List of Publications by Year in descending order

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		11608	12558
223	19,759	70	132
papers	citations	h-index	g-index
223	223	223	16392
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	The darkest microbiome—a postâ€human biosphere. Microbial Biotechnology, 2022, 15, 176-185.	2.0	14
2	Microbial biotechnology to assure national security of supplies of essential resources: energy, food and water, medical reagents, waste disposal and a circular economy. Microbial Biotechnology, 2022, 15, 1021-1025.	2.0	6
3	Multiple intertwined crises facing humanity necessitate a European Environmental Research Organization. Microbial Biotechnology, 2022, 15, 1031-1034.	2.0	1
4	Bacterial <scp>tRNA</scp> landscape revisited. Environmental Microbiology, 2022, , .	1.8	2
5	Microbiome transplants to save the planetary surface biosphere. Environmental Microbiology Reports, 2021, 13, 50-53.	1.0	0
6	The soil crisis: the need to treat as a global health problem and the pivotal role of microbes in prophylaxis and therapy. Microbial Biotechnology, 2021, 14, 769-797.	2.0	53
7	<scp>SARSâ€CoV</scp> â€2 biology and variants: anticipation of viral evolution and what needs to be done. Environmental Microbiology, 2021, 23, 2339-2363.	1.8	30
8	<scp>COVID</scp> â€19: long covid and its societal consequences. Environmental Microbiology, 2021, 23, 4077-4091.	1.8	27
9	Microbiome Yarns: bacterial predators, tissue tropism and molecular decoys. Microbial Biotechnology, 2021, 14, 51-58.	2.0	0
10	Microbial Biotechnology is 15! An adventure in journal parenting. Microbial Biotechnology, 2021, , .	2.0	0
11	COVID â€19 transmission: economyâ€boosting investment should target innovation in pandemic containment strategies to minimize restrictions of civil liberties. Environmental Microbiology, 2020, 22, 4527-4531.	1.8	3
12	The contribution of microbiology toward attainment of sustainable development goals: the need to conserve soil health while maximizing its productivity. Environmental Microbiology Reports, 2020, 13, 425-427.	1.0	7
13	The urgent need for microbiology literacy in society: children as educators. Microbial Biotechnology, 2020, 13, 1300-1303.	2.0	14
14	Strategies to minimize preventable morbidity and mortality resulting from pandemics like COVID â€19. Environmental Microbiology, 2020, 22, 4085-4092.	1.8	2
15	SARS oV â€2 variants: Relevance for symptom granularity, epidemiology, immunity (herd, vaccines), virus origin and containment?. Environmental Microbiology, 2020, 22, 2001-2006.	1.8	20
16	Visualizing the invisible: class excursions to ignite children's enthusiasm for microbes. Microbial Biotechnology, 2020, 13, 844-887.	2.0	26
17	The Home Clinic <i>or</i> All in a Day's Work of Dr. Fics. Microbial Biotechnology, 2020, 13, 3-10.	2.0	1
18	<scp>The importance of naturally attenuated SARSâ€CoV</scp> â€2 <scp>in the fight against COVID</scp> â€19.	1.8	54

Environmental Microbiology, 2020, 22, 1997-2000.

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19	The COVID â€19 pandemic: some lessons learned about crisis preparedness and management, and the need for international benchmarking to reduce deficits. Environmental Microbiology, 2020, 22, 1986-1996.	1.8	43
20	The long journey towards standards for engineering biosystems. EMBO Reports, 2020, 21, e50521.	2.0	46
21	Mikrobiologisches Wissen für alle bedeutet Klimaschutz!. BioSpektrum, 2019, 25, 595-595.	0.0	0
22	Scientists' warning to humanity: microorganisms and climate change. Nature Reviews Microbiology, 2019, 17, 569-586.	13.6	1,138
23	The urgent need for microbiology literacy in society. Environmental Microbiology, 2019, 21, 1513-1528.	1.8	99
24	Microbiome yarns: The Global Phenotypeâ€Genotype Survey. Episode <scp>III</scp> : importance of microbiota diversification for microbiome function and biome health. Microbial Biotechnology, 2019, 12, 421-433.	2.0	1
25	Microbiome yarns: the Global Phenotype–Genotype Survey. Microbial Biotechnology, 2019, 12, 191-199.	2.0	1
26	Microbiome yarns: The Global Phenotype-Genotype Survey. Microbial Biotechnology, 2019, 12, 11-24.	2.0	1
27	Synthetic consortia of nanobodyâ€coupled and formatted bacteria for prophylaxis and therapy interventions targeting microbiome dysbiosisâ€associated diseases and coâ€morbidities. Microbial Biotechnology, 2019, 12, 58-65.	2.0	17
28	Microbiome Yarns: human milk oligosaccharides, <i>Bifidobacterium</i> and immunopowergames1,2,3,4. Microbial Biotechnology, 2018, 11, 437-441.	2.0	3
29	Microbiome Yarns: human biome reproduction, evolution and visual acuity,,,. Microbial Biotechnology, 2018, 11, 149-159.	2.0	1
30	<i>Environmental Microbiology Reports</i> is 10!. Environmental Microbiology Reports, 2018, 10, 5-6.	1.0	2
31	Viable cyanobacteria in the deep continental subsurface. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10702-10707.	3.3	124
32	Environmental microbiology – the next 20 years: bioconnectivity and meta'omics 2.0. Environmental Microbiology, 2018, 20, 1949-1954.	1.8	3
33	Environmental Microbiology is 20!. Environmental Microbiology, 2018, 20, 1936-1944.	1.8	3
34	Microbiome Yarns: microbiome of the built environment, paranormal microbiology, and the power of single cell genomics1,2,3,4. Microbial Biotechnology, 2018, 11, 575-587.	2.0	2
35	Microbiome yarns: microbiomology of curly and straight hair. Microbial Biotechnology, 2017, 10, 231-237.	2.0	1
36	Microbiome yarns: microbiomology of winter rosy face [,] [,] [,] . Microbial Biotechnology, 2017, 10, 520-524.	2.0	0

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37	Microbiomes, metabolic errors and detection of performance enhancing drug abuse. Environmental Microbiology Reports, 2017, 9, 25-26.	1.0	Ο
38	Pristine but metal-rich RÃo Sucio (Dirty River) is dominated by Gallionella and other iron-sulfur oxidizing microbes. Extremophiles, 2017, 21, 235-243.	0.9	17
39	The contribution of microbial biotechnology to sustainable development goals. Microbial Biotechnology, 2017, 10, 984-987.	2.0	73
40	The <scp>DIY</scp> Digital Medical Centre. Microbial Biotechnology, 2017, 10, 1084-1093.	2.0	18
41	Protein complex formation during denitrification by <i>Pseudomonas aeruginosa</i> . Microbial Biotechnology, 2017, 10, 1523-1534.	2.0	43
42	The contribution of microbial biotechnology to economic growth and employment creation. Microbial Biotechnology, 2017, 10, 1137-1144.	2.0	30
43	A routine checkâ€up at the digital medical centre. Microbial Biotechnology, 2017, 10, 25-27.	2.0	3
44	Microbiome yarns: microbial forensics for auditing provenance in global food chains [,] [,] . Microbial Biotechnology, 2017, 10, 678-682.	2.0	1
45	<i>Microbial Biotechnology</i> is 10!. Microbial Biotechnology, 2017, 10, 1277-1278.	2.0	1
46	Microbiome yarns: microbiome basis of memory,,,. Microbial Biotechnology, 2017, 10, 1283-1292.	2.0	0
47	<scp>S</scp> ingh <scp>C</scp> hhatwal: A magical scholar and exceptional <scp><i>S</i></scp> <i>treptococcus</i> researcher. Environmental Microbiology Reports, 2016, 8, 550-552.	1.0	0
48	Protein Network of the Pseudomonas aeruginosa Denitrification Apparatus. Journal of Bacteriology, 2016, 198, 1401-1413.	1.0	60
49	Microbiomes, metabolic errors and detection of performance enhancing drug abuse ^{1,2} . Environmental Microbiology Reports, 2016, , .	1.0	Ο
50	Is there a common water-activity limit for the three domains of life?. ISME Journal, 2015, 9, 1333-1351.	4.4	229
51	A Periplasmic Complex of the Nitrite Reductase NirS, the Chaperone DnaK, and the Flagellum Protein FliC Is Essential for Flagellum Assembly and Motility in Pseudomonas aeruginosa. Journal of Bacteriology, 2015, 197, 3066-3075.	1.0	24
52	Farewell to Bernard Witholt, A pioneering microbial biotechnologist. Microbial Biotechnology, 2015, 8, 621-622.	2.0	0
53	Concomitant osmotic and chaotropicity-induced stresses in Aspergillus wentii: compatible solutes determine the biotic window. Current Genetics, 2015, 61, 457-477.	0.8	101
54	Multiplication of microbes below 0.690 water activity: implications for terrestrial and extraterrestrial life. Environmental Microbiology, 2015, 17, 257-277.	1.8	131

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55	Pipelines for New Chemicals: a strategy to create new value chains and stimulate innovation-based economic revival in Southern European countries. Environmental Microbiology, 2014, 16, 9-18.	1.8	16
56	Impact of a simulated oil spill on benthic phototrophs and nitrogenâ€fixing bacteria in mudflat mesocosms. Environmental Microbiology, 2013, 15, 242-252.	1.8	52
57	Adaptation of the Hydrocarbonoclastic Bacterium Alcanivorax borkumensis SK2 to Alkanes and Toxic Organic Compounds: a Physiological and Transcriptomic Approach. Applied and Environmental Microbiology, 2013, 79, 4282-4293.	1.4	85
58	Central Role of Dynamic Tidal Biofilms Dominated by Aerobic Hydrocarbonoclastic Bacteria and Diatoms in the Biodegradation of Hydrocarbons in Coastal Mudflats. Applied and Environmental Microbiology, 2012, 78, 3638-3648.	1.4	90
59	Transcriptional profiling of the marine oil-degrading bacterium Alcanivorax borkumensis during growth on n-alkanes. FEMS Microbiology Letters, 2011, 319, 160-168.	0.7	65
60	Effect of the Earthworms Lumbricus terrestris and Aporrectodea caliginosa on Bacterial Diversity in Soil. Microbial Ecology, 2010, 59, 574-587.	1.4	92
61	Fate of prions in soil: Degradation of recombinant prion in aqueous extracts from soil and casts of two earthworm species. Soil Biology and Biochemistry, 2010, 42, 1168-1171.	4.2	10
62	Novel Hybrid Esteraseâ€Haloacid Dehalogenase Enzyme. ChemBioChem, 2010, 11, 1975-1978.	1.3	16
63	Halophilic archaea in the human intestinal mucosa. Environmental Microbiology, 2010, 12, 2398-2410.	1.8	105
64	Consortia modulation of the stress response: proteomic analysis of single strain versus mixed culture. Environmental Microbiology, 2010, 12, 2436-2449.	1.8	28
65	Human biome biotechnology and the personalization of odour profiles*. Microbial Biotechnology, 2009, 2, 150-152.	2.0	1
66	Bacterial consortium proteomics under 4â€chlorosalicylate carbonâ€limiting conditions. Proteomics, 2009, 9, 2273-2285.	1.3	14
67	Microbial consortia in mesocosm bioremediation trial using oil sorbents, slow-release fertilizer and bioaugmentation. FEMS Microbiology Ecology, 2009, 69, 288-300.	1.3	44
68	â€~ <i>Candidatus</i> Lumbricincola', a novel lineage of uncultured <i>Mollicutes</i> from earthworms of family <i>Lumbricidae</i> . Environmental Microbiology, 2009, 11, 1016-1026.	1.8	57
69	Characterization of marine isopreneâ€degrading communities. Environmental Microbiology, 2009, 11, 3280-3291.	1.8	111
70	Reactome Array: Forging a Link Between Metabolome and Genome. Science, 2009, 326, 252-257.	6.0	39
71	Niche-specificity factors of a marine oil-degrading bacterium <i>Alcanivorax borkumensis</i> SK2. FEMS Microbiology Letters, 2008, 285, 89-96.	0.7	36
72	High benzene concentrations can favour Gram-positive bacteria in groundwaters from a contaminated aquifer. FEMS Microbiology Ecology, 2008, 65, 526-533.	1.3	18

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73	Fungi and inflammatory bowel diseases: Alterations of composition and diversity. Scandinavian Journal of Gastroenterology, 2008, 43, 831-841.	0.6	375
74	A purple acidophilic di-ferric DNA ligase from <i>Ferroplasma</i> . Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8878-8883.	3.3	27
75	Genome-Scale Reconstruction and Analysis of the Pseudomonas putida KT2440 Metabolic Network Facilitates Applications in Biotechnology. PLoS Computational Biology, 2008, 4, e1000210.	1.5	237
76	Dynamics of Reductive Genome Evolution in Mitochondria and Obligate Intracellular Microbes. Molecular Biology and Evolution, 2007, 24, 449-456.	3.5	37
77	Analysis of Storage Lipid Accumulation in Alcanivorax borkumensis : Evidence for Alternative Triacylglycerol Biosynthesis Routes in Bacteria. Journal of Bacteriology, 2007, 189, 918-928.	1.0	133
78	Obligate oil-degrading marine bacteria. Current Opinion in Biotechnology, 2007, 18, 257-266.	3.3	769
79	Primary producing prokaryotic communities of brine, interface and seawater above the halocline of deep anoxic lake L'Atalante, Eastern Mediterranean Sea. ISME Journal, 2007, 1, 743-755.	4.4	99
80	The cellular machinery of Ferroplasma acidiphilum is iron-protein-dominated. Nature, 2007, 445, 91-94.	13.7	88
81	Determining the identity and roles of oil-metabolizing marine bacteria from the Thames estuary, UK. Environmental Microbiology, 2007, 9, 165-176.	1.8	201
82	Effects of temperature and biostimulation on oil-degrading microbial communities in temperate estuarine waters. Environmental Microbiology, 2007, 9, 177-186.	1.8	242
83	Limits of life in MgCl2-containing environments: chaotropicity defines the window. Environmental Microbiology, 2007, 9, 801-813.	1.8	254
84	Efficacy of intervention strategies for bioremediation of crude oil in marine systems and effects on indigenous hydrocarbonoclastic bacteria. Environmental Microbiology, 2007, 9, 1562-1571.	1.8	146
85	Widespread capacity to metabolize polychlorinated biphenyls by diverse microbial communities in soils with no significant exposure to PCB contamination. Environmental Microbiology, 2007, 9, 1890-1897.	1.8	41
86	Characterization of a chitinolytic enzyme from Serratia sp. KCK isolated from kimchi juice. Applied Microbiology and Biotechnology, 2007, 75, 1275-1283.	1.7	32
87	Characterization and role of a metalloprotease induced by chitin in Serratia sp. KCK. Journal of Industrial Microbiology and Biotechnology, 2007, 34, 715-721.	1.4	10
88	Proteomic Insights into Metabolic Adaptations in Alcanivorax borkumensis Induced by Alkane Utilization. Journal of Bacteriology, 2006, 188, 3763-3773.	1.0	139
89	Novel Polyphenol Oxidase Mined from a Metagenome Expression Library of Bovine Rumen. Journal of Biological Chemistry, 2006, 281, 22933-22942.	1.6	168
90	Low temperature-induced systems failure inEscherichia coli: Insights from rescue by cold-adapted chaperones. Proteomics, 2006, 6, 193-206.	1.3	73

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91	The 'pH optimum anomaly' of intracellular enzymes of Ferroplasma acidiphilum. Environmental Microbiology, 2006, 8, 416-425.	1.8	48
92	16S rRNA gene sequence analyses and inter- and intrageneric relationships of Xanthomonas species and Stenotrophomonas maltophilia. FEMS Microbiology Letters, 2006, 151, 145-153.	0.7	64
93	Heterogeneous aerobic benzene-degrading communities in oxygen-depleted groundwaters. FEMS Microbiology Ecology, 2006, 58, 260-270.	1.3	87
94	Genome sequence of the ubiquitous hydrocarbon-degrading marine bacterium Alcanivorax borkumensis. Nature Biotechnology, 2006, 24, 997-1004.	9.4	417
95	Stratified prokaryote network in the oxic–anoxic transition of a deep-sea halocline. Nature, 2006, 440, 203-207.	13.7	215
96	7- O -Malonyl Macrolactin A, a New Macrolactin Antibiotic from Bacillus subtilis Active against Methicillin-Resistant Staphylococcus aureus , Vancomycin-Resistant Enterococci, and a Small-Colony Variant of Burkholderia cepacia. Antimicrobial Agents and Chemotherapy, 2006, 50, 1701-1709.	1.4	129
97	Mutation in a " tesB -Like―Hydroxyacyl-Coenzyme A-Specific Thioesterase Gene Causes Hyperproduction of Extracellular Polyhydroxyalkanoates by Alcanivorax borkumensis SK2. Journal of Bacteriology, 2006, 188, 8452-8459.	1.0	79
98	Stable isotope probing reveals the dominant role of Burkholderia species in aerobic degradation of PCBs. FEMS Microbiology Ecology, 2005, 52, 207-217.	1.3	55
99	Microbial Enzymes Mined from the Urania Deep-Sea Hypersaline Anoxic Basin. Chemistry and Biology, 2005, 12, 895-904.	6.2	142
100	The Enigma of Prokaryotic Life in Deep Hypersaline Anoxic Basins. Science, 2005, 307, 121-123.	6.0	275
101	Effects of long-term benzene pollution on bacterial diversity and community structure in groundwater. Environmental Microbiology, 2005, 7, 1192-1199.	1.8	55
102	Ferroplasma and relatives, recently discovered cell wall-lacking archaea making a living in extremely acid, heavy metal-rich environments. Environmental Microbiology, 2005, 7, 1277-1288.	1.8	143
103	Novel hydrolase diversity retrieved from a metagenome library of bovine rumen microflora. Environmental Microbiology, 2005, 7, 1996-2010.	1.8	258
104	Golden age of drug discovery or dark age of missed chances?. Environmental Microbiology, 2005, 7, 1861-1863.	1.8	1
105	Natural microbial diversity in superficial sediments of Milazzo Harbor (Sicily) and community successions during microcosm enrichment with various hydrocarbons. Environmental Microbiology, 2005, 7, 1426-1441.	1.8	194
106	Conversion of a Carboxylesterase into a Triacylglycerol Lipase by a Random Mutation. Angewandte Chemie - International Edition, 2005, 44, 7553-7557.	7.2	32
107	Three Stages of a Biofilm Community Developing at the Liquid-Liquid Interface between Polychlorinated Biphenyls and Water. Applied and Environmental Microbiology, 2005, 71, 7301-7309.	1.4	64
108	Uracil content of 16S rRNA of thermophilic and psychrophilic prokaryotes correlates inversely with their optimal growth temperatures. Nucleic Acids Research, 2005, 33, 4016-4022.	6.5	54

7

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109	Expression of a Temperature-Sensitive Esterase in a Novel Chaperone-Based Escherichia coli Strain. Applied and Environmental Microbiology, 2004, 70, 4499-4504.	1.4	71
110	Functional consequences of single:double ring transitions in chaperonins: life in the cold. Molecular Microbiology, 2004, 53, 167-182.	1.2	42
111	In vitro alterations of intestinal bacterial microbiota in fecal samples during storage. Diagnostic Microbiology and Infectious Disease, 2004, 50, 237-245.	0.8	105
112	Compatible Solutes Protect against Chaotrope (Ethanol)-Induced, Nonosmotic Water Stress. Applied and Environmental Microbiology, 2003, 69, 7032-7034.	1.4	72
113	Leitbakteria of microbial biofilm communities causing occlusion of biliary stents. Environmental Microbiology, 2003, 5, 859-866.	1.8	15
114	Chaotropic solutes cause water stress in Pseudomonas putida. Environmental Microbiology, 2003, 5, 1270-1280.	1.8	153
115	Genome sequence completed of Alcanivorax borkumensis, a hydrocarbon-degrading bacterium that plays a global role in oil removal from marine systems. Journal of Biotechnology, 2003, 106, 215-220.	1.9	126
116	Chaperonins govern growth of Escherichia coli at low temperatures. Nature Biotechnology, 2003, 21, 1266-1267.	9.4	228
117	Substrate Specificity and Expression of Three 2,3-Dihydroxybiphenyl 1,2-Dioxygenases from Rhodococcus globerulus Strain P6. Journal of Bacteriology, 2003, 185, 2944-2951.	1.0	58
118	Detection and Diversity of Expressed Denitrification Genes in Estuarine Sediments after Reverse Transcription-PCR Amplification from mRNA. Applied and Environmental Microbiology, 2002, 68, 5017-5025.	1.4	174
119	Polychlorinated biphenyl-degrading microbial communities in soils and sediments. Current Opinion in Microbiology, 2002, 5, 246-253.	2.3	263
120	Microbial community of a saline mud volcano at San Biagio-Belpasso, Mt. Etna (Italy). Environmental Microbiology, 2002, 4, 249-256.	1.8	64
121	Pseudomonas putida: a cosmopolitan opportunist par excellence. Environmental Microbiology, 2002, 4, 779-781.	1.8	278
122	Upstream-independent ribosomal RNA amplification analysis (URA): a new approach to characterizing the diversity of natural microbial communities. Environmental Microbiology, 2001, 3, 662-666.	1.8	8
123	Biological land mines: bioterrorism underscores major knowledge deficits in the ecology of infectious agents. Environmental Microbiology, 2001, 3, 741-742.	1.8	2
124	Combined Use of 16S Ribosomal DNA and 16S rRNA To Study the Bacterial Community of Polychlorinated Biphenyl-Polluted Soil. Applied and Environmental Microbiology, 2001, 67, 1874-1884.	1.4	276
125	The Essential HupB and HupN Proteins of Pseudomonas putida Provide Redundant and Nonspecific DNA-bending Functions. Journal of Biological Chemistry, 2001, 276, 16641-16648.	1.6	18
126	[26] Approach to analyze interactions of microorganisms, hydrophobic substrates, and soil colloids leading to formation of composite biofilms, and to study initial events in microbiogeological processes. Methods in Enzymology, 2001, 336, 317-IN14.	0.4	36

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127	An evaluation of terminal-restriction fragment length polymorphism (T-RFLP) analysis for the study of microbial community structure and dynamics. Environmental Microbiology, 2000, 2, 39-50.	1.8	720
128	A gene containment strategy based on a restriction-modification system. Environmental Microbiology, 2000, 2, 555-563.	1.8	26
129	A Second [2Fe-2S] Ferredoxin from Sphingomonas sp. Strain RW1 Can Function as an Electron Donor for the Dioxin Dioxygenase. Journal of Bacteriology, 2000, 182, 2238-2244.	1.0	37
130	Removal of Mercury from Chemical Wastewater by Microoganisms in Technical Scale. Environmental Science & Technology, 2000, 34, 4628-4634.	4.6	126
131	Regiospecificity of Dioxygenation of Di- to Pentachlorobiphenyls and Their Degradation to Chlorobenzoates by the <i>bph</i> -Encoded Catabolic Pathway of <i>Burkholderia</i> sp. Strain LB400. Applied and Environmental Microbiology, 1999, 65, 3614-3621.	1.4	109
132	Towards elucidation of microbial community metabolic pathways: unravelling the network of carbon sharing in a pollutant-degrading bacterial consortium by immunocapture and isotopic ratio mass spectrometry. Environmental Microbiology, 1999, 1, 167-174.	1.8	136
133	Identification of the metabolically active members of a bacterial community in a polychlorinated biphenyl-polluted moorland soil. Environmental Microbiology, 1999, 1, 199-212.	1.8	148
134	Thermal Gradient Gel Electrophoresis Analysis of Bioprotection from Pollutant Shocks in the Activated Sludge Microbial Community. Applied and Environmental Microbiology, 1999, 65, 102-109.	1.4	291
135	Degradation of Chlorobenzenes at Nanomolar Concentrations by <i>Burkholderia</i> sp. Strain PS14 in Liquid Cultures and in Soil. Applied and Environmental Microbiology, 1999, 65, 2547-2552.	1.4	39
136	3-Nitroadipate, a Metabolic Intermediate for Mineralization of 2,4-Dinitrophenol by a New Strain of a Rhodococcus Species. Journal of Bacteriology, 1999, 181, 149-152.	1.0	52
137	Genetic and Biochemical Analyses of the <i>tec</i> Operon Suggest a Route for Evolution of Chlorobenzene Degradation Genes. Journal of Bacteriology, 1999, 181, 341-346.	1.0	55
138	A Functional 4-Hydroxysalicylate/Hydroxyquinol Degradative Pathway Gene Cluster Is Linked to the Initial Dibenzo- <i>p</i> -Dioxin Pathway Genes in <i>Sphingomonas</i> sp. Strain RW1. Journal of Bacteriology, 1999, 181, 3452-3461.	1.0	74
139	Mini-transposons in microbial ecology and environmental biotechnology. FEMS Microbiology Ecology, 1998, 27, 211-224.	1.3	43
140	Genetic requirements for the expression of benzylamine dehydrogenase activity in Pseudomonas putida. FEMS Microbiology Letters, 1998, 166, 109-114.	0.7	6
141	Multifunctional g3p-peptide tag for current phage display systems. Journal of Immunological Methods, 1998, 212, 131-138.	0.6	13
142	The reductase RedA2 of the multi-component dioxin dioxygenase system of Sphingomonas sp. RW1 is related to class-I cytochrome P450-type reductases. FEBS Journal, 1998, 253, 437-444.	0.2	37
143	Crystal structure of cisâ€biphenylâ€2,3â€dihydrodiolâ€2,3â€dehydrogenase from a PCB degrader at 2.0 Ã resolution. Protein Science, 1998, 7, 1286-1293.	3.1	69
144	Ecology and industrial microbiology Strange bedfellows. Current Opinion in Microbiology, 1998, 1, 267-270.	2.3	8

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145	Characterization of a gene cluster from Ralstonia eutropha JMP134 encoding metabolism of 4-methylmuconolactone. Gene, 1998, 206, 53-62.	1.0	16
146	A Novel [2Fe-2S] Ferredoxin from Pseudomonas putidamt2 Promotes the Reductive Reactivation of Catechol 2,3-Dioxygenase. Journal of Biological Chemistry, 1998, 273, 9622-9629.	1.6	63
147	Use of Subtractive Hybridization To Design Habitat-Based Oligonucleotide Probes for Investigation of Natural Bacterial Communities. Applied and Environmental Microbiology, 1998, 64, 185-191.	1.4	11
148	Degradation of 1,2,3,4-Tetrachlorobenzene by <i>Pseudomonas chlororaphis</i> RW71. Applied and Environmental Microbiology, 1998, 64, 3798-3806.	1.4	65
149	Activation and Repression of Transcription at the Double Tandem Divergent Promoters for the <i>xylR</i> and <i>xylS</i> Genes of the TOL Plasmid of <i>Pseudomonas putida</i> . Journal of Bacteriology, 1998, 180, 2889-2894.	1.0	69
150	Genetic Analysis of Dioxin Dioxygenase of <i>Sphingomonas</i> sp. Strain RW1: Catabolic Genes Dispersed on the Genome. Journal of Bacteriology, 1998, 180, 3954-3966.	1.0	165
151	Biochemical and Genetic Characterization of a Gentisate 1,2-Dioxygenase from <i>Sphingomonas</i> sp. Strain RW5. Journal of Bacteriology, 1998, 180, 4171-4176.	1.0	71
152	Detoxification of Protoanemonin by Dienelactone Hydrolase. Journal of Bacteriology, 1998, 180, 400-402.	1.0	27
153	Identification of Chlorobenzene Dioxygenase Sequence Elements Involved in Dechlorination of 1,2,4,5-Tetrachlorobenzene. Journal of Bacteriology, 1998, 180, 5520-5528.	1.0	80
154	TRANSCRIPTIONAL CONTROL OF THEPSEUDOMONASTOL PLASMID CATABOLIC OPERONS IS ACHIEVED THROUGH AN INTERPLAY OF HOST FACTORS AND PLASMID-ENCODED REGULATORS. Annual Review of Microbiology, 1997, 51, 341-373.	2.9	315
155	Temperature dependent expression of an acid phosphatase byBordetella bronchiseptica: role in intracellular survival. Microbial Pathogenesis, 1997, 22, 257-264.	1.3	26
156	Construction and characterization of genetically-marked bivalent anti-Shigella dysenteriae1 and anti-Shigella flexneriY live vaccine candidates. Microbial Pathogenesis, 1997, 22, 363-376.	1.3	10
157	Oral Somatic Transgene Vaccination Using Attenuated S. typhimurium. Cell, 1997, 91, 765-775.	13.5	400
158	Green fluorescent protein-based reporter systems for genetic analysis of bacteria including monocopy applications. Gene, 1997, 196, 69-74.	1.0	130
159	Bioprotection of microbial communities from toxic phenol mixtures by a genetically designed pseudomonad. Nature Biotechnology, 1997, 15, 378-382.	9.4	72
160	Genetic and Biochemical Characterization of the Broad Spectrum Chlorobenzene Dioxygenase from Burkholderia Sp. Strain PS12 - Dechlorination of 1,2,4,5-Tetrachlorobenzene. FEBS Journal, 1997, 247, 190-199.	0.2	74
161	Molecular Characterization of Fdx1, a Putidaredoxin-Type [2Fe-2S] Ferredoxin Able to Transfer Electrons to the Dioxin Dioxygenase of Sphingomonas sp. RW1. FEBS Journal, 1997, 247, 833-842.	0.2	56
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