i> , 2005, 7, 1985-1995.	1.8	758
5	Simultaneous Assessment of Soil Microbial Community Structure and Function through Analysis of the Meta-Transcriptome. <i>PLoS ONE</i> , 2008, 3, e2527.	1.1	667
6	Pathways of Carbon Assimilation and Ammonia Oxidation Suggested by Environmental Genomic Analyses of Marine Crenarchaeota. <i>PLoS Biology</i> , 2006, 4, e95.	2.6	554
7	Genomic studies of uncultivated archaea. <i>Nature Reviews Microbiology</i> , 2005, 3, 479-488.	13.6	531
8	The Thaumarchaeota: an emerging view of their phylogeny and ecophysiology. <i>Current Opinion in Microbiology</i> , 2011, 14, 300-306.	2.3	511
9	Diversity and abundance of Crenarchaeota in terrestrial habitats studied by 16S RNA surveys and real time PCR. <i>Environmental Microbiology</i> , 2003, 5, 787-797.	1.8	431
10	Distinct gene set in two different lineages of ammonia-oxidizing archaea supports the phylum Thaumarchaeota. <i>Trends in Microbiology</i> , 2010, 18, 331-340.	3.5	431
11	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.	3.3	420
12	Archaea in Biogeochemical Cycles. <i>Annual Review of Microbiology</i> , 2013, 67, 437-457.	2.9	393
13	The genome of the ammonia-oxidizing <i>Candidatus Nitrososphaera gargensis</i> : insights into metabolic versatility and environmental adaptations. <i>Environmental Microbiology</i> , 2012, 14, 3122-3145.	1.8	332
14	Methylotrophic methanogenic Thermoplasmata implicated in reduced methane emissions from bovine rumen. <i>Nature Communications</i> , 2013, 4, 1428.	5.8	328
15	Ammonia-oxidising Crenarchaeota: important players in the nitrogen cycle?. <i>Trends in Microbiology</i> , 2006, 14, 207-212.	3.5	315
16	Phylotype-level 16S rRNA analysis reveals new bacterial indicators of health state in acute murine colitis. <i>ISME Journal</i> , 2012, 6, 2091-2106.	4.4	291
17	Complex nitrogen cycling in the sponge <i>Geodia barretti</i> . <i>Environmental Microbiology</i> , 2009, 11, 2228-2243.	1.8	286
18	Correlating microbial community profiles with geochemical data in highly stratified sediments from the Arctic Mid-Ocean Ridge. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E2846-55.	3.3	282

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19	Pathways and key intermediates required for obligate aerobic ammonia-dependent chemolithotrophy in bacteria and Thaumarchaeota. <i>ISME Journal</i> , 2016, 10, 1836-1845.	4.4	281
20	Dynamics and functional relevance of ammonia-oxidizing archaea in two agricultural soils. <i>Environmental Microbiology</i> , 2009, 11, 446-456.	1.8	276
21	Aerobic nitrous oxide production through N-nitrosating hybrid formation in ammonia-oxidizing archaea. <i>ISME Journal</i> , 2014, 8, 1135-1146.	4.4	270
22	<i>Nitrososphaera viennensis</i> gen. nov., sp. nov., an aerobic and mesophilic, ammonia-oxidizing archaeon from soil and a member of the archaeal phylum Thaumarchaeota. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 2738-2752.	0.8	256
23	Unifying the global phylogeny and environmental distribution of ammonia-oxidising archaea based on <i>amoA</i> genes. <i>Nature Communications</i> , 2018, 9, 1517.	5.8	256
24	Ammonia-Oxidising Archaea – Physiology, Ecology and Evolution. <i>Advances in Microbial Physiology</i> , 2010, 57, 1-41.	1.0	244
25	Acidobacteria form a coherent but highly diverse group within the bacterial domain: evidence from environmental genomics. <i>Molecular Microbiology</i> , 2003, 50, 563-575.	1.2	231
26	Biochar Decelerates Soil Organic Nitrogen Cycling but Stimulates Soil Nitrification in a Temperate Arable Field Trial. <i>PLoS ONE</i> , 2014, 9, e86388.	1.1	231
27	Screening for Sulfolobales, their Plasmids and their Viruses in Icelandic Solfataras. <i>Systematic and Applied Microbiology</i> , 1993, 16, 609-628.	1.2	205
28	Ammonia oxidation: different niches for bacteria and archaea?. <i>ISME Journal</i> , 2010, 4, 1092-1094.	4.4	180
29	Proteomics and comparative genomics of <i>Nitrososphaera viennensis</i> reveal the core genome and adaptations of archaeal ammonia oxidizers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7937-E7946.	3.3	178
30	Longitudinal study of murine microbiota activity and interactions with the host during acute inflammation and recovery. <i>ISME Journal</i> , 2014, 8, 1101-1114.	4.4	174
31	Nitrification in terrestrial hot springs of Iceland and Kamchatka. <i>FEMS Microbiology Ecology</i> , 2008, 64, 167-174.	1.3	173
32	Responses of the terrestrial ammonia-oxidizing archaeon <i>Ca</i> . <i>Nitrososphaera viennensis</i> and the ammonia-oxidizing bacterium <i>Nitrospira multififormis</i> to nitrification inhibitors. <i>FEMS Microbiology Letters</i> , 2013, 344, 121-129.	0.7	172
33	Complete nucleotide sequence of the virus SSV1 of the archaeobacterium <i>Sulfolobus shibatae</i> . <i>Virology</i> , 1991, 185, 242-250.	1.1	166
34	Nitrification rates in Arctic soils are associated with functionally distinct populations of ammonia-oxidizing archaea. <i>ISME Journal</i> , 2013, 7, 1620-1631.	4.4	163
35	First insight into the genome of an uncultivated crenarchaeote from soil. <i>Environmental Microbiology</i> , 2002, 4, 603-611.	1.8	161
36	Viruses, plasmids and other genetic elements of thermophilic and hyperthermophilic Archaea. <i>FEMS Microbiology Reviews</i> , 1996, 18, 225-236.	3.9	160

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37	Physiological and genomic characterization of two novel marine thaumarchaeal strains indicates niche differentiation. <i>ISME Journal</i> , 2016, 10, 1051-1063.	4.4	160
38	Intact Polar and Core Glycerol Dibiphytanyl Glycerol Tetraether Lipids of Group I.1a and I.1b Thaumarchaeota in Soil. <i>Applied and Environmental Microbiology</i> , 2012, 78, 6866-6874.	1.4	156
39	Dibiphytanyl Ether Lipids in Nonthermophilic Crenarchaeotes. <i>Applied and Environmental Microbiology</i> , 1998, 64, 1133-1138.	1.4	151
40	UV-Inducible cellular aggregation of the hyperthermophilic archaeon <i>Sulfolobus solfataricus</i> is mediated by pili formation. <i>Molecular Microbiology</i> , 2008, 70, 938-952.	1.2	137
41	Homologues of nitrite reductases in ammonia-oxidizing archaea: diversity and genomic context. <i>Environmental Microbiology</i> , 2010, 12, 1075-1088.	1.8	137
42	Distinct microbial communities associated with buried soils in the Siberian tundra. <i>ISME Journal</i> , 2014, 8, 841-853.	4.4	137
43	Genomic Analysis Reveals Chromosomal Variation in Natural Populations of the Uncultured Psychrophilic Archaeon <i>Cenarchaeum symbiosum</i> . <i>Journal of Bacteriology</i> , 1998, 180, 5003-5009.	1.0	137
44	Ammonia-oxidizing archaea as main drivers of nitrification in cold-water sponges. <i>Environmental Microbiology</i> , 2012, 14, 909-923.	1.8	135
45	A reporter gene system for the hyperthermophilic archaeon <i>Sulfolobus solfataricus</i> based on a selectable and integrative shuttle vector. <i>Molecular Microbiology</i> , 2003, 48, 1241-1252.	1.2	132
46	Response of the Hyperthermophilic Archaeon <i>Sulfolobus solfataricus</i> to UV Damage. <i>Journal of Bacteriology</i> , 2007, 189, 8708-8718.	1.0	128
47	Metatranscriptomics of the marine sponge <i>Geodia barretti</i> : tackling phylogeny and function of its microbial community. <i>Environmental Microbiology</i> , 2012, 14, 1308-1324.	1.8	124
48	Back to the Future of Soil Metagenomics. <i>Frontiers in Microbiology</i> , 2016, 7, 73.	1.5	120
49	Life at extremely low pH. <i>Nature</i> , 1995, 375, 741-742.	13.7	117
50	Chemotaxonomic characterisation of the thaumarchaeal lipidome. <i>Environmental Microbiology</i> , 2017, 19, 2681-2700.	1.8	117
51	High Spontaneous Mutation Rate in the Hyperthermophilic Archaeon <i>Sulfolobus solfataricus</i> Is Mediated by Transposable Elements. <i>Journal of Bacteriology</i> , 2000, 182, 2574-2581.	1.0	116
52	UV-inducible DNA exchange in hyperthermophilic archaea mediated by type IV pili. <i>Molecular Microbiology</i> , 2011, 82, 807-817.	1.2	113
53	Diversity of Archaea in hypersaline environments characterized by molecular-phylogenetic and cultivation studies. <i>Extremophiles</i> , 2002, 6, 267-274.	0.9	110
54	Phylogenetic and genomic analysis of <i>Methanomassiliicoccales</i> in wetlands and animal intestinal tracts reveals clade-specific habitat preferences. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv149.	1.3	110

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55	Microbial community structure and functioning in marine sediments associated with diffuse hydrothermal venting assessed by integrated metaomics. <i>Environmental Microbiology</i> , 2014, 16, 2699-2710.	1.8	109
56	Intestinal Microbiota Signatures Associated with Inflammation History in Mice Experiencing Recurring Colitis. <i>Frontiers in Microbiology</i> , 2015, 6, 1408.	1.5	106
57	Characterization of large-insert DNA libraries from soil for environmental genomic studies of Archaea. <i>Environmental Microbiology</i> , 2004, 6, 970-980.	1.8	101
58	A plant-microbe interaction framework explaining nutrient effects on primary production. <i>Nature Ecology and Evolution</i> , 2018, 2, 1588-1596.	3.4	100
59	CRISPR-mediated targeted mRNA degradation in the archaeon <i>Sulfolobus solfataricus</i> . <i>Nucleic Acids Research</i> , 2014, 42, 5280-5288.	6.5	93
60	Biological methane production under putative Enceladus-like conditions. <i>Nature Communications</i> , 2018, 9, 748.	5.8	91
61	<i>In vivo</i> activity of CRISPR-mediated virus defence in a hyperthermophilic archaeon. <i>Molecular Microbiology</i> , 2011, 80, 481-491.	1.2	89
62	A hydrophobic ammonia-oxidizing archaeon of the <i>Nitrosocosmicus</i> clade isolated from coal tar-contaminated sediment. <i>Environmental Microbiology Reports</i> , 2016, 8, 983-992.	1.0	89
63	Plant-derived compounds stimulate the decomposition of organic matter in arctic permafrost soils. <i>Scientific Reports</i> , 2016, 6, 25607.	1.6	87
64	Candidatus <i>Nitrosocaldus cavascurensis</i> , an Ammonia Oxidizing, Extremely Thermophilic Archaeon with a Highly Mobile Genome. <i>Frontiers in Microbiology</i> , 2018, 9, 28.	1.5	86
65	Genetic Requirements for the Function of the Archaeal Virus SSV1 in <i>Sulfolobus solfataricus</i> : Construction and Testing of Viral Shuttle Vectors. <i>Genetics</i> , 1999, 152, 1397-1405.	1.2	86
66	Four newly isolated fuselloviruses from extreme geothermal environments reveal unusual morphologies and a possible interviral recombination mechanism. <i>Environmental Microbiology</i> , 2009, 11, 2849-2862.	1.8	85
67	Variability of the transporter gene complement in ammonia-oxidizing archaea. <i>Trends in Microbiology</i> , 2014, 22, 665-675.	3.5	81
68	Holistic Assessment of Rumen Microbiome Dynamics through Quantitative Metatranscriptomics Reveals Multifunctional Redundancy during Key Steps of Anaerobic Feed Degradation. <i>MSystems</i> , 2018, 3, .	1.7	74
69	Metagenome—a challenging source of enzyme discovery. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2002, 19-20, 13-19.	1.8	73
70	Site- and horizon-specific patterns of microbial community structure and enzyme activities in permafrost-affected soils of Greenland. <i>Frontiers in Microbiology</i> , 2014, 5, 541.	1.5	73
71	Analysis of the first genome fragment from the marine sponge-associated, novel candidate phylum Poribacteria by environmental genomics. <i>Environmental Microbiology</i> , 2006, 8, 612-624.	1.8	68
72	The effect of warming on the vulnerability of subducted organic carbon in arctic soils. <i>Soil Biology and Biochemistry</i> , 2015, 90, 19-29.	4.2	68

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73	Unexpectedly broad target recognition of the CRISPR-mediated virus defence system in the archaeon <i>Sulfolobus solfataricus</i> . <i>Nucleic Acids Research</i> , 2013, 41, 10509-10517.	6.5	66
74	An insertion element of the extremely thermophilic archaeon <i>Sulfolobus solfataricus</i> transposes into the endogenous β -galactosidase gene. <i>Molecular Genetics and Genomics</i> , 1994, 243, 91-96.	2.4	63
75	Complete Nucleotide Sequence of the <i>Sulfolobus islandicus</i> Multicopy Plasmid pRN1. <i>Plasmid</i> , 1996, 35, 141-144.	0.4	63
76	Diversity and abundance of <i>Korarchaeota</i> in terrestrial hot springs of Iceland and Kamchatka. <i>ISME Journal</i> , 2010, 4, 346-356.	4.4	61
77	Significance of dark CO ₂ fixation in arctic soils. <i>Soil Biology and Biochemistry</i> , 2018, 119, 11-21.	4.2	58
78	Elucidating the transcription cycle of the UV-inducible hyperthermophilic archaeal virus SSV1 by DNA microarrays. <i>Virology</i> , 2007, 365, 48-59.	1.1	56
79	Distribution of <i>Crenarchaeota</i> Representatives in Terrestrial Hot Springs of Russia and Iceland. <i>Applied and Environmental Microbiology</i> , 2008, 74, 7620-7628.	1.4	56
80	“Hot standards” for the thermoacidophilic archaeon <i>Sulfolobus solfataricus</i> . <i>Extremophiles</i> , 2010, 14, 119-142.	0.9	55
81	Assessing the Ecophysiology of Methanogens in the Context of Recent Astrobiological and Planetological Studies. <i>Life</i> , 2015, 5, 1652-1686.	1.1	55
82	Diversity of radA Genes from Cultured and Uncultured Archaea : Comparative Analysis of Putative RadA Proteins and Their Use as a Phylogenetic Marker. <i>Journal of Bacteriology</i> , 1999, 181, 907-915.	1.0	54
83	The Phylum Thaumarchaeota. , 2014, , 347-362.		52
84	Ammonia Oxidation by the Arctic Terrestrial Thaumarchaeote Candidatus <i>Nitrosocosmicus arcticus</i> Is Stimulated by Increasing Temperatures. <i>Frontiers in Microbiology</i> , 2019, 10, 1571.	1.5	51
85	A thaumarchaeal provirus testifies for an ancient association of tailed viruses with archaea. <i>Biochemical Society Transactions</i> , 2011, 39, 82-88.	1.6	50
86	Metagenomics of Kamchatkan hot spring filaments reveal two new major (hyper)thermophilic lineages related to Thaumarchaeota. <i>Research in Microbiology</i> , 2013, 164, 425-438.	1.0	46
87	Quantitative and phylogenetic study of the Deep Sea Archaeal Group in sediments of the Arctic mid-ocean spreading ridge. <i>Frontiers in Microbiology</i> , 2013, 4, 299.	1.5	45
88	Regulation of expression of the arabinose and glucose transporter genes in the thermophilic archaeon <i>Sulfolobus solfataricus</i> . <i>Extremophiles</i> , 2006, 10, 383-391.	0.9	43
89	Metagenomic Analysis of Ammonia-Oxidizing Archaea Affiliated with the Soil Group. <i>Frontiers in Microbiology</i> , 2012, 3, 208.	1.5	41
90	Intestinal Epithelial Cell Tyrosine Kinase 2 Transduces IL-22 Signals To Protect from Acute Colitis. <i>Journal of Immunology</i> , 2015, 195, 5011-5024.	0.4	40

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91	Transformation of the extremely thermoacidophilic archaeon <i>Sulfolobus solfataricus</i> via a self-spreading vector. <i>FEMS Microbiology Letters</i> , 1996, 137, 31-35.	0.7	39
92	Type I interferons have opposing effects during the emergence and recovery phases of colitis. <i>European Journal of Immunology</i> , 2014, 44, 2749-2760.	1.6	39
93	Reactions to UV damage in the model archaeon <i>Sulfolobus solfataricus</i> . <i>Biochemical Society Transactions</i> , 2009, 37, 36-41.	1.6	36
94	Sulfur-Oxidizing Chemolithotrophic Proteobacteria Dominate the Microbiota in High Arctic Thermal Springs on Svalbard. <i>Astrobiology</i> , 2011, 11, 665-678.	1.5	36
95	Geochemical transition zone powering microbial growth in subsurface sediments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 32617-32626.	3.3	36
96	CRISPR-mediated gene silencing reveals involvement of the archaeal S-layer in cell division and virus infection. <i>Nature Communications</i> , 2019, 10, 4797.	5.8	35
97	Seasonal and vertical distribution of putative ammonia-oxidizing thaumarchaeotal communities in an oligotrophic lake. <i>FEMS Microbiology Ecology</i> , 2013, 83, 515-526.	1.3	33
98	Archaeal nitrification is a key driver of high nitrous oxide emissions from arctic peatlands. <i>Soil Biology and Biochemistry</i> , 2019, 137, 107539.	4.2	33
99	Genome wide transcriptomic analysis of the soil ammonia oxidizing archaeon <i>Nitrososphaera viennensis</i> upon exposure to copper limitation. <i>ISME Journal</i> , 2020, 14, 2659-2674.	4.4	33
100	Gene expression of lactobacilli in murine forestomach biofilms. <i>Microbial Biotechnology</i> , 2014, 7, 347-359.	2.0	31
101	Intact polar lipid and core lipid inventory of the hydrothermal vent methanogens <i>Methanocaldococcus villosus</i> and <i>Methanothermococcus okinawensis</i> . <i>Organic Geochemistry</i> , 2018, 126, 33-42.	0.9	29
102	Nucleotide sequence, transcription and phylogeny of the gene encoding the superoxide dismutase of <i>Sulfolobus acidocaldarius</i> . <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1993, 1174, 95-98.	2.4	28
103	The legacy of Carl Woese and Wolfram Zillig: from phylogeny to landmark discoveries. <i>Nature Reviews Microbiology</i> , 2013, 11, 713-719.	13.6	28
104	Temporal and Spatial Coexistence of Archaeal and Bacterial <i>amoA</i> Genes and Gene Transcripts in Lake Lucerne. <i>Archaea</i> , 2013, 2013, 1-11.	2.3	27
105	Ancestral Reconstructions Decipher Major Adaptations of Ammonia-Oxidizing Archaea upon Radiation into Moderate Terrestrial and Marine Environments. <i>MBio</i> , 2020, 11, .	1.8	27
106	Genomes of Thaumarchaeota from deep sea sediments reveal specific adaptations of three independently evolved lineages. <i>ISME Journal</i> , 2021, 15, 2792-2808.	4.4	27
107	A phylogenetic and proteomic reconstruction of eukaryotic chromatin evolution. <i>Nature Ecology and Evolution</i> , 2022, 6, 1007-1023.	3.4	26
108	SulfoSYS (<i>Sulfolobus</i> Systems Biology): towards a silicon cell model for the central carbohydrate metabolism of the archaeon <i>Sulfolobus solfataricus</i> under temperature variation. <i>Biochemical Society Transactions</i> , 2009, 37, 58-64.	1.6	25

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109	Efficient CRISPR-Mediated Post-Transcriptional Gene Silencing in a Hyperthermophilic Archaeon Using Multiplexed crRNA Expression. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3161-3168.	0.8	25
110	CRISPR-mediated defense mechanisms in the hyperthermophilic archaeal genus <i>Sulfolobus</i> . <i>RNA Biology</i> , 2013, 10, 671-678.	1.5	21
111	Exploring the microbial biotransformation of extraterrestrial material on nanometer scale. <i>Scientific Reports</i> , 2019, 9, 18028.	1.6	21
112	Distribution and Activity of Ammonia-Oxidizing Archaea in Natural Environments. , 0, , 157-178.		19
113	Metagenomes from Coastal Marine Sediments Give Insights into the Ecological Role and Cellular Features of <i>Loki</i> - and <i>Thorarchaeota</i> . <i>MBio</i> , 2019, 10, .	1.8	16
114	Heavily Armed Ancestors: CRISPR Immunity and Applications in Archaea with a Comparative Analysis of CRISPR Types in Sulfolobales. <i>Biomolecules</i> , 2020, 10, 1523.	1.8	14
115	Preparation of High-Molecular Weight DNA and Metagenomic Libraries from Soils and Hot Springs. <i>Methods in Enzymology</i> , 2011, 496, 319-344.	0.4	12
116	Copper limiting threshold in the terrestrial ammonia oxidizing archaeon <i>Nitrososphaera viennensis</i> . <i>Research in Microbiology</i> , 2020, 171, 134-142.	1.0	12
117	The Impact of Non-cultivated Biodiversity on Enzyme Discovery and Evolution. <i>Biocatalysis and Biotransformation</i> , 2003, 21, 87-91.	1.1	11
118	Indications for a moonlighting function of translation factor <i>alF5A</i> in the crenarchaeum <i>Sulfolobus solfataricus</i> . <i>RNA Biology</i> , 2019, 16, 675-685.	1.5	11
119	Nitrogen Isotope Fractionation During Archaeal Ammonia Oxidation: Coupled Estimates From Measurements of Residual Ammonium and Accumulated Nitrite. <i>Frontiers in Microbiology</i> , 2020, 11, 1710.	1.5	10
120	Comparative CRISPR type III-based knockdown of essential genes in hyperthermophilic <i>Sulfolobales</i> and the evasion of lethal gene silencing. <i>RNA Biology</i> , 2021, 18, 421-434.	1.5	10
121	Archaea: very diverse, often different but never bad?. <i>Current Opinion in Microbiology</i> , 2011, 14, 271-273.	2.3	9
122	Linking 16S rRNA Gene Classification to <i>amoA</i> Gene Taxonomy Reveals Environmental Distribution of Ammonia-Oxidizing Archaeal Clades in Peatland Soils. <i>MSystems</i> , 2021, 6, e0054621.	1.7	9
123	Metabolism of the deep. <i>Nature</i> , 2008, 456, 712-713.	13.7	8
124	Meet the relatives of our cellular ancestor. <i>Nature</i> , 2020, 577, 478-479.	13.7	8
125	Phylogeny of DNA-Dependent RNA Polymerases: Testimony for the Origin of Eukaryotes. , 1991, , 321-332.		8
126	Comment on "A Critical Review on Nitrous Oxide Production by Ammonia-Oxidizing Archaea" by Lan Wu, Xueming Chen, Wei Wei, Yiwen Liu, Dongbo Wang, and Bing-Jie Ni. <i>Environmental Science & Technology</i> , 2021, 55, 797-798.	4.6	6

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127	Microbial diversity of a closed salt lagoon in the Puertecitos area, Upper Gulf of California. <i>Ciencias Marinas</i> , 2018, 44, 71-90.	0.4	5
128	Draft Genome Sequence of the Growth-Promoting Endophyte <i>Paenibacillus</i> sp. P22, Isolated from <i>Populus</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	4
129	The Microbial Soil Flora: Novel Approaches for Accessing the Phylogenetic and Physiological Diversity of Prokaryotes. , 2006, , 407-424.		2
130	Simulating putative Enceladus-like conditions: The possibility of biological methane production on Saturn's icy moon. <i>Proceedings of the International Astronomical Union</i> , 2018, 14, 219-221.	0.0	1