

Hongyue Dang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9651932/publications.pdf>

Version: 2024-02-01

31
papers

3,041
citations

304743

22
h-index

434195

31
g-index

31
all docs

31
docs citations

31
times ranked

3542
citing authors

#	ARTICLE	IF	CITATIONS
1	Understanding Interaction Patterns within Deep-Sea Microbial Communities and Their Potential Applications. <i>Marine Drugs</i> , 2022, 20, 108.	4.6	10
2	Electrostimulated bio-dechlorination of a PCB mixture (Aroclor 1260) in a marine-originated dechlorinating culture. <i>Environmental Pollution</i> , 2021, 291, 118157.	7.5	15
3	Grand Challenges in Microbe-Driven Marine Carbon Cycling Research. <i>Frontiers in Microbiology</i> , 2020, 11, 1039.	3.5	10
4	Redox characteristics of humins and their coupling with potential PCB dechlorinators in southern Yellow Sea sediments. <i>Environmental Pollution</i> , 2019, 252, 296-304.	7.5	20
5	Climate tipping-point potential and paradoxical production of methane in a changing ocean. <i>Science China Earth Sciences</i> , 2018, 61, 1714-1727.	5.2	4
6	Ecological Energetic Perspectives on Responses of Nitrogen-Transforming Chemolithoautotrophic Microbiota to Changes in the Marine Environment. <i>Frontiers in Microbiology</i> , 2017, 8, 1246.	3.5	49
7	Environmental Conditions Outweigh Geographical Contiguity in Determining the Similarity of <i>nifH</i> -Harboring Microbial Communities in Sediments of Two Disconnected Marginal Seas. <i>Frontiers in Microbiology</i> , 2016, 7, 1111.	3.5	14
8	Microbial Surface Colonization and Biofilm Development in Marine Environments. <i>Microbiology and Molecular Biology Reviews</i> , 2016, 80, 91-138.	6.6	864
9	Inspirations from the scientific discovery of the anammox bacteria: A classic example of how scientific principles can guide discovery and development. <i>Science China Earth Sciences</i> , 2016, 59, 449-455.	5.2	3
10	Ubiquity and Diversity of Heterotrophic Bacterial <i>nasA</i> Genes in Diverse Marine Environments. <i>PLoS ONE</i> , 2015, 10, e0117473.	2.5	15
11	Deep-sea methane seep sediments in the Okhotsk Sea sustain diverse and abundant anammox bacteria. <i>FEMS Microbiology Ecology</i> , 2014, 87, 503-516.	2.7	44
12	Environment-Dependent Distribution of the Sediment <i>nifH</i> -Harboring Microbiota in the Northern South China Sea. <i>Applied and Environmental Microbiology</i> , 2013, 79, 121-132.	3.1	39
13	Thaumarchaeotal Signature Gene Distribution in Sediments of the Northern South China Sea: an Indicator of the Metabolic Intersection of the Marine Carbon, Nitrogen, and Phosphorus Cycles?. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2137-2147.	3.1	58
14	Molecular Detection of <i>Candidatus Scalindua pacifica</i> and Environmental Responses of Sediment Anammox Bacterial Community in the Bohai Sea, China. <i>PLoS ONE</i> , 2013, 8, e61330.	2.5	86
15	Molecular characterization of putative biocorroding microbiota with a novel niche detection of <i>Epsilon</i> - and <i>Zetaproteobacteria</i> in Pacific Ocean coastal seawaters. <i>Environmental Microbiology</i> , 2011, 13, 3059-3074.	3.8	124
16	Gene cloning, expression and characterization of a cold-adapted lipase from a psychrophilic deep-sea bacterium <i>Psychrobacter</i> sp. C18. <i>World Journal of Microbiology and Biotechnology</i> , 2011, 27, 431-441.	3.6	39
17	Diversity, abundance and distribution of <i>amoA</i> -encoding archaea in deep-sea methane seep sediments of the Okhotsk Sea. <i>FEMS Microbiology Ecology</i> , 2010, 72, 370-385.	2.7	68
18	Environmental Factors Shape Sediment Anammox Bacterial Communities in Hypernutriented Jiaozhou Bay, China. <i>Applied and Environmental Microbiology</i> , 2010, 76, 7036-7047.	3.1	140

#	ARTICLE	IF	CITATIONS
19	Diverse and Novel <i>nifH</i> and <i>nifH</i> -Like Gene Sequences in the Deep-Sea Methane Seep Sediments of the Okhotsk Sea. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2238-2245.	3.1	61
20	Molecular characterizations of chloramphenicol- and oxytetracycline-resistant bacteria and resistance genes in mariculture waters of China. <i>Marine Pollution Bulletin</i> , 2009, 58, 987-994.	5.0	32
21	Extracellular hydrolytic enzyme screening of culturable heterotrophic bacteria from deep-sea sediments of the Southern Okinawa Trough. <i>World Journal of Microbiology and Biotechnology</i> , 2009, 25, 71-79.	3.6	62
22	Fine-scale vertical distribution of bacteria in the East Pacific deep-sea sediments determined via 16S rRNA gene T-RFLP and clone library analyses. <i>World Journal of Microbiology and Biotechnology</i> , 2009, 25, 179-188.	3.6	26
23	Diversity and Distribution of Sediment NirS-Encoding Bacterial Assemblages in Response to Environmental Gradients in the Eutrophied Jiaozhou Bay, China. <i>Microbial Ecology</i> , 2009, 58, 161-169.	2.8	82
24	Dominant chloramphenicol-resistant bacteria and resistance genes in coastal marine waters of Jiaozhou Bay, China. <i>World Journal of Microbiology and Biotechnology</i> , 2008, 24, 209-217.	3.6	59
25	Incidence of diverse integrons and β -lactamase genes in environmental Enterobacteriaceae isolates from Jiaozhou Bay, China. <i>World Journal of Microbiology and Biotechnology</i> , 2008, 24, 2889-2896.	3.6	15
26	Diverse Tetracycline Resistant Bacteria and Resistance Genes from Coastal Waters of Jiaozhou Bay. <i>Microbial Ecology</i> , 2008, 55, 237-246.	2.8	47
27	Diversity and spatial distribution of sediment ammonia-oxidizing crenarchaeota in response to estuarine and environmental gradients in the Changjiang Estuary and East China Sea. <i>Microbiology (United Kingdom)</i> , 2008, 154, 2084-2095.	1.8	146
28	Cross-Ocean Distribution of <i>Rhodobacterales</i> Bacteria as Primary Surface Colonizers in Temperate Coastal Marine Waters. <i>Applied and Environmental Microbiology</i> , 2008, 74, 52-60.	3.1	394
29	Concurrence of cat and tet Genes in Multiple Antibiotic-Resistant Bacteria Isolated from a Sea Cucumber and Sea Urchin Mariculture Farm in China. <i>Microbial Ecology</i> , 2006, 52, 634-643.	2.8	39
30	Molecular characterizations of oxytetracycline resistant bacteria and their resistance genes from mariculture waters of China. <i>Marine Pollution Bulletin</i> , 2006, 52, 1494-1503.	5.0	50
31	Bacterial Primary Colonization and Early Succession on Surfaces in Marine Waters as Determined by Amplified rRNA Gene Restriction Analysis and Sequence Analysis of 16S rRNA Genes. <i>Applied and Environmental Microbiology</i> , 2000, 66, 467-475.	3.1	426