

Andrew J Weightman

List of Publications by Year in descending order

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123
papers

12,031
citations

30070

54
h-index

26613

107
g-index

126
all docs

126
docs citations

126
times ranked

11555
citing authors

#	ARTICLE	IF	CITATIONS
1	Design and Evaluation of Useful Bacterium-Specific PCR Primers That Amplify Genes Coding for Bacterial 16S rRNA. <i>Applied and Environmental Microbiology</i> , 1998, 64, 795-799.	3.1	1,498
2	At Least 1 in 20 16S rRNA Sequence Records Currently Held in Public Repositories Is Estimated To Contain Substantial Anomalies. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7724-7736.	3.1	716
3	Deep bacterial biosphere in Pacific Ocean sediments. <i>Nature</i> , 1994, 371, 410-413.	27.8	653
4	New Screening Software Shows that Most Recent Large 16S rRNA Gene Clone Libraries Contain Chimeras. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5734-5741.	3.1	621
5	Cultivation-Dependent and -Independent Approaches for Determining Bacterial Diversity in Heavy-Metal-Contaminated Soil. <i>Applied and Environmental Microbiology</i> , 2003, 69, 3223-3230.	3.1	465
6	Deep sub-seafloor prokaryotes stimulated at interfaces over geological time. <i>Nature</i> , 2005, 436, 390-394.	27.8	414
7	Transposon mutagenesis and cloning analysis of the pathways for degradation of 2,4-dichlorophenoxyacetic acid and 3-chlorobenzoate in <i>Alcaligenes eutrophus</i> JMP134(pJP4). <i>Journal of Bacteriology</i> , 1985, 161, 85-90.	2.2	306
8	A review of prokaryotic populations and processes in sub-seafloor sediments, including biosphere:geosphere interactions. <i>Marine Geology</i> , 2014, 352, 409-425.	2.1	265
9	Assessment of bacterial community structure in the deep sub-seafloor biosphere by 16S rDNA-based techniques: a cautionary tale. <i>Journal of Microbiological Methods</i> , 2003, 55, 155-164.	1.6	225
10	Molecular and Cultural Analysis of the Microflora Associated with Endodontic Infections. <i>Journal of Dental Research</i> , 2002, 81, 761-766.	5.2	220
11	Development of a <i>recA</i> Gene-Based Identification Approach for the Entire <i>Burkholderia</i> Genus. <i>Applied and Environmental Microbiology</i> , 2005, 71, 3917-3927.	3.1	217
12	Prokaryotic biodiversity and activity in the deep subseafloor biosphere. <i>FEMS Microbiology Ecology</i> , 2008, 66, 181-196.	2.7	217
13	PRIMROSE: a computer program for generating and estimating the phylogenetic range of 16S rRNA oligonucleotide probes and primers in conjunction with the RDP-II database. <i>Nucleic Acids Research</i> , 2002, 30, 3481-3489.	14.5	206
14	Bacteria in decomposing wood and their interactions with wood-decay fungi. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw179.	2.7	191
15	Diversity of prokaryotes and methanogenesis in deep subsurface sediments from the Nankai Trough, Ocean Drilling Program Leg 190. <i>Environmental Microbiology</i> , 2004, 6, 274-287.	3.8	183
16	Prokaryotic community composition and biogeochemical processes in deep subseafloor sediments from the Peru Margin. <i>FEMS Microbiology Ecology</i> , 2006, 58, 65-85.	2.7	168
17	Phylogeny and physiology of candidate phylum "Atribacteria"™ (OP9/JJS1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016, 10, 273-286.	9.8	166
18	Bacterial community structure, compartmentalization and activity in a microbial fuel cell. <i>Journal of Applied Microbiology</i> , 2006, 101, 698-710.	3.1	164

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19	Methanogen and bacterial diversity and distribution in deep gas hydrate sediments from the Cascadia Margin as revealed by 16S rRNA molecular analysis. <i>FEMS Microbiology Ecology</i> , 2001, 34, 221-228.	2.7	160
20	The family Coriobacteriaceae: reclassification of <i>Eubacterium exiguum</i> (Poco et al. 1996) and <i>Peptostreptococcus heliotrinireducens</i> (Lanigan 1976) as <i>Slackia exigua</i> gen. nov., comb. nov. and <i>Slackia heliotrinireducens</i> gen. nov., comb. nov., and <i>Eubacterium lentum</i> (Prevot 1938) as <i>Eggerthella lenta</i> gen. nov., comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 1999, 49, 595-600.	1.7	149
21	<i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> in the Catchment Area and Water of the River Taff in South Wales, United Kingdom, and Its Potential Relationship to Clustering of Crohn's Disease Cases in the City of Cardiff. <i>Applied and Environmental Microbiology</i> , 2005, 71, 2130-2139.	3.1	147
22	Bacterial populations and processes in sediments containing gas hydrates (ODP Leg 146: Cascadia) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5</i>	4.4	138
23	Biogeochemistry and biodiversity of methane cycling in subsurface marine sediments (Skagerrak,) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 130</i>	3.8	130
24	Novel subgingival bacterial phylotypes detected using multiple universal polymerase chain reaction primer sets. <i>Oral Microbiology and Immunology</i> , 2006, 21, 61-68.	2.8	128
25	Effect of sample handling on estimation of bacterial diversity in marine sediments by 16S rRNA gene sequence analysis. <i>FEMS Microbiology Ecology</i> , 1994, 15, 215-225.	2.7	118
26	The effect of anthropogenic arsenic contamination on the earthworm microbiome. <i>Environmental Microbiology</i> , 2015, 17, 1884-1896.	3.8	118
27	New Degenerate Cytophaga - Flexibacter - Bacteroides -Specific 16S Ribosomal DNA-Targeted Oligonucleotide Probes Reveal High Bacterial Diversity in River Taff Epilithon. <i>Applied and Environmental Microbiology</i> , 2002, 68, 201-210.	3.1	117
28	Widespread Occurrence of a Novel Division of Bacteria Identified by 16S rRNA Gene Sequences Originally Found in Deep Marine Sediments. <i>Applied and Environmental Microbiology</i> , 2004, 70, 5708-5713.	3.1	113
29	Culturable prokaryotic diversity of deep, gas hydrate sediments: first use of a continuous high-pressure, anaerobic, enrichment and isolation system for seafloor sediments (DeepIsoBUG). <i>Environmental Microbiology</i> , 2009, 11, 3140-3153.	3.8	107
30	A comparison of stable-isotope probing of DNA and phospholipid fatty acids to study prokaryotic functional diversity in sulfate-reducing marine sediment enrichment slurries. <i>Environmental Microbiology</i> , 2006, 8, 1575-1589.	3.8	103
31	Comparison of microbial and meiofaunal community analyses for determining impact of heavy metal contamination. <i>Journal of Microbiological Methods</i> , 2001, 45, 171-185.	1.6	101
32	DNA extraction for 16S rRNA gene analysis to determine genetic diversity in deep sediment communities. <i>FEMS Microbiology Letters</i> , 1992, 100, 59-65.	1.8	101
33	Prokaryotic Populations and Activities in an Interbedded Coal Deposit, Including a Previously Deeply Buried Section (1.6–2.3 km) Above ¼ 150 Ma Basement Rock. <i>Geomicrobiology Journal</i> , 2009, 26, 163-178.	2.0	99
34	Culturable phylogenetic diversity of the phylum 'Bacteroidetes' from river epilithon and coastal water and description of novel members of the family Flavobacteriaceae: <i>Epilithonimonas tenax</i> gen. nov., sp. nov. and <i>Persicivirga xylanidelens</i> gen. nov., sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2006, 56, 169-180.	1.7	94
35	The complete nucleotide sequence and environmental distribution of the cryptic, conjugative, broad-host-range plasmid pIPO2 isolated from bacteria of the wheat rhizosphere The GenBank accession number for the pIPO2T sequence reported in this paper is AJ297913.. <i>Microbiology (United)</i> <i>Tj ETQq1 1 0.784314 rgBT /Overlock 94</i>	1.8	94
36	Investigation of Two Evolutionarily Unrelated Halocarboxylic Acid Dehalogenase Gene Families. <i>Journal of Bacteriology</i> , 1999, 181, 2535-2547.	2.2	93

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37	Prokaryotic functional diversity in different biogeochemical depth zones in tidal sediments of the Severn Estuary, UK, revealed by stable-isotope probing. <i>FEMS Microbiology Ecology</i> , 2010, 72, 179-197.	2.7	87
38	Investigation of the methanogen population structure and activity in a brackish lake sediment. <i>Environmental Microbiology</i> , 2005, 7, 947-960.	3.8	86
39	Distribution and culturability of the uncultivated AGG58 cluster™ of the Bacteroidetes phylum in aquatic environments. <i>FEMS Microbiology Ecology</i> , 2004, 47, 359-370.	2.7	83
40	Applications of molecular ecology in the characterization of uncultured microorganisms associated with human disease. <i>Reviews in Medical Microbiology</i> , 1997, 8, 91-102.	0.9	82
41	<i>Fluviicola taffensis</i> gen. nov., sp. nov., a novel freshwater bacterium of the family Cryomorphaceae in the phylum Bacteroidetes™. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005, 55, 2189-2194.	1.7	81
42	Diversity of gut microbiota increases with aging and starvation in the desert locust. <i>Antonie Van Leeuwenhoek</i> , 2010, 97, 69-77.	1.7	78
43	Archaeal community diversity and abundance changes along a natural salinity gradient in estuarine sediments. <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-18.	2.7	77
44	Biofilm microbial community of a thermophilic trickling biofilter used for continuous biohydrogen production. <i>FEMS Microbiology Letters</i> , 2005, 249, 31-38.	1.8	71
45	Enrichment and cultivation of prokaryotes associated with the sulphate-methane transition zone of diffusion-controlled sediments of Aarhus Bay, Denmark, under heterotrophic conditions. <i>FEMS Microbiology Ecology</i> , 2011, 77, 248-263.	2.7	70
46	Subsurface microbiology and biogeochemistry of a deep, cold-water carbonate mound from the Porcupine Seabight (IODP Expedition 307). <i>Environmental Microbiology</i> , 2009, 11, 239-257.	3.8	68
47	Dissimilatory Fe(III) reduction by an electrochemically active lactic acid bacterium phylogenetically related to <i>Enterococcus gallinarum</i> isolated from submerged soil. <i>Journal of Applied Microbiology</i> , 2005, 99, 978-987.	3.1	67
48	Molecular monitoring of culturable bacteria from deep-sea sediment of the Nankai Trough, Leg 190 Ocean Drilling Program. <i>FEMS Microbiology Ecology</i> , 2004, 48, 357-367.	2.7	65
49	Haloalkane-Utilizing <i>Rhodococcus</i> Strains Isolated from Geographically Distinct Locations Possess a Highly Conserved Gene Cluster Encoding Haloalkane Catabolism. <i>Journal of Bacteriology</i> , 2000, 182, 2725-2731.	2.2	64
50	DNA extraction for 16S rRNA gene analysis to determine genetic diversity in deep sediment communities. <i>FEMS Microbiology Letters</i> , 1992, 100, 59-65.	1.8	64
51	Dehalogenase genes of <i>Pseudomonas putida</i> PP3 on chromosomally located transposable elements.. <i>Molecular Biology and Evolution</i> , 1985, 2, 557-67.	8.9	60
52	The dehalogenase gene <i>dehI</i> from <i>Pseudomonas putida</i> PP3 is carried on an unusual mobile genetic element designated DEH. <i>Journal of Bacteriology</i> , 1992, 174, 1932-1940.	2.2	60
53	Survival of <i>Desulfotomaculum</i> spores from estuarine sediments after serial autoclaving and high-temperature exposure. <i>ISME Journal</i> , 2015, 9, 922-933.	9.8	58
54	Design and Evaluation of Useful Bacterium-Specific PCR Primers That Amplify Genes Coding for Bacterial 16S rRNA. <i>Applied and Environmental Microbiology</i> , 1998, 64, 2333-2333.	3.1	56

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55	Distribution of candidate division JS1 and other Bacteria in tidal sediments of the German Wadden Sea using targeted 16S rRNA gene PCR-DGGE. <i>FEMS Microbiology Ecology</i> , 2007, 62, 78-89.	2.7	56
56	Molecular cloning and heterologous expression of a <i>Klebsiella pneumoniae</i> gene encoding alginate lyase. <i>Gene</i> , 1989, 75, 127-134.	2.2	55
57	Composition of Acridid gut bacterial communities as revealed by 16S rRNA gene analysis. <i>Journal of Invertebrate Pathology</i> , 2008, 97, 265-272.	3.2	53
58	Isolation of sulfate-reducing bacteria from deep sediment layers of the Pacific Ocean. <i>Geomicrobiology Journal</i> , 1998, 15, 67-83.	2.0	52
59	Prokaryotes stimulate mineral H ₂ formation for the deep biosphere and subsequent thermogenic activity. <i>Geology</i> , 2011, 39, 219-222.	4.4	50
60	Identification and Discrimination of Oral Asaccharolytic Eubacterium spp. by Pyrolysis Mass Spectrometry and Artificial Neural Networks. <i>Current Microbiology</i> , 1996, 32, 77-84.	2.2	49
61	Diversity of oral asaccharolytic Eubacterium species in periodontitis - identification of novel phylotypes representing uncultivated taxa. <i>Oral Microbiology and Immunology</i> , 1999, 14, 56-59.	2.8	49
62	Identifying the genetic basis of ecologically and biotechnologically useful functions of the bacterium <i>Burkholderia vietnamiensis</i> . <i>Environmental Microbiology</i> , 2007, 9, 1017-1034.	3.8	48
63	The Crystal Structure of DehI Reveals a New α -Haloacid Dehalogenase Fold and Active-Site Mechanism. <i>Journal of Molecular Biology</i> , 2008, 378, 284-294.	4.2	48
64	Analysis of DGGE profiles to explore the relationship between prokaryotic community composition and biogeochemical processes in deep seafloor sediments from the Peru Margin. <i>FEMS Microbiology Ecology</i> , 2006, 58, 86-98.	2.7	47
65	Title is missing!. <i>Biotechnology Letters</i> , 1998, 20, 1073-1076.	2.2	45
66	Uncultured Microbial Phyla Suggest Mechanisms for Multi-Thousand-Year Subsistence in Baltic Sea Sediments. <i>MBio</i> , 2019, 10, .	4.1	45
67	Depth variation of bacterial extracellular enzyme activity and population diversity in the northeastern North Atlantic Ocean. <i>Deep-Sea Research Part II: Topical Studies in Oceanography</i> , 2001, 48, 1003-1017.	1.4	44
68	Localization and functional analysis of structural and regulatory dehalogenase genes carried on DEH from <i>Pseudomonas putida</i> PP3. <i>Journal of Bacteriology</i> , 1992, 174, 1941-1947.	2.2	42
69	Changes in methanogenic substrate utilization and communities with depth in a salt-marsh, creek sediment in southern England. <i>Estuarine, Coastal and Shelf Science</i> , 2012, 96, 170-178.	2.1	42
70	Culture-Independent Identification of Periodontitis-Associated <i>Porphyromonas</i> and <i>Tannerella</i> Populations by Targeted Molecular Analysis. <i>Journal of Clinical Microbiology</i> , 2004, 42, 5523-5527.	3.9	41
71	Similarity of microbial and meiofaunal community analyses for mapping ecological effects of heavy-metal contamination in soil. <i>FEMS Microbiology Ecology</i> , 2002, 40, 113-122.	2.7	40
72	Culture-Independent Analysis of Bacterial Fuel Contamination Provides Insight into the Level of Concordance with the Standard Industry Practice of Aerobic Cultivation. <i>Applied and Environmental Microbiology</i> , 2011, 77, 4527-4538.	3.1	40

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73	The Challenges of Linking Ecosystem Services to Biodiversity. <i>Advances in Ecological Research</i> , 2016, 54, 87-134.	2.7	39
74	The partial purification of two dehalogenases from <i>Pseudomonas putida</i> PP3. <i>FEMS Microbiology Letters</i> , 1979, 6, 231-234.	1.8	38
75	Modified linker-PCR primers facilitate complete sequencing of DGGE DNA fragments. <i>Journal of Microbiological Methods</i> , 2008, 75, 579-581.	1.6	38
76	Dynamic Microbial Community Associated with Iron-Arsenic Co-Precipitation Products from a Groundwater Storage System in Bangladesh. <i>Microbial Ecology</i> , 2012, 64, 171-186.	2.8	38
77	Transposition of DEH, a Broad-Host-Range Transposon Flanked by IS Ppu12, in <i>Pseudomonas putida</i> Is Associated with Genomic Rearrangements and Dehalogenase Gene Silencing. <i>Journal of Bacteriology</i> , 2002, 184, 6581-6591.	2.2	36
78	Microbial dehalogenation of trichloroacetic acid. <i>World Journal of Microbiology and Biotechnology</i> , 1992, 8, 512-518.	3.6	35
79	Comparing the Dehalogenase Gene Pool in Cultivated \pm -Halocarboxylic Acid-Degrading Bacteria with the Environmental Metagene Pool. <i>Applied and Environmental Microbiology</i> , 2003, 69, 4375-4382.	3.1	35
80	Environmentally directed mutations in the dehalogenase system of <i>Pseudomonas putida</i> strain PP3. <i>Archives of Microbiology</i> , 1992, 158, 176-182.	2.2	34
81	Complex coupled metabolic and prokaryotic community responses to increasing temperatures in anaerobic marine sediments: critical temperatures and substrate changes. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv084.	2.7	34
82	Highly competitive fungi manipulate bacterial communities in decomposing beech wood (<i>Fagus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.7	34
83	Impact of flow hydrodynamics and pipe material properties on biofilm development within drinking water systems. <i>Environmental Technology (United Kingdom)</i> , 2020, 41, 3732-3744.	2.2	31
84	Chemosynthetic bacteria found in bivalve species from mud volcanoes of the Gulf of Cadiz. <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	2.7	29
85	Microbial diversity in <i>Frenulata</i> (Siboglinidae, Polychaeta) species from mud volcanoes in the Gulf of Cadiz (NE Atlantic). <i>Antonie Van Leeuwenhoek</i> , 2011, 100, 83-98.	1.7	27
86	Toxic effects of chlorinated and brominated alkanolic acids on <i>Pseudomonas putida</i> PP3: selection at high frequencies of mutations in genes encoding dehalogenases. <i>Applied and Environmental Microbiology</i> , 1985, 49, 1494-1501.	3.1	27
87	Chronic effects of temperature and nitrate pollution on <i>Daphnia magna</i> : Is this cladoceran suitable for widespread use as a tertiary treatment?. <i>Water Research</i> , 2015, 83, 141-152.	11.3	26
88	Not all <i>Pseudomonas aeruginosa</i> are equal: strains from industrial sources possess uniquely large multireplicon genomes. <i>Microbial Genomics</i> , 2019, 5, .	2.0	26
89	Application of <i>arecA</i> -gene-based identification approach to the maize rhizosphere reveals novel diversity in <i>Burkholderia</i> species. <i>FEMS Microbiology Letters</i> , 2006, 259, 126-132.	1.8	23
90	Using microcosms to study gene transfer in aquatic habitats. <i>FEMS Microbiology Ecology</i> , 2006, 23, 81-94.	2.7	22

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91	<i>Mycobacterium avium</i> Subspecies <i>paratuberculosis</i> : Human Exposure through Environmental and Domestic Aerosols. <i>Pathogens</i> , 2014, 3, 577-595.	2.8	22
92	Evaluation of five selective media for the detection of <i>Pseudomonas aeruginosa</i> using a strain panel from clinical, environmental and industrial sources. <i>Journal of Microbiological Methods</i> , 2014, 99, 8-14.	1.6	22
93	Fungal control of early-stage bacterial community development in decomposing wood. <i>Fungal Ecology</i> , 2019, 42, 100868.	1.6	22
94	Rapid differentiation of <i>Prevotella intermedia</i> and <i>P. nigrescens</i> by 16S rDNA PCR-RFLP. <i>Journal of Medical Microbiology</i> , 1996, 44, 41-43.	1.8	20
95	Contrasting relationships between biogeochemistry and prokaryotic diversity depth profiles along an estuarine sediment gradient. <i>FEMS Microbiology Ecology</i> , 2013, 85, 143-157.	2.7	20
96	Detection of alginate lyases by isoelectric focusing and activity staining. <i>International Journal of Biological Macromolecules</i> , 1986, 8, 337-341.	7.5	19
97	The nucleotide sequence of a transposable haloalkanoic acid dehalogenase regulatory gene (<i>dehR I</i>) from <i>Pseudomonas putida</i> strain PP3 and its relationship with γ -54-dependent activators. <i>Biodegradation</i> , 1995, 6, 247-255.	3.0	19
98	Inter-laboratory quantification of Bacteria and Archaea in deeply buried sediments of the Baltic Sea (IODP Expedition 347). <i>FEMS Microbiology Ecology</i> , 2017, 93, fix007.	2.7	18
99	Retrotransfer of IncP1-like plasmids from aquatic bacteria. <i>Letters in Applied Microbiology</i> , 1995, 20, 317-322.	2.2	16
100	Diversity of alpha-halocarboxylic acid dehalogenases in bacteria isolated from a pristine soil after enrichment and selection on the herbicide 2,2-dichloropropionic acid (Dalapon). <i>Environmental Microbiology</i> , 2003, 5, 48-54.	3.8	14
101	Rock crushing derived hydrogen directly supports a methanogenic community: significance for the deep biosphere. <i>Environmental Microbiology Reports</i> , 2019, 11, 165-172.	2.4	13
102	Specificity of the oral microflora in dental caries, endodontic infections and periodontitis. <i>International Congress Series</i> , 2005, 1284, 150-157.	0.2	12
103	Bacterial Diversity and Community Structure in High Arsenic Aquifers in Hetao Plain of Inner Mongolia, China. <i>Geomicrobiology Journal</i> , 2014, 31, 338-349.	2.0	12
104	Methanogen and bacterial diversity and distribution in deep gas hydrate sediments from the Cascadia Margin as revealed by 16S rRNA molecular analysis. <i>FEMS Microbiology Ecology</i> , 2001, 34, 221-228.	2.7	11
105	<i>Eubacterium minutum</i> is an earlier synonym of <i>Eubacterium tardum</i> and has priority. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 1999, 49, 1939-1941.	1.7	10
106	Modified Primers Facilitate Rapid Screening of 16S rRNA Gene Libraries. <i>BioTechniques</i> , 2000, 29, 48-50.	1.8	10
107	<i>Arabidopsis thaliana</i> and <i>Pisum sativum</i> models demonstrate that root colonization is an intrinsic trait of <i>Burkholderia cepacia</i> complex bacteria. <i>Microbiology (United Kingdom)</i> , 2014, 160, 373-384.	1.8	9
108	Genetic Engineering for Wastewater Treatment. <i>Water and Environment Journal</i> , 1991, 5, 608-616.	2.2	8

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109	Presence of <i>Mycobacterium avium</i> Subspecies <i>paratuberculosis</i> Monitored Over Varying Temporal and Spatial Scales in River Catchments: Persistent Routes for Human Exposure. <i>Microorganisms</i> , 2019, 7, 136.	3.6	8
110	The influence of migratory Paraburkholderia on growth and competition of wood-decay fungi. <i>Fungal Ecology</i> , 2020, 45, 100937.	1.6	7
111	Effect of sample handling on estimation of bacterial diversity in marine sediments by 16S rRNA gene sequence analysis. <i>FEMS Microbiology Ecology</i> , 1994, 15, 215-225.	2.7	6
112	Genome Sequences of Two Choline-Utilizing Methanogenic Archaea, <i>Methanococoides</i> spp., Isolated from Marine Sediments. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	5
113	DNA extraction for 16S rRNA gene analysis to determine genetic diversity in deep sediment communities. <i>FEMS Microbiology Letters</i> , 1992, 100, 59-65.	1.8	5
114	Horizontal transfer of dehalogenase genes on IncP1 α plasmids during bacterial adaptation to degrade α -halocarboxylic acids. <i>FEMS Microbiology Ecology</i> , 2003, 45, 273-282.	2.7	3
115	1. Studies on prokaryotic populations and processes in subseafloor sediments – an update. , 0, , 1-28.		2
116	Mitochondrial DNA variation in River Usk brown trout, <i>Salmo trutta</i> . <i>Journal of Fish Biology</i> , 1994, 44, 717-723.	1.6	2
117	Genetic analysis of <i>Klebsiella pneumoniae</i> alginate lyase by transposon Tn10 mutagenesis. <i>Hydrobiologia</i> , 1987, 151-152, 571-575.	2.0	1
118	Purification, crystallization and preliminary crystallographic analysis of Dehl, a group I α -haloacid dehalogenase from <i>Pseudomonas putida</i> strain PP3. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 596-598.	0.7	1
119	Distribution, growth and movement of River Usk brown trout (<i>Salmo trutta</i>). <i>Journal of Fish Biology</i> , 1993, 43, 45-52.	1.6	1
120	Similarity of microbial and meiofaunal community analyses for mapping ecological effects of heavy-metal contamination in soil. <i>FEMS Microbiology Ecology</i> , 2002, 40, 113-122.	2.7	1
121	Towards passive bioremediation of dye-bearing effluents using hydrous ferric oxide wastes: Mechanisms, products and microbiology. <i>Journal of Environmental Management</i> , 2022, 317, 115332.	7.8	1
122	Changes in Metal Leachability through Stimulation of Iron Reducing Communities within Waste Sludge. <i>Solid State Phenomena</i> , 0, 262, 269-272.	0.3	0
123	Using microcosms to study gene transfer in aquatic habitats. <i>FEMS Microbiology Ecology</i> , 1997, 23, 81-94.	2.7	0