

Yong Wang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8902141/publications.pdf>

Version: 2024-02-01

86
papers

4,067
citations

172457

29
h-index

123424

61
g-index

89
all docs

89
docs citations

89
times ranked

5862
citing authors

#	ARTICLE	IF	CITATIONS
1	Carbon metabolism and adaptation of hyperalkaliphilic microbes in serpentinizing spring of Manleluag, the Philippines. <i>Environmental Microbiology Reports</i> , 2022, 14, 308-319.	2.4	2
2	Microbiomes in the Challenger Deep slope and bottom-axis sediments. <i>Nature Communications</i> , 2022, 13, 1515.	12.8	31
3	Deep sea sediments associated with cold seeps are a subsurface reservoir of viral diversity. <i>ISME Journal</i> , 2021, 15, 2366-2378.	9.8	93
4	Asgard archaea in the haima cold seep: Spatial distribution and genomic insights. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2021, 170, 103489.	1.4	11
5	Phylogenomic Insights into Distribution and Adaptation of Bdellovibrionota in Marine Waters. <i>Microorganisms</i> , 2021, 9, 757.	3.6	14
6	Functional diversity of microbial communities in inactive seafloor sulfide deposits. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	16
7	Deep-Sea Carbonates Are a Reservoir of Fossil Microbes Previously Inhabiting Cold Seeps. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	1
8	Microbial ecology of sulfur cycling near the sulfate–methane transition of deep-sea cold seep sediments. <i>Environmental Microbiology</i> , 2021, 23, 6844-6858.	3.8	31
9	Genomic differences within the phylum Marinimicrobia: From waters to sediments in the Mariana Trench. <i>Marine Genomics</i> , 2020, 50, 100699.	1.1	12
10	“Unicorn from Hades”, a new genus of Mysidae (Malacostraca: Mysida) from the Mariana Trench, with a systematic analysis of the deep-sea mysids. <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106666.	2.7	2
11	Metagenomic studies of SAR202 bacteria at the full-ocean depth in the Mariana Trench. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 165, 103396.	1.4	14
12	Rediscovery of the abyssal species <i>Peniagone leander</i> Pawson and Foell, 1986 (Holothuroidea). <i>Limnology</i> , 2020, 38, 1319-1327.	1.3	3
13	Metabolic diversification of anaerobic methanotrophic archaea in a deep-sea cold seep. <i>Marine Life Science and Technology</i> , 2020, 2, 431-441.	4.6	17
14	A novel bacterial phylum that participates in carbon and osmolyte cycling in the Challenger Deep sediments. <i>Environmental Microbiology</i> , 2020, 23, 3758-3772.	3.8	4
15	Phylogenomics of expanding uncultured environmental <i>Tenericutes</i> provides insights into their pathogenicity and evolutionary relationship with <i>Bacilli</i> . <i>BMC Genomics</i> , 2020, 21, 408.	2.8	65
16	Multiple in situ Nucleic Acid Collections (MISNAC) From Deep-Sea Waters. <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	13
17	Comparative analysis of the gut microbial communities between two dominant amphipods from the Challenger Deep, Mariana Trench. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2019, 151, 103081.	1.4	16
18	In situ metagenomic insights into the community compositions and ecological roles of hadal microbes in the Mariana Trench. <i>Environmental Microbiology</i> , 2019, 21, 4092-4108.	3.8	40

#	ARTICLE	IF	CITATIONS
19	Hadal water sampling by in situ microbial filtration and fixation (ISMIFF) apparatus. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2019, 144, 132-137.	1.4	29
20	New Microbial Lineages Capable of Carbon Fixation and Nutrient Cycling in Deep-Sea Sediments of the Northern South China Sea. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	36
21	Genomics insights into ecotype formation of ammonia-oxidizing archaea in the deep ocean. <i>Environmental Microbiology</i> , 2019, 21, 716-729.	3.8	39
22	Deepest record of <i>Eucopia sculpticauda</i> (Crustacea: Lophogastrida: Eucopiidae) and the order, with new insights into the distribution and genetic diversity of the species. <i>Bulletin of Marine Science</i> , 2019, 95, 327-335.	0.8	2
23	Periodic and Spatial Spreading of Alkanes and <i>Alcanivorax</i> Bacteria in Deep Waters of the Mariana Trench. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	17
24	Genomic Characterization of a Novel Gut Symbiont From the Hadal Snailfish. <i>Frontiers in Microbiology</i> , 2019, 10, 2978.	3.5	29
25	The vertical distribution of prokaryotes in the surface sediment of Jiaolong cold seep at the northern South China Sea. <i>Extremophiles</i> , 2018, 22, 499-510.	2.3	24
26	Unique tRNA gene profile suggests paucity of nucleotide modifications in anticodons of a deep-sea symbiotic <i>Spiroplasma</i> . <i>Nucleic Acids Research</i> , 2018, 46, 2197-2203.	14.5	4
27	The Enigmatic Genome of an Obligate Ancient <i>Spiroplasma</i> Symbiont in a Hadal Holothurian. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	38
28	Rediscovery of the hadal species <i>Amblyops magnus</i> Birstein & Tchindonova, 1958 (Crustacea: Tj ETQq0 0,0 rgBT /Qverlock 10	0.5	2
29	Molecular Characterization of a Novel N-Acetylneuraminase Lyase from a Deep-Sea Symbiotic <i>Mycoplasma</i> . <i>Marine Drugs</i> , 2018, 16, 80.	4.6	10
30	Toward understanding barnacle cementing by characterization of one cement protein-100kDa in <i>Amphibalanus amphitrite</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 969-975.	2.1	16
31	New species of the giant deep-sea isopod genus <i>Bathynomus</i> (Crustacea, Isopoda, Cirolanidae) from Hainan Island, South China Sea. <i>Integrative Zoology</i> , 2017, 12, 283-291.	2.6	7
32	Draft Genome of <i>Scalindua rubra</i> , Obtained from the Interface Above the Discovery Deep Brine in the Red Sea, Sheds Light on Potential Salt Adaptation Strategies in Anammox Bacteria. <i>Microbial Ecology</i> , 2017, 74, 1-5.	2.8	73
33	<i>Deinococcus planocerae</i> sp. nov., isolated from a marine flatworm. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 811-817.	1.7	8
34	Lirex: A Package for Identification of Long Inverted Repeats in Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 141-146.	6.9	4
35	Comparative Transcriptomic Analysis Reveals Candidate Genes and Pathways Involved in Larval Settlement of the Barnacle <i>Megabalanus volcano</i> . <i>International Journal of Molecular Sciences</i> , 2017, 18, 2253.	4.1	11
36	Oxidative Weathering and Microbial Diversity of an Inactive Seafloor Hydrothermal Sulfide Chimney. <i>Frontiers in Microbiology</i> , 2017, 8, 1378.	3.5	28

#	ARTICLE	IF	CITATIONS
37	The Cyanobacteria-Dominated Sponge <i>Dactylospongia elegans</i> in the South China Sea: Prokaryotic Community and Metagenomic Insights. <i>Frontiers in Microbiology</i> , 2017, 8, 1387.	3.5	15
38	Archive of bacterial community in anhydrite crystals from a deep-sea basin provides evidence of past oil-spilling in a benthic environment in the Red Sea. <i>Biogeosciences</i> , 2016, 13, 6405-6417.	3.3	1
39	Genomic characterization of symbiotic mycoplasmas from the stomach of deep-sea isopod <i>Bathynomus</i> sp. <i>Environmental Microbiology</i> , 2016, 18, 2646-2659.	3.8	49
40	Draft genome of an <i>Aerophobetes</i> bacterium reveals a facultative lifestyle in deep-sea anaerobic sediments. <i>Science Bulletin</i> , 2016, 61, 1176-1186.	9.0	16
41	An evaluation of multiple annealing and looping based genome amplification using a synthetic bacterial community. <i>Acta Oceanologica Sinica</i> , 2016, 35, 131-136.	1.0	8
42	Sensitivity and correlation of hypervariable regions in 16S rRNA genes in phylogenetic analysis. <i>BMC Bioinformatics</i> , 2016, 17, 135.	2.6	374
43	Pathway mining-based integration of critical enzyme parts for de novo biosynthesis of steviolglycosides sweetener in <i>Escherichia coli</i> . <i>Cell Research</i> , 2016, 26, 258-261.	12.0	57
44	Species sorting during biofilm assembly by artificial substrates deployed in a cold seep system. <i>Scientific Reports</i> , 2015, 4, 6647.	3.3	43
45	Synchronized dynamics of bacterial niche-specific functions during biofilm development in a cold seep brine pool. <i>Environmental Microbiology</i> , 2015, 17, 4089-4104.	3.8	24
46	Microbial community changes along the active seepage site of one cold seep in the Red Sea. <i>Frontiers in Microbiology</i> , 2015, 6, 739.	3.5	12
47	Luminescence dating of marine sediments from the Sea of Japan using quartz OSL and polymineral pIRIR signals of fine grains. <i>Quaternary Geochronology</i> , 2015, 30, 257-263.	1.4	16
48	Assembly of plant communities in coastal wetlands—the role of saltcedar <i>Tamarix chinensis</i> during early succession. <i>Journal of Plant Ecology</i> , 2015, 8, 539-548.	2.3	5
49	Changing composition of microbial communities indicates seepage fluid difference of the Thuwal Seeps in the Red Sea. <i>Antonie Van Leeuwenhoek</i> , 2015, 108, 461-471.	1.7	2
50	Roles of phenotypic and genetic characteristics in the social mating pattern of Silver-throated Tits (<i>Aegithalos glaucogularis</i>). <i>Journal of Ornithology</i> , 2015, 156, 687-697.	1.1	3
51	Atroposelective Synthesis of Axially Chiral Biaryldiols via Organocatalytic Arylation of 2-Naphthols. <i>Journal of the American Chemical Society</i> , 2015, 137, 15062-15065.	13.7	242
52	Conserved Regions in 16S Ribosome RNA Sequences and Primer Design for Studies of Environmental Microbes. , 2015, , 106-110.		1
53	Zonation of Microbial Communities by a Hydrothermal Mound in the Atlantis II Deep (the Red Sea). <i>PLoS ONE</i> , 2015, 10, e0140766.	2.5	6
54	Pyrosequencing revealed shifts of prokaryotic communities between healthy and disease-like tissues of the Red Sea sponge <i>Crella cyathophora</i> . <i>PeerJ</i> , 2015, 3, e890.	2.0	20

#	ARTICLE	IF	CITATIONS
55	Optimal Eukaryotic 18S and Universal 16S/18S Ribosomal RNA Primers and Their Application in a Study of Symbiosis. PLoS ONE, 2014, 9, e90053.	2.5	104
56	Toward Understanding the Dynamics of Microbial Communities in an Estuarine System. PLoS ONE, 2014, 9, e94449.	2.5	24
57	Microbial Sulfur Cycle in Two Hydrothermal Chimneys on the Southwest Indian Ridge. MBio, 2014, 5, e00980-13.	4.1	71
58	Genomic analysis reveals versatile heterotrophic capacity of a potentially symbiotic sulfur-oxidizing bacterium in sponge. Environmental Microbiology, 2014, 16, 3548-3561.	3.8	76
59	Symbiotic Adaptation Drives Genome Streamlining of the Cyanobacterial Sponge Symbiont <i>Candidatus</i> <i>Synechococcus spongiarum</i> . MBio, 2014, 5, e00079-14.	4.1	83
60	Effect of Copper Treatment on the Composition and Function of the Bacterial Community in the Sponge <i>Haliclona cymaeformis</i> . MBio, 2014, 5, e01980.	4.1	39
61	Molecular Techniques Revealed Highly Diverse Microbial Communities in Natural Marine Biofilms on Polystyrene Dishes for Invertebrate Larval Settlement. Microbial Ecology, 2014, 68, 81-93.	2.8	28
62	Pyrosequencing Reveals the Microbial Communities in the Red Sea Sponge <i>Carteriospongia foliascens</i> and Their Impressive Shifts in Abnormal Tissues. Microbial Ecology, 2014, 68, 621-632.	2.8	37
63	Diversity and distribution of eukaryotic microbes in and around a brine pool adjacent to the Thuwal cold seeps in the Red Sea. Frontiers in Microbiology, 2014, 5, 37.	3.5	30
64	In situ environment rather than substrate type dictates microbial community structure of biofilms in a cold seep system. Scientific Reports, 2014, 4, 3587.	3.3	49
65	Effect of polybrominated diphenyl ether (PBDE) treatment on the composition and function of the bacterial community in the sponge <i>Haliclona cymaeformis</i> . Frontiers in Microbiology, 2014, 5, 799.	3.5	9
66	Deep Sequencing of <i>Myxilla</i> (<i>Ectyomyxilla</i>) <i>methanophila</i> , an Epibiotic Sponge on Cold-Seep Tubeworms, Reveals Methylophilic, Thiophilic, and Putative Hydrocarbon-Degrading Microbial Associations. Microbial Ecology, 2013, 65, 450-461.	2.8	25
67	Autotrophic Microbe Metagenomes and Metabolic Pathways Differentiate Adjacent Red Sea Brine Pools. Scientific Reports, 2013, 3, 1748.	3.3	25
68	Adaptation of intertidal biofilm communities is driven by metal ion and oxidative stresses. Scientific Reports, 2013, 3, 3180.	3.3	31
69	Distinctive Microbial Community Structure in Highly Stratified Deep-Sea Brine Water Columns. Applied and Environmental Microbiology, 2013, 79, 3425-3437.	3.1	57
70	Artifactual pyrosequencing reads in multiple-displacement-amplified sediment metagenomes from the Red Sea. PeerJ, 2013, 1, e69.	2.0	4
71	Spatial and Species Variations in Bacterial Communities Associated with Corals from the Red Sea as Revealed by Pyrosequencing. Applied and Environmental Microbiology, 2012, 78, 7173-7184.	3.1	97
72	Vertical stratification of microbial communities in the Red Sea revealed by 16S rDNA pyrosequencing. ISME Journal, 2011, 5, 507-518.	9.8	151

#	ARTICLE	IF	CITATIONS
73	Pyrosequencing reveals highly diverse and species-specific microbial communities in sponges from the Red Sea. ISME Journal, 2011, 5, 650-664.	9.8	265
74	Hydrothermally generated aromatic compounds are consumed by bacteria colonizing in Atlantis II Deep of the Red Sea. ISME Journal, 2011, 5, 1652-1659.	9.8	34
75	Bacterial Niche-Specific Genome Expansion Is Coupled with Highly Frequent Gene Disruptions in Deep-Sea Sediments. PLoS ONE, 2011, 6, e29149.	2.5	10
76	Study of monocyte membrane proteome perturbation during lipopolysaccharide-induced tolerance using iTRAQ-based quantitative proteomic approach. Proteomics, 2010, 10, 2780-2789.	2.2	45
77	Conservative Fragments in Bacterial 16S rRNA Genes and Primer Design for 16S Ribosomal DNA Amplicons in Metagenomic Studies. PLoS ONE, 2009, 4, e7401.	2.5	960
78	In Silico Prediction of Two Classes of Honeybee Genes with CpG Deficiency or CpG Enrichment and Sorting According to Gene Ontology Classes. Journal of Molecular Evolution, 2009, 68, 700-705.	1.8	21
79	A study on genomic distribution and sequence features of human long inverted repeats reveals species-specific intronic inverted repeats. FEBS Journal, 2009, 276, 1986-1998.	4.7	19
80	Discovery of a long inverted repeat in human POTE genes. Genomics, 2009, 94, 278-283.	2.9	4
81	Acquisition of inverted GSTM exons by an intron of primate GSTM5 gene. Journal of Human Genetics, 2009, 54, 271-276.	2.3	2
82	The mitochondrial genome of the Basidiomycete fungus <i>Pleurotus ostreatus</i> (oyster) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 Td	1.8	53
83	Comparative Genomic Study Reveals a Transition from TA Richness in Invertebrates to GC Richness in Vertebrates at CpG Flanking Sites: An Indication for Context-Dependent Mutagenicity of Methylated CpG Sites. Genomics, Proteomics and Bioinformatics, 2008, 6, 144-154.	6.9	3
84	GC Content Increased at CpG Flanking Positions of Fish Genes Compared with Sea Squirt Orthologs as a Mechanism for Reducing Impact of DNA Methylation. PLoS ONE, 2008, 3, e3612.	2.5	9
85	Database for chicken full-length cDNAs. Physiological Genomics, 2007, 28, 141-145.	2.3	4
86	Long inverted repeats in eukaryotic genomes: Recombinogenic motifs determine genomic plasticity. FEBS Letters, 2006, 580, 1277-1284.	2.8	35