Jian-Qiang Su

List of Publications by Year
in descending order

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148	13,419	23567	23533
papers	citations	58 h-index	111 g-index

151	151	151	9519
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Discarded masks as hotspots of antibiotic resistance genes during COVID-19 pandemic. Journal of Hazardous Materials, 2022, 425, 127774.	12.4	22
2	Prevalence of antibiotic resistance genes in Pangasianodon hypophthalmus and Oreochromis niloticus aquaculture production systems in Bangladesh. Science of the Total Environment, 2022, 813, 151915.	8.0	8
3	Earthworms reduce the dissemination potential of antibiotic resistance genes by changing bacterial co-occurrence patterns in soil. Journal of Hazardous Materials, 2022, 426, 128127.	12.4	20
4	Nanopore sequencing analysis of integron gene cassettes in sewages and soils. Science of the Total Environment, 2022, 817, 152766.	8.0	9
5	Conurbation size drives antibiotic resistance along the river. Science of the Total Environment, 2022, 823, 153822.	8.0	9
6	Globally distributed mining-impacted environments are underexplored hotspots of multidrug resistance genes. ISME Journal, 2022, 16, 2099-2113.	9.8	35
7	HiLi-chip: A high-throughput library construction chip for comprehensive profiling of environmental microbial communities. Environmental Research, 2022, 213, 113650.	7.5	1
8	Response of syntrophic bacterial and methanogenic archaeal communities in paddy soil to soil type and phenological period of rice growth. Journal of Cleaner Production, 2021, 278, 123418.	9.3	8
9	Earthworm gut: An overlooked niche for anaerobic ammonium oxidation in agricultural soil. Science of the Total Environment, 2021, 752, 141874.	8.0	6
10	Co-selection of antibiotic resistance genes, and mobile genetic elements in the presence of heavy metals in poultry farm environments. Science of the Total Environment, 2021, 755, 142702.	8.0	122
11	Air pollution could drive global dissemination of antibiotic resistance genes. ISME Journal, 2021, 15, 270-281.	9.8	95
12	Cadmium enhances conjugative plasmid transfer to a fresh water microbial community. Environmental Pollution, 2021, 268, 115903.	7.5	25
13	Changes in the diversity and abundance of syntrophic and methanogenic communities in response to rice phenology. Applied Soil Ecology, 2021, 159, 103851.	4.3	2
14	Deciphering Potential Roles of Earthworms in Mitigation of Antibiotic Resistance in the Soils from Diverse Ecosystems. Environmental Science & Technology, 2021, 55, 7445-7455.	10.0	49
15	Developing Surrogate Markers for Predicting Antibiotic Resistance â€œHot Spotsâ€•in Rivers Where Limited Data Are Available. Environmental Science & Technology, 2021, 55, 7466-7478.	10.0	21
16	Dynamics of antibiotic resistance and its association with bacterial community in a drinking water treatment plant and the residential area. Environmental Science and Pollution Research, 2021, 28, 55690-55699.	5.3	10
17	Vertical distribution of antibiotic resistance genes in an urban green facade. Environment International, 2021, 152, 106502.	10.0	24
18	Co-effect of cadmium and iron oxide nanoparticles on plasmid-mediated conjugative transfer of antibiotic resistance genes. Environment International, 2021, 152, 106453.	10.0	37

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19	Urban greenness and plant species are key factors in shaping air microbiomes and reducing airborne pathogens. Environment International, 2021, 153, 106539.	10.0	25
20	Environmental antimicrobial resistance is associated with faecal pollution in Central Thailandâ€™s coastal aquaculture region. Journal of Hazardous Materials, 2021, 416, 125718.	12.4	25
21	Longitudinal study on the effects of growth-promoting and therapeutic antibiotics on the dynamics of chicken cloacal and litter microbiomes and resistomes. Microbiome, 2021, 9, 178.	11.1	30
22	Anammox Bacteria Are Potentially Involved in Anaerobic Ammonium Oxidation Coupled to Iron(III) Reduction in the Wastewater Treatment System. Frontiers in Microbiology, 2021, 12, 717249.	3.5	3
23	Fecal pollution mediates the dominance of stochastic assembly of antibiotic resistome in an urban lagoon (Yundang lagoon), China. Journal of Hazardous Materials, 2021, 417, 126083.	12.4	22
24	Distinct patterns of abundant and rare subcommunities in paddy soil during wettingâ€“drying cycles. Science of the Total Environment, 2021, 785, 147298.	8.0	14
25	Arsenic contribution of poultry manure towards soils and food plants contamination and associated cancer risk in Khyber Pakhtunkhwa, Pakistan. Environmental Geochemistry and Health, 2021, , 1.	3.4	2
26	Soil pH has a stronger effect than arsenic content on shaping plastisphere bacterial communities in soil. Environmental Pollution, 2021, 287, 117339.	7.5	35
27	Viral Community and Virus-Associated Antibiotic Resistance Genes in Soils Amended with Organic Fertilizers. Environmental Science & Technology, 2021, 55, 13881-13890.	10.0	49
28	Field aging alters biochar's effect on antibiotic resistome in manured soil. Environmental Pollution, 2021, 288, 117719.	7.5	16
29	Influence of Legacy Mercury on Antibiotic Resistomes: Evidence from Agricultural Soils with Different Cropping Systems. Environmental Science & Technology, 2021, 55, 13913-13922.	10.0	19
30	Spatial and temporal dynamics of microbiomes and resistomes in broiler litter stockpiles. Computational and Structural Biotechnology Journal, 2021, 19, 6201-6211.	4.1	5
31	Antibiotics in poultry manure and their associated health issues: a systematic review. Journal of Soils and Sediments, 2020, 20, 486-497.	3.0	87
32	Antibiotic resistome in a landfill leachate treatment plant and effluent-receiving river. Chemosphere, 2020, 242, 125207.	8.2	41
33	Response of prokaryotic communities to extreme precipitation events in an urban coastal lagoon: A case study of Yundang lagoon, China. Science of the Total Environment, 2020, 706, 135937.	8.0	14
34	Phenotypic Tracking of Antibiotic Resistance Spread via Transformation from Environment to Clinic by Reverse D₂O Single-Cell Raman Probing. Analytical Chemistry, 2020, 92, 15472-15479.	6.5	15
35	High-throughput diagnosis of human pathogens and fecal contamination in marine recreational water. Environmental Research, 2020, 190, 109982.	7.5	43
36	Cyanobacterial blooms contribute to the diversity of antibiotic-resistance genes in aquatic ecosystems. Communications Biology, 2020, 3, 737.	4.4	66

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37	Changes in gut bacterial communities and the incidence of antibiotic resistance genes during degradation of antibiotics by black soldier fly larvae. Environment International, 2020, 142, 105834.	10.0	51
38	Enhanced removal of ciprofloxacin and reduction of antibiotic resistance genes by earthworm Metaphire vulgaris in soil. Science of the Total Environment, 2020, 742, 140409.	8.0	42
39	Manure fertilization increase antibiotic resistance in soils from typical greenhouse vegetable production bases, China. Journal of Hazardous Materials, 2020, 391, 122267.	12.4	61
40	Microbial Flow Within an Air-Phyllosphere-Soil Continuum. Frontiers in Microbiology, 2020, 11, 615481.	3.5	25
41	GLOBAL TRENDS AND PERFORMANCES OF STUDIES ON ANTIBIOTIC RESISTANCE GENES. Environmental Engineering and Management Journal, 2020, 19, 485-495.	0.6	1
42	Soil amendment with sewage sludge affects soil prokaryotic community composition, mobilome and resistome. FEMS Microbiology Ecology, 2019, 95, .	2.7	12
43	High-throughput characterization of antibiotic resistome in soil amended with commercial organic fertilizers. Journal of Soils and Sediments, 2019, 19, 641-651.	3.0	11
44	Loss of soil microbial diversity exacerbates spread of antibiotic resistance. Soil Ecology Letters, 2019, 1, 3-13.	4.5	66
45	Metabolic Inactivity and Re-awakening of a Nitrate Reduction Dependent Iron(II)-Oxidizing Bacterium Bacillus ferrooxidans. Frontiers in Microbiology, 2019, 10, 1494.	3.5	4
46	State of the art of tertiary treatment technologies for controlling antibiotic resistance in wastewater treatment plants. Environment International, 2019, 131, 105026.	10.0	125
47	Spatial ecology of a wastewater network defines the antibiotic resistance genes in downstream receiving waters. Water Research, 2019, 162, 347-357.	11.3	108
48	Changes in archaeal ether lipid composition in response to agriculture alternation in ancient and modern paddy soils. Organic Geochemistry, 2019, 138, 103912.	1.8	1
49	Understanding drivers of antibiotic resistance genes in High Arctic soil ecosystems. Environment International, 2019, 125, 497-504.	10.0	137
50	Manure and Doxycycline Affect the Bacterial Community and Its Resistome in Lettuce Rhizosphere and Bulk Soil. Frontiers in Microbiology, 2019, 10, 725.	3.5	46
51	Effects of diet on gut microbiota of soil collembolans. Science of the Total Environment, 2019, 676, 197-205.	8.0	28
52	Fate of Antibiotic Resistant Pseudomonas putida and Broad Host Range Plasmid in Natural Soil Microcosms. Frontiers in Microbiology, 2019, 10, 194.	3.5	48
53	Identification of dominant sulfamethoxazole-degraders in pig farm-impacted soil by DNA and protein stable isotope probing. Environment International, 2019, 126, 118-126.	10.0	49
54	Antibiotic Resistomes in Plant Microbiomes. Trends in Plant Science, 2019, 24, 530-541.	8.8	233

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55	RNA Stable Isotope Probing of Potential Feammox Population in Paddy Soil. Environmental Science & Technology, 2019, 53, 4841-4849.	10.0	70
56	Rapid Antibiotic Susceptibility Testing of Pathogenic Bacteria Using Heavy-Water-Labeled Single-Cell Raman Spectroscopy in Clinical Samples. Analytical Chemistry, 2019, 91, 6296-6303.	6.5	104
57	Spatial and seasonal variation of the airborne microbiome in a rapidly developing city of China. Science of the Total Environment, 2019, 665, 61-68.	8.0	70
58	Distinct rhizosphere effect on active and total bacterial communities in paddy soils. Science of the Total Environment, 2019, 649, 422-430.	8.0	62
59	Turning pig manure into biochar can effectively mitigate antibiotic resistance genes as organic fertilizer. Science of the Total Environment, 2019, 649, 902-908.	8.0	83
60	High-throughput profiling of antibiotic resistance gene dynamic in a drinking water river-reservoir system. Water Research, 2019, 149, 179-189.	11.3	150
61	AsChip: A High-Throughput qPCR Chip for Comprehensive Profiling of Genes Linked to Microbial Cycling of Arsenic. Environmental Science & Technology, 2019, 53, 798-807.	10.0	34
62	Evidence for co-selection of antibiotic resistance genes and mobile genetic elements in metal polluted urban soils. Science of the Total Environment, 2019, 656, 512-520.	8.0	183
63	Nitrogen inputs are more important than denitrifier abundances in controlling denitrification-derived N2O emission from both urban and agricultural soils. Science of the Total Environment, 2019, 650, 2807-2817.	8.0	11
64	Impact of Wastewater Treatment on the Prevalence of Integrons and the Genetic Diversity of Integron Gene Cassettes. Applied and Environmental Microbiology, 2018, 84, .	3.1	62
65	Co-optimization of sponge-core bioreactors for removing total nitrogen and antibiotic resistance genes from domestic wastewater. Science of the Total Environment, 2018, 634, 1417-1423.	8.0	16
66	Increased microbial functional diversity under long-term organic and integrated fertilization in a paddy soil. Applied Microbiology and Biotechnology, 2018, 102, 1969-1982.	3.6	57
67	Spatial and temporal distribution of antibiotic resistomes in a peri-urban area is associated significantly with anthropogenic activities. Environmental Pollution, 2018, 235, 525-533.	7.5	74
68	Effect of biochar amendment on the alleviation of antibiotic resistance in soil and phyllosphere of Brassica chinensis L.. Soil Biology and Biochemistry, 2018, 119, 74-82.	8.8	105
69	Functional Single-Cell Approach to Probing Nitrogen-Fixing Bacteria in Soil Communities by Resonance Raman Spectroscopy with ¹⁵N₂ Labeling. Analytical Chemistry, 2018, 90, 5082-5089.	6.5	67
70	Distinct effects of struvite and biochar amendment on the class 1 integron antibiotic resistance gene cassettes in phyllosphere and rhizosphere. Science of the Total Environment, 2018, 631-632, 668-676.	8.0	40
71	Feed additives shift gut microbiota and enrich antibiotic resistance in swine gut. Science of the Total Environment, 2018, 621, 1224-1232.	8.0	141
72	Diversity, abundance, and persistence of antibiotic resistance genes in various types of animal manure following industrial composting. Journal of Hazardous Materials, 2018, 344, 716-722.	12.4	301

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73	Seasonal comparison of bacterial communities in rhizosphere of alpine cushion plants in the Himalayan Hengduan Mountains. Plant Diversity, 2018, 40, 209-216.	3.7	12
74	Long-term effects of manure and chemical fertilizers on soil antibiotic resistome. Soil Biology and Biochemistry, 2018, 122, 111-119.	8.8	98
75	Long-term organic fertilization increased antibiotic resistome in phyllosphere of maize. Science of the Total Environment, 2018, 645, 1230-1237.	8.0	97
76	Tracking antibiotic resistome during wastewater treatment using high throughput quantitative PCR. Environment International, 2018, 117, 146-153.	10.0	152
77	QMEC: a tool for high-throughput quantitative assessment of microbial functional potential in C, N, P, and S biogeochemical cycling. Science China Life Sciences, 2018, 61, 1451-1462.	4.9	181
78	Large-scale biogeographical patterns of bacterial antibiotic resistome in the waterbodies of China. Environment International, 2018, 117, 292-299.	10.0	106
79	Bacillus ferrooxidans sp. nov., an iron(II)-oxidizing bacterium isolated from paddy soil. Journal of Microbiology, 2018, 56, 472-477.	2.8	5
80	Propionicimonas ferrireducens sp. nov., isolated from dissimilatory iron(III)-reducing microbial enrichment obtained from paddy soil. International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 1914-1918.	1.7	8
81	Continental-scale pollution of estuaries with antibiotic resistance genes. Nature Microbiology, 2017, 2, 16270.	13.3	812
82	Quantitative detection of fecal contamination with domestic poultry feces in environments in China. AMB Express, 2017, 7, 80.	3.0	19
83	Land scale biogeography of arsenic biotransformation genes in estuarine wetland. Environmental Microbiology, 2017, 19, 2468-2482.	3.8	45
84	Application of Struvite Alters the Antibiotic Resistome in Soil, Rhizosphere, and Phyllosphere. Environmental Science & Technology, 2017, 51, 8149-8157.	10.0	196
85	Application of genomic technologies to measure and monitor antibiotic resistance in animals. Annals of the New York Academy of Sciences, 2017, 1388, 121-135.	3.8	41
86	Metagenomic assembly unravel microbial response to redox fluctuation in acid sulfate soil. Soil Biology and Biochemistry, 2017, 105, 244-252.	8.8	27
87	From chemical mixtures to antibiotic resistance. Journal of Environmental Sciences, 2017, 62, 138-144.	6.1	39
88	Do manure-borne or indigenous soil microorganisms influence the spread of antibiotic resistance genes in manured soil?. Soil Biology and Biochemistry, 2017, 114, 229-237.	8.8	170
89	An underappreciated hotspot of antibiotic resistance: The groundwater near the municipal solid waste landfill. Science of the Total Environment, 2017, 609, 966-973.	8.0	133
90	Bacterial succession along a long-term chronosequence of paddy soil in the Yangtze River Delta, China. Soil Biology and Biochemistry, 2017, 104, 59-67.	8.8	70

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91	The antibiotic resistome of swine manure is significantly altered by association with the Musca domestica larvae gut microbiome. ISME Journal, 2017, 11, 100-111.	9.8	101
92	Biochar Addition Increases the Rates of Dissimilatory Iron Reduction and Methanogenesis in Ferrihydrite Enrichments. Frontiers in Microbiology, 2017, 8, 589.	3.5	31
93	Metagenomics of urban sewage identifies an extensively shared antibiotic resistome in China. Microbiome, 2017, 5, 84.	11.1	247
94	Transcriptomic Analysis Reveals Adaptive Responses of an Enterobacteriaceae Strain LSJC7 to Arsenic Exposure. Frontiers in Microbiology, 2016, 7, 636.	3.5	38
95	Electron Shuttles Enhance Anaerobic Ammonium Oxidation Coupled to Iron(III) Reduction. Environmental Science & Technology, 2016, 50, 9298-9307.	10.0	217
96	The patterns of bacterial community and relationships between sulfate-reducing bacteria and hydrochemistry in sulfate-polluted groundwater of Baogang rare earth tailings. Environmental Science and Pollution Research, 2016, 23, 21766-21779.	5.3	10
97	Long-Term Impact of Field Applications of Sewage Sludge on Soil Antibiotic Resistome. Environmental Science & Technology, 2016, 50, 12602-12611.	10.0	97
98	A buried Neolithic paddy soil reveals loss of microbial functional diversity after modern rice cultivation. Science Bulletin, 2016, 61, 1052-1060.	9.0	41
99	The phenological stage of rice growth determines anaerobic ammonium oxidation activity in rhizosphere soil. Soil Biology and Biochemistry, 2016, 100, 59-65.	8.8	58
100	Responses of endophytic and rhizospheric bacterial communities of salt marsh plant (Spartina) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 38 2016, 16, 707-715.	3.0	33
101	Heavy Metal Induced Antibiotic Resistance in Bacterium LSJC7. International Journal of Molecular Sciences, 2015, 16, 23390-23404.	4.1	126
102	Diversity and Abundance of Arsenic Biotransformation Genes in Paddy Soils from Southern China. Environmental Science & Technology, 2015, 49, 4138-4146.	10.0	195
103	Antibiotic Resistome and Its Association with Bacterial Communities during Sewage Sludge Composting. Environmental Science & Technology, 2015, 49, 7356-7363.	10.0	736
104	Antibiotic resistance genes in manure-amended soil and vegetables at harvest. Journal of Hazardous Materials, 2015, 299, 215-221.	12.4	263
105	Increased levels of antibiotic resistance in urban stream of Jiulongjiang River, China. Applied Microbiology and Biotechnology, 2015, 99, 5697-5707.	3.6	196
106	Insights into the role of plant on ammonia-oxidizing bacteria and archaea in the mangrove ecosystem. Journal of Soils and Sediments, 2015, 15, 1212-1223.	3.0	31
107	A comprehensive study of the impact of polycyclic aromatic hydrocarbons (PAHs) contamination on salt marsh plants Spartina alterniflora: implication for plant-microbe interactions in phytoremediation. Environmental Science and Pollution Research, 2015, 22, 7071-7081.	5.3	51
108	Diversity of endophytic and rhizoplane bacterial communities associated with exotic Spartina alterniflora and native mangrove using Illumina amplicon sequencing. Canadian Journal of Microbiology, 2015, 61, 723-733.	1.7	67

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109	Variability in responses of bacterial communities and nitrogen oxide emission to urea fertilization among various flooded paddy soils. FEMS Microbiology Ecology, 2015, 91, .	2.7	21
110	Bacterial community composition at anodes of microbial fuel cells for paddy soils: the effects of soil properties. Journal of Soils and Sediments, 2015, 15, 926-936.	3.0	51
111	pH regulates ammonia-oxidizing bacteria and archaea in paddy soils in Southern China. Applied Microbiology and Biotechnology, 2015, 99, 6113-6123.	3.6	70
112	Performance of vertical up-flow constructed wetlands on swine wastewater containing tetracyclines and tet genes. Water Research, 2015, 70, 109-117.	11.3	162
113	Potential Contribution of Anammox to Nitrogen Loss from Paddy Soils in Southern China. Applied and Environmental Microbiology, 2015, 81, 938-947.	3.1	118
114	Longâ€term balanced fertilization increases the soil microbial functional diversity in a phosphorusâ€limited paddy soil. Molecular Ecology, 2015, 24, 136-150.	3.9	197
115	Long-term nitrogen fertilization of paddy soil shifts iron-reducing microbial community revealed by RNA-13C-acetate probing coupled with pyrosequencing. ISME Journal, 2015, 9, 721-734.	9.8	118
116	Phyllosphere Bacterial Community of Floating Macrophytes in Paddy Soil Environments as Revealed by Illumina High-Throughput Sequencing. Applied and Environmental Microbiology, 2015, 81, 522-532.	3.1	65
117	Quantitative analyses of ribulose-1,5-bisphosphate carboxylase/oxygenase (RubisCO) large-subunit genes (cbbL) in typical paddy soils. FEMS Microbiology Ecology, 2014, 87, 89-101.	2.7	63
118	Does urbanization shape bacterial community composition in urban park soils? A case study in 16 representative Chinese cities based on the pyrosequencing method. FEMS Microbiology Ecology, 2014, 87, 182-192.	2.7	80
119	Functional metagenomic characterization of antibiotic resistance genes in agricultural soils from China. Environment International, 2014, 65, 9-15.	10.0	149
120	Relationships Between Abundance of Microbial Functional Genes and the Status and Fluxes of Carbon and Nitrogen in Rice Rhizosphere and Bulk Soils. Pedosphere, 2014, 24, 645-651.	4.0	19
121	Impacts of vegetation, tidal process, and depth on the activities, abundances, and community compositions of denitrifiers in mangrove sediment. Applied Microbiology and Biotechnology, 2014, 98, 9375-9387.	3.6	45
122	Arsenite Oxidation by the Phyllosphere Bacterial Community Associated with Wolffia australiana. Environmental Science & Technology, 2014, 48, 9668-9674.	10.0	31
123	Biochar Impacts Soil Microbial Community Composition and Nitrogen Cycling in an Acidic Soil Planted with Rape. Environmental Science & Technology, 2014, 48, 9391-9399.	10.0	390
124	High Throughput Profiling of Antibiotic Resistance Genes in Urban Park Soils with Reclaimed Water Irrigation. Environmental Science & Technology, 2014, 48, 9079-9085.	10.0	351
125	Illumina sequencing-based analyses of bacterial communities during short-chain fatty-acid production from food waste and sewage sludge fermentation at different pH values. World Journal of Microbiology and Biotechnology, 2014, 30, 2387-2395.	3.6	15
126	Genome sequence of the anaerobic bacterium Bacillus sp. strain ZYK, a selenite and nitrate reducer from paddy soil. Standards in Genomic Sciences, 2014, 9, 646-654.	1.5	6

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127	A marine algicidal actinomycete and its active substance against the harmful algal bloom species Phaeocystis globosa. Applied Microbiology and Biotechnology, 2013, 97, 9207-9215.	3.6	82
128	Response of bacterial communities to short-term pyrene exposure in red soil. Frontiers of Environmental Science and Engineering, 2013, 7, 559-567.	6.0	6
129	Abundance and composition of denitrifiers in response toSpartina alterniflorainvasion in estuarine sediment. Canadian Journal of Microbiology, 2013, 59, 825-836.	1.7	19
130	Diverse and abundant antibiotic resistance genes in Chinese swine farms. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3435-3440.	7.1	1,925
131	Draft Genome Sequence of a Novel Bacterial Strain, LSJC7, Belonging to the Family Enterobacteriaceae with Dual Resistance to Arsenic and Tetracycline. Journal of Bacteriology, 2012, 194, 7005-7006.	2.2	7
132	Fate of tetracyclines in swine manure of three selected swine farms in China. Journal of Environmental Sciences, 2012, 24, 1047-1052.	6.1	105
133	An Attempt to Quantify Cu-Resistant Microorganisms in a Paddy Soil from Jiaxing, China. Pedosphere, 2012, 22, 201-205.	4.0	19
134	A marine bacterium producing protein with algicidal activity against Alexandrium tamarense. Harmful Algae, 2012, 13, 83-88.	4.8	71
135	Marine bacteria antagonistic to the harmful algal bloom species Alexandrium tamarense (Dinophyceae). Biological Control, 2011, 56, 132-138.	3.0	57
136	Algicidal Effects of a Novel Marine Actinomycete on the Toxic Dinoflagellate Alexandrium tamarense. Current Microbiology, 2011, 62, 1774-1781.	2.2	60
137	Lysis of a red-tide causing alga, Alexandrium tamarense, caused by bacteria from its phycosphere. Biological Control, 2010, 52, 123-130.	3.0	98
138	A novel marine bacterium algicidal to the toxic dinoflagellate Alexandrium tamarense. Letters in Applied Microbiology, 2010, 51, 552-557.	2.2	37
139	Bacterial decolorization and degradation of the reactive dye Reactive Red 180 by Citrobacter sp. CK3. International Biodeterioration and Biodegradation, 2009, 63, 395-399.	3.9	191
140	Biological decolorization of the reactive dyes Reactive Black 5 by a novel isolated bacterial strain Enterobacter sp. EC3. Journal of Hazardous Materials, 2009, 171, 654-659.	12.4	146
141	An efficient method to obtain axenic cultures of Alexandrium tamarenseâ€"a PSP-producing dinoflagellate. Journal of Microbiological Methods, 2007, 69, 425-430.	1.6	57
142	Isolation and characterization of a marine algicidal bacterium against the toxic dinoflagellate Alexandrium tamarense. Harmful Algae, 2007, 6, 799-810.	4.8	107
143	Microbial modulation in the biomass and toxin production of a red-tide causing alga. Marine Pollution Bulletin, 2005, 51, 1018-1025.	5.0	23
144	Biological activity of a red-tide alga--A. tamarense under co-cultured condition with bacteria. Journal of Environmental Sciences, 2005, 17, 1047-50.	6.1	2

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145	The distribution characteristics of bacterial Î²-glucosidase activity in Taiwan strait. Marine Pollution Bulletin, 2002, 45, 168-176.	5.0	8
146	Research on Modeling and Simulation of Engine-Generator in the Electric Drive Vehicle. Advanced Materials Research, 0, 512-515, 2615-2619.	0.3	0
147	Co-Simulation Research of In-Wheel Motor Drive Vehicle Steering Control. Applied Mechanics and Materials, 0, 415, 578-581.	0.2	0
148	Engine-Generator's Optimized Control Strategy for Electric Drive Armored Vehicle. Applied Mechanics and Materials, 0, 415, 574-577.	0.2	0