

Yong Wang

List of Publications by Year in descending order

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172457

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#	ARTICLE	IF	CITATIONS
1	Conservative Fragments in Bacterial 16S rRNA Genes and Primer Design for 16S Ribosomal DNA Amplicons in Metagenomic Studies. <i>PLoS ONE</i> , 2009, 4, e7401.	2.5	960
2	Sensitivity and correlation of hypervariable regions in 16S rRNA genes in phylogenetic analysis. <i>BMC Bioinformatics</i> , 2016, 17, 135.	2.6	374
3	Pyrosequencing reveals highly diverse and species-specific microbial communities in sponges from the Red Sea. <i>ISME Journal</i> , 2011, 5, 650-664.	9.8	265
4	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
5	Vertical stratification of microbial communities in the Red Sea revealed by 16S rDNA pyrosequencing. <i>ISME Journal</i> , 2011, 5, 507-518.	9.8	151
6	Optimal Eukaryotic 18S and Universal 16S/18S Ribosomal RNA Primers and Their Application in a Study of Symbiosis. <i>PLoS ONE</i> , 2014, 9, e90053.	2.5	104
7	Spatial and Species Variations in Bacterial Communities Associated with Corals from the Red Sea as Revealed by Pyrosequencing. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7173-7184.	3.1	97
8	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
9	Symbiotic Adaptation Drives Genome Streamlining of the Cyanobacterial Sponge Symbiont <i>Candidatus Synechococcus spongiarum</i> . <i>MBio</i> , 2014, 5, e00079-14.	4.1	83
10	Genomic analysis reveals versatile heterotrophic capacity of a potentially symbiotic sulfur-oxidizing bacterium in sponge. <i>Environmental Microbiology</i> , 2014, 16, 3548-3561.	3.8	76
11	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
12	Microbial Sulfur Cycle in Two Hydrothermal Chimneys on the Southwest Indian Ridge. <i>MBio</i> , 2014, 5, e00980-13.	4.1	71
13	Phylogenomics of expanding uncultured environmental Tenericutes provides insights into their pathogenicity and evolutionary relationship with Bacilli. <i>BMC Genomics</i> , 2020, 21, 408.	2.8	65
14	Distinctive Microbial Community Structure in Highly Stratified Deep-Sea Brine Water Columns. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3425-3437.	3.1	57
15	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
16	The mitochondrial genome of the Basidiomycete fungus <i>Pleurotus ostreatus</i> (oyster) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 142 Td	1.8	53
17	In situ environment rather than substrate type dictates microbial community structure of biofilms in a cold seep system. <i>Scientific Reports</i> , 2014, 4, 3587.	3.3	49
18	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

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19	Study of monocyte membrane proteome perturbation during lipopolysaccharide-induced tolerance using iTRAQ-based quantitative proteomic approach. <i>Proteomics</i> , 2010, 10, 2780-2789.	2.2	45
20	Species sorting during biofilm assembly by artificial substrates deployed in a cold seep system. <i>Scientific Reports</i> , 2015, 4, 6647.	3.3	43
21	<i>In situ</i> meta-omic 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
22	Effect of Copper Treatment on the Composition and Function of the Bacterial Community in the Sponge <i>Haliclona cymaeformis</i> . <i>MBio</i> , 2014, 5, e01980.	4.1	39
23	Genomics insights into ecotype formation of ammonia-oxidizing archaea in the deep ocean. <i>Environmental Microbiology</i> , 2019, 21, 716-729.	3.8	39
24	The Enigmatic Genome of an Obligate Ancient Spiroplasma Symbiont in a Hadal Holothurian. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	38
25	Pyrosequencing Reveals the Microbial Communities in the Red Sea Sponge <i>Carteriospongia foliascens</i> and Their Impressive Shifts in Abnormal Tissues. <i>Microbial Ecology</i> , 2014, 68, 621-632.	2.8	37
26	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
27	Long inverted repeats in eukaryotic genomes: Recombinogenic motifs determine genomic plasticity. <i>FEBS Letters</i> , 2006, 580, 1277-1284.	2.8	35
28	Hydrothermally generated aromatic compounds are consumed by bacteria colonizing in Atlantis II Deep of the Red Sea. <i>ISME Journal</i> , 2011, 5, 1652-1659.	9.8	34
29	Adaptation of intertidal biofilm communities is driven by metal ion and oxidative stresses. <i>Scientific Reports</i> , 2013, 3, 3180.	3.3	31
30	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
31	Microbiomes in the Challenger Deep slope and bottom-axis sediments. <i>Nature Communications</i> , 2022, 13, 1515.	12.8	31
32	Diversity and distribution of eukaryotic microbes in and around a brine pool adjacent to the Thuwal cold seeps in the Red Sea. <i>Frontiers in Microbiology</i> , 2014, 5, 37.	3.5	30
33	Hadal water sampling by in situ microbial filtration and fixation (ISMIF) apparatus. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2019, 144, 132-137.	1.4	29
34	Genomic Characterization of a Novel Gut Symbiont From the Hadal Snailfish. <i>Frontiers in Microbiology</i> , 2019, 10, 2978.	3.5	29
35	Molecular Techniques Revealed Highly Diverse Microbial Communities in Natural Marine Biofilms on Polystyrene Dishes for Invertebrate Larval Settlement. <i>Microbial Ecology</i> , 2014, 68, 81-93.	2.8	28
36	Oxidative Weathering and Microbial Diversity of an Inactive Seafloor Hydrothermal Sulfide Chimney. <i>Frontiers in Microbiology</i> , 2017, 8, 1378.	3.5	28

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37	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. <i>Microbial Ecology</i> , 2013, 65, 450-461.	2.8	25
38	Autotrophic Microbe Metagenomes and Metabolic Pathways Differentiate Adjacent Red Sea Brine Pools. <i>Scientific Reports</i> , 2013, 3, 1748.	3.3	25
39	Toward Understanding the Dynamics of Microbial Communities in an Estuarine System. <i>PLoS ONE</i> , 2014, 9, e94449.	2.5	24
40	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
41	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
42	In Silico Prediction of Two Classes of Honeybee Genes with CpG Deficiency or CpG Enrichment and Sorting According to Gene Ontology Classes. <i>Journal of Molecular Evolution</i> , 2009, 68, 700-705.	1.8	21
43	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
44	A study on genomic distribution and sequence features of human long inverted repeats reveals species-specific intronic inverted repeats. <i>FEBS Journal</i> , 2009, 276, 1986-1998.	4.7	19
45	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
46	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
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	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
49	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
50	Functional diversity of microbial communities in inactive seafloor sulfide deposits. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	16
51	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
52	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
53	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
54	Phylogenomic Insights into Distribution and Adaptation of Bdellovibrionota in Marine Waters. <i>Microorganisms</i> , 2021, 9, 757.	3.6	14

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55	Multiple in situ Nucleic Acid Collections (MISNAC) From Deep-Sea Waters. <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	13
56	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
57	Genomic differences within the phylum Marinimicrobia: From waters to sediments in the Mariana Trench. <i>Marine Genomics</i> , 2020, 50, 100699.	1.1	12
58	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
59	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
60	Molecular Characterization of a Novel N-Acetylneuraminate Lyase from a Deep-Sea Symbiotic <i>Mycoplasma</i> . <i>Marine Drugs</i> , 2018, 16, 80.	4.6	10
61	Bacterial Niche-Specific Genome Expansion Is Coupled with Highly Frequent Gene Disruptions in Deep-Sea Sediments. <i>PLoS ONE</i> , 2011, 6, e29149.	2.5	10
62	GC Content Increased at CpG Flanking Positions of Fish Genes Compared with Sea Squirt Orthologs as a Mechanism for Reducing Impact of DNA Methylation. <i>PLoS ONE</i> , 2008, 3, e3612.	2.5	9
63	Effect of polybrominated diphenyl ether (PBDE) treatment on the composition and function of the bacterial community in the sponge <i>Haliclona cymaeformis</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 799.	3.5	9
64	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
65	<i>Deinococcus planocerae</i> sp. nov., isolated from a marine flatworm. <i>Antonie Van Leeuwenhoek</i> , 2017, 110, 811-817.	1.7	8
66	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
67	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
68	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
69	Database for chicken full-length cDNAs. <i>Physiological Genomics</i> , 2007, 28, 141-145.	2.3	4
70	Discovery of a long inverted repeat in human POTE genes. <i>Genomics</i> , 2009, 94, 278-283.	2.9	4
71	Lirex: A Package for Identification of Long Inverted Repeats in Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 141-146.	6.9	4
72	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

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73	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
74	Artifactual pyrosequencing reads in multiple-displacement-amplified sediment metagenomes from the Red Sea. <i>PeerJ</i> , 2013, 1, e69.	2.0	4
75	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. <i>Genomics, Proteomics and Bioinformatics</i> , 2008, 6, 144-154.	6.9	3
76	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
77	Rediscovery of the abyssal species <i>Peniagone leander</i> Pawson and Foell, 1986 (Holothuroidea: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Limnology, 2020, 38, 1319-1327.	1.3	3
78	Acquisition of inverted GSTM exons by an intron of primate GSTM5 gene. <i>Journal of Human Genetics</i> , 2009, 54, 271-276.	2.3	2
79	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
80	Rediscovery of the hadal species <i>Amblyops magnus</i> Birstein & Tchindonova, 1958 (Crustacea: Tj ETQq0 0.0 rgBT /Overlock 10	0.5	2
81	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
82	“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
83	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
84	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
85	Deep-Sea Carbonates Are a Reservoir of Fossil Microbes Previously Inhabiting Cold Seeps. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	1
86	Conserved Regions in 16S Ribosome RNA Sequences and Primer Design for Studies of Environmental Microbes. , 2015, , 106-110.		1