

Andrew J Weightman

List of Publications by Year in descending order

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120
papers

12,031
citations

29994

54
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26548

107
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126
all docs

126
docs citations

126
times ranked

11555
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	3.8	1
2	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.	1.2	31
3	The influence of migratory Paraburkholderia on growth and competition of wood-decay fungi. <i>Fungal Ecology</i> , 2020, 45, 100937.	0.7	7
4	Fungal control of early-stage bacterial community development in decomposing wood. <i>Fungal Ecology</i> , 2019, 42, 100868.	0.7	22
5	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.	1.6	8
6	Uncultured Microbial Phyla Suggest Mechanisms for Multi-Thousand-Year Subsistence in Baltic Sea Sediments. <i>MBio</i> , 2019, 10, .	1.8	45
7	Genome Sequences of Two Choline-Utilizing Methanogenic Archaea, <i>Methanococcoides</i> spp., Isolated from Marine Sediments. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	5
8	Rock-crushing derived hydrogen directly supports a methanogenic community: significance for the deep biosphere. <i>Environmental Microbiology Reports</i> , 2019, 11, 165-172.	1.0	13
9	Highly competitive fungi manipulate bacterial communities in decomposing beech wood (<i>Fagus</i>) Tj ETQq1 1 0.784314 rgBT /Overl 1.3 34	1.3	34
10	Not all <i>Pseudomonas aeruginosa</i> are equal: strains from industrial sources possess uniquely large multireplicon genomes. <i>Microbial Genomics</i> , 2019, 5, .	1.0	26
11	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.	1.3	18
12	The Challenges of Linking Ecosystem Services to Biodiversity. <i>Advances in Ecological Research</i> , 2016, 54, 87-134.	1.4	39
13	Bacteria in decomposing wood and their interactions with wood-decay fungi. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw179.	1.3	191
14	Phylogeny and physiology of candidate phylum "Atribacteria" (OP9/S1) inferred from cultivation-independent genomics. <i>ISME Journal</i> , 2016, 10, 273-286.	4.4	166
15	The effect of anthropogenic arsenic contamination on the earthworm microbiome. <i>Environmental Microbiology</i> , 2015, 17, 1884-1896.	1.8	118
16	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.	1.3	34
17	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.	5.3	26
18	Survival of <i>Desulfotomaculum</i> spores from estuarine sediments after serial autoclaving and high-temperature exposure. <i>ISME Journal</i> , 2015, 9, 922-933.	4.4	58

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19	Archaeal community diversity and abundance changes along a natural salinity gradient in estuarine sediments. <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-18.	1.3	77
20	Bacterial Diversity and Community Structure in High Arsenic Aquifers in Hetao Plain of Inner Mongolia, China. <i>Geomicrobiology Journal</i> , 2014, 31, 338-349.	1.0	12
21	<i>Mycobacterium avium</i> Subspecies <i>paratuberculosis</i> : Human Exposure through Environmental and Domestic Aerosols. <i>Pathogens</i> , 2014, 3, 577-595.	1.2	22
22	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.	0.7	22
23	<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.	0.7	9
24	A review of prokaryotic populations and processes in sub-seafloor sediments, including biosphere:geosphere interactions. <i>Marine Geology</i> , 2014, 352, 409-425.	0.9	265
25	Contrasting relationships between biogeochemistry and prokaryotic diversity depth profiles along an estuarine sediment gradient. <i>FEMS Microbiology Ecology</i> , 2013, 85, 143-157.	1.3	20
26	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.	1.4	38
27	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.	0.9	42
28	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.	1.3	70
29	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.	0.7	27
30	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.	1.4	40
31	Prokaryotes stimulate mineral H ₂ formation for the deep biosphere and subsequent thermogenic activity. <i>Geology</i> , 2011, 39, 219-222.	2.0	50
32	Diversity of gut microbiota increases with aging and starvation in the desert locust. <i>Antonie Van Leeuwenhoek</i> , 2010, 97, 69-77.	0.7	78
33	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.	1.3	87
34	Chemosynthetic bacteria found in bivalve species from mud volcanoes of the Gulf of Cadiz. <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	1.3	29
35	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.	1.8	68
36	Culturable prokaryotic diversity of deep, gas hydrate sediments: first use of a continuous high-pressure, anaerobic, enrichment and isolation system for subseafloor sediments (DeepSoBUG). <i>Environmental Microbiology</i> , 2009, 11, 3140-3153.	1.8	107

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37	Prokaryotic Populations and Activities in an Interbedded Coal Deposit, Including a Previously Deeply Buried Section (1.6–2.3 km) Above \sim 150 Ma Basement Rock. <i>Geomicrobiology Journal</i> , 2009, 26, 163-178.	1.0	99
38	Purification, crystallization and preliminary crystallographic analysis of Dehl, a group I $\hat{\iota}$ -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
39	Prokaryotic biodiversity and activity in the deep seafloor biosphere. <i>FEMS Microbiology Ecology</i> , 2008, 66, 181-196.	1.3	217
40	Composition of Acridid gut bacterial communities as revealed by 16S rRNA gene analysis. <i>Journal of Invertebrate Pathology</i> , 2008, 97, 265-272.	1.5	53
41	The Crystal Structure of Dehl Reveals a New $\hat{\iota}$ -Haloacid Dehalogenase Fold and Active-Site Mechanism. <i>Journal of Molecular Biology</i> , 2008, 378, 284-294.	2.0	48
42	Modified linker-PCR primers facilitate complete sequencing of DGGE DNA fragments. <i>Journal of Microbiological Methods</i> , 2008, 75, 579-581.	0.7	38
43	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.	1.8	48
44	Biogeochemistry and biodiversity of methane cycling in subsurface marine sediments (Skagerrak, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.8	130
45	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.	1.3	56
46	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
47	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.	1.8	103
48	Application of arecAgene-based identification approach to the maize rhizosphere reveals novel diversity in <i>Burkholderia</i> species. <i>FEMS Microbiology Letters</i> , 2006, 259, 126-132.	0.7	23
49	Using microcosms to study gene transfer in aquatic habitats. <i>FEMS Microbiology Ecology</i> , 2006, 23, 81-94.	1.3	22
50	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.	1.3	47
51	Prokaryotic community composition and biogeochemical processes in deep seafloor sediments from the Peru Margin. <i>FEMS Microbiology Ecology</i> , 2006, 58, 65-85.	1.3	168
52	Bacterial community structure, compartmentalization and activity in a microbial fuel cell. <i>Journal of Applied Microbiology</i> , 2006, 101, 698-710.	1.4	164
53	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.	0.8	94
54	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.	1.4	621

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55	Biofilm microbial community of a thermophilic trickling biofilter used for continuous biohydrogen production. <i>FEMS Microbiology Letters</i> , 2005, 249, 31-38.	0.7	71
56	Investigation of the methanogen population structure and activity in a brackish lake sediment. <i>Environmental Microbiology</i> , 2005, 7, 947-960.	1.8	86
57	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.	1.4	67
58	Deep sub-seafloor prokaryotes stimulated at interfaces over geological time. <i>Nature</i> , 2005, 436, 390-394.	13.7	414
59	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.	1.4	716
60	<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.	0.8	81
61	<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.	1.4	147
62	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.	1.4	217
63	Specificity of the oral microflora in dental caries, endodontic infections and periodontitis. <i>International Congress Series</i> , 2005, 1284, 150-157.	0.2	12
64	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.	1.8	41
65	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.	1.4	113
66	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.	1.8	183
67	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.	1.3	65
68	Distribution and culturability of the uncultivated "AGG58 cluster" of the Bacteroidetes phylum in aquatic environments. <i>FEMS Microbiology Ecology</i> , 2004, 47, 359-370.	1.3	83
69	Horizontal transfer of dehalogenase genes on <i>IncP1</i> plasmids during bacterial adaptation to degrade α -halocarboxylic acids. <i>FEMS Microbiology Ecology</i> , 2003, 45, 273-282.	1.3	3
70	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.	1.8	14
71	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.	0.7	225
72	Cultivation-Dependent and -Independent Approaches for Determining Bacterial Diversity in Heavy-Metal-Contaminated Soil. <i>Applied and Environmental Microbiology</i> , 2003, 69, 3223-3230.	1.4	465

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73	Comparing the Dehalogenase Gene Pool in Cultivated $\hat{\pm}$ -Halocarboxylic Acid-Degrading Bacteria with the Environmental Metagene Pool. Applied and Environmental Microbiology, 2003, 69, 4375-4382.	1.4	35
74	New Degenerate Cytophaga - Flexibacter - Bacteroides -Specific 16S Ribosomal DNA-Targeted Oligonucleotide Probes Reveal High Bacterial Diversity in River Taff Epilithon. Applied and Environmental Microbiology, 2002, 68, 201-210.	1.4	117
75	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. Nucleic Acids Research, 2002, 30, 3481-3489.	6.5	206
76	Transposition of DEH , a Broad-Host-Range Transposon Flanked by IS Ppu12 , in Pseudomonas putida Is Associated with Genomic Rearrangements and Dehalogenase Gene Silencing. Journal of Bacteriology, 2002, 184, 6581-6591.	1.0	36
77	Molecular and Cultural Analysis of the Microflora Associated with Endodontic Infections. Journal of Dental Research, 2002, 81, 761-766.	2.5	220
78	Similarity of microbial and meiofaunal community analyses for mapping ecological effects of heavy-metal contamination in soil. FEMS Microbiology Ecology, 2002, 40, 113-122.	1.3	40
79	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.. Microbiology (United Tj ETQq1 1 0.784314 94 rGT /Over	0.7	94
80	Comparison of microbial and meiofaunal community analyses for determining impact of heavy metal contamination. Journal of Microbiological Methods, 2001, 45, 171-185.	0.7	101
81	Depth variation of bacterial extracellular enzyme activity and population diversity in the northeastern North Atlantic Ocean. Deep-Sea Research Part II: Topical Studies in Oceanography, 2001, 48, 1003-1017.	0.6	44
82	Methanogen and bacterial diversity and distribution in deep gas hydrate sediments from the Cascadia Margin as revealed by 16S rRNA molecular analysis. FEMS Microbiology Ecology, 2001, 34, 221-228.	1.3	160
83	Modified Primers Facilitate Rapid Screening of 16S rRNA Gene Libraries. BioTechniques, 2000, 29, 48-50.	0.8	10
84	Haloalkane-Utilizing Rhodococcus Strains Isolated from Geographically Distinct Locations Possess a Highly Conserved Gene Cluster Encoding Haloalkane Catabolism. Journal of Bacteriology, 2000, 182, 2725-2731.	1.0	64
85	The family Coriobacteriaceae: reclassification of Eubacterium exiguum (Poco et al. 1996) and Peptostreptococcus heliotrinireducens (Lanigan 1976) as Slackia exigua gen. nov., comb. nov. and Slackia heliotrinireducens gen. nov., comb. nov., and Eubacterium lentum (Prevot 1938) as Eggerthella lenta gen. nov., comb. nov.. International Journal of Systematic and Evolutionary Microbiology, 1999, 49, 595-600.	0.8	149
86	Eubacterium minutum is an earlier synonym of Eubacterium tardum and has priority. International Journal of Systematic and Evolutionary Microbiology, 1999, 49, 1939-1941.	0.8	10
87	Diversity of oral asaccharolytic Eubacterium species in periodontitis - identification of novel phylotypes representing uncultivated taxa. Oral Microbiology and Immunology, 1999, 14, 56-59.	2.8	49
88	Investigation of Two Evolutionarily Unrelated Halocarboxylic Acid Dehalogenase Gene Families. Journal of Bacteriology, 1999, 181, 2535-2547.	1.0	93
89	Title is missing!. Biotechnology Letters, 1998, 20, 1073-1076.	1.1	45
90	Isolation of sulfate-reducing bacteria from deep sediment layers of the pacific ocean. Geomicrobiology Journal, 1998, 15, 67-83.	1.0	52

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91	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.	1.4	56
92	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.	1.4	1,498
93	Applications of molecular ecology in the characterization of uncultured microorganisms associated with human disease. <i>Reviews in Medical Microbiology</i> , 1997, 8, 91-102.	0.4	82
94	Bacterial populations and processes in sediments containing gas hydrates (ODP Leg 146: Cascadia) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.8	138
95	Identification and Discrimination of Oral Asaccharolytic Eubacterium spp. by Pyrolysis Mass Spectrometry and Artificial Neural Networks. <i>Current Microbiology</i> , 1996, 32, 77-84.	1.0	49
96	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.	0.7	20
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.	1.5	19
98	Retrotransfer of IncP1-like plasmids from aquatic bacteria. <i>Letters in Applied Microbiology</i> , 1995, 20, 317-322.	1.0	16
99	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.	1.3	118
100	Deep bacterial biosphere in Pacific Ocean sediments. <i>Nature</i> , 1994, 371, 410-413.	13.7	653
101	Mitochondrial DNA variation in River Usk brown trout, <i>Salmo trutta</i> . , 1994, 44, 717.		2
102	Distribution, growth and movement of River Usk brown trout (<i>Salmo trutta</i>). <i>Journal of Fish Biology</i> , 1993, 43, 45-52.	0.7	1
103	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.	1.0	60
104	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.	1.0	42
105	Environmentally directed mutations in the dehalogenase system of <i>Pseudomonas putida</i> strain PP3. <i>Archives of Microbiology</i> , 1992, 158, 176-182.	1.0	34
106	Microbial dehalogenation of trichloroacetic acid. <i>World Journal of Microbiology and Biotechnology</i> , 1992, 8, 512-518.	1.7	35
107	DNA extraction for 16S rRNA gene analysis to determine genetic diversity in deep sediment communities. <i>FEMS Microbiology Letters</i> , 1992, 100, 59-65.	0.7	101
108	DNA extraction for 16S rRNA gene analysis to determine genetic diversity in deep sediment communities. <i>FEMS Microbiology Letters</i> , 1992, 100, 59-65.	0.7	64

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109	Genetic Engineering for Wastewater Treatment. <i>Water and Environment Journal</i> , 1991, 5, 608-616.	1.0	8
110	Molecular cloning and heterologous expression of a <i>Klebsiella pneumoniae</i> gene encoding alginate lyase. <i>Gene</i> , 1989, 75, 127-134.	1.0	55
111	Genetic analysis of <i>Klebsiella pneumoniae</i> alginate lyase by transposon Tn10 mutagenesis. <i>Hydrobiologia</i> , 1987, 151-152, 571-575.	1.0	1
112	Detection of alginate lyases by isoelectric focusing and activity staining. <i>International Journal of Biological Macromolecules</i> , 1986, 8, 337-341.	3.6	19
113	Dehalogenase genes of <i>Pseudomonas putida</i> PP3 on chromosomally located transposable elements.. <i>Molecular Biology and Evolution</i> , 1985, 2, 557-67.	3.5	60
114	Toxic effects of chlorinated and brominated alkanic 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.	1.4	27
115	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.	1.0	306
116	The partial purification of two dehalogenases from <i>Pseudomonas putida</i> PP3. <i>FEMS Microbiology Letters</i> , 1979, 6, 231-234.	0.7	38
117	1. Studies on prokaryotic populations and processes in subseafloor sediments – an update. , 0, , 1-28.		2
118	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
119	Effect of sample handling on estimation of bacterial diversity in marine sediments by 16S rRNA gene sequence analysis. , 0, .		6
120	Methanogen and bacterial diversity and distribution in deep gas hydrate sediments from the Cascadia Margin as revealed by 16S rRNA molecular analysis. , 0, .		11