

Sen-Lin Tang

List of Publications by Year in descending order

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98
papers

2,925
citations

147801

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107
docs citations

107
times ranked

3126
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of DNA Polymerase Families: Evidences for Multiple Gene Exchange Between Cellular and Viral Proteins. <i>Journal of Molecular Evolution</i> , 2002, 54, 763-773.	1.8	219
2	Analysis of SD sequences in completed microbial genomes: Non-SD-led genes are as common as SD-led genes. <i>Gene</i> , 2006, 373, 90-99.	2.2	109
3	The dynamics of microbial partnerships in the coral <i>Isopora palifera</i> . <i>ISME Journal</i> , 2011, 5, 728-740.	9.8	105
4	Genomic Insight into the Host-Endosymbiont Relationship of <i>Endozoicomonas montiporae</i> CL-33T with its Coral Host. <i>Frontiers in Microbiology</i> , 2016, 7, 251.	3.5	101
5	Comparative genomics: Dominant coral-bacterium <i>Endozoicomonas acroporae</i> metabolizes dimethylsulfoniopropionate (DMSP). <i>ISME Journal</i> , 2020, 14, 1290-1303.	9.8	96
6	Haloarchaeal viruses: how diverse are they?. <i>Research in Microbiology</i> , 2003, 154, 309-313.	2.1	91
7	Mucus Sugar Content Shapes the Bacterial Community Structure in Thermally Stressed <i>Acropora muricata</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 371.	3.5	86
8	HF2: a double-stranded DNA tailed haloarchaeal virus with a mosaic genome. <i>Molecular Microbiology</i> , 2002, 44, 283-296.	2.5	81
9	Microbial and viral metagenomes of a subtropical freshwater reservoir subject to climatic disturbances. <i>ISME Journal</i> , 2013, 7, 2374-2386.	9.8	81
10	An unsupervised hierarchical dynamic self-organizing approach to cancer class discovery and marker gene identification in microarray data. <i>Bioinformatics</i> , 2003, 19, 2131-2140.	4.1	80
11	Binning sequences using very sparse labels within a metagenome. <i>BMC Bioinformatics</i> , 2008, 9, 215.	2.6	74
12	Influence of Species Specificity and Other Factors on Bacteria Associated with the Coral <i>Stylophora pistillata</i> in Taiwan. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7797-7806.	3.1	73
13	Successive shifts in the microbial community of the surface mucus layer and tissues of the coral <i>Acropora muricata</i> under thermal stress. <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv142.	2.7	70
14	Haloviruses HF1 and HF2: Evidence for a Recent and Large Recombination Event. <i>Journal of Bacteriology</i> , 2004, 186, 2810-2817.	2.2	62
15	Changes in the Soil Bacterial Communities in a Cedar Plantation Invaded by Moso Bamboo. <i>Microbial Ecology</i> , 2014, 67, 421-429.	2.8	62
16	Prevalence of potential nitrogen-fixing, green sulfur bacteria in the skeleton of reef-building coral <i>Stylophora palifera</i> . <i>Limnology and Oceanography</i> , 2016, 61, 1078-1086.	3.1	59
17	Unsupervised discovery of microbial population structure within metagenomes using nucleotide base composition. <i>Nucleic Acids Research</i> , 2012, 40, e34-e34.	14.5	58
18	Bacterial Communities of Three Saline Meromictic Lakes in Central Asia. <i>PLoS ONE</i> , 2016, 11, e0150847.	2.5	56

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19	Metabolic stratification driven by surface and subsurface interactions in a terrestrial mud volcano. ISME Journal, 2012, 6, 2280-2290.	9.8	54
20	Using Growing Self-Organising Maps to Improve the Binning Process in Environmental Whole-Genome Shotgun Sequencing. Journal of Biomedicine and Biotechnology, 2008, 2008, 1-10.	3.0	50
21	Role of flagellins from A and B loci in flagella formation of <i>Halobacterium salinarum</i> . Molecular Microbiology, 2000, 35, 69-78.	2.5	48
22	Anaerobic and aerobic cleavage of the steroid core ring structure by <i>Steroidobacter denitrificans</i> . Journal of Lipid Research, 2013, 54, 1493-1504.	4.2	48
23	Integrated multi-omics analyses reveal the biochemical mechanisms and phylogenetic relevance of anaerobic androgen biodegradation in the environment. ISME Journal, 2016, 10, 1967-1983.	9.8	48
24	Metagenomic, phylogenetic, and functional characterization of predominant endolithic green sulfur bacteria in the coral <i>Isopora palifera</i> . Microbiome, 2019, 7, 3.	11.1	44
25	Bacterial Community Diversity in Undisturbed Perhumid Montane Forest Soils in Taiwan. Microbial Ecology, 2010, 59, 369-378.	2.8	43
26	Long-Term Survey Is Necessary to Reveal Various Shifts of Microbial Composition in Corals. Frontiers in Microbiology, 2017, 8, 1094.	3.5	38
27	PH1: An Archaeovirus of <i>Haloarcula hispanica</i> Related to SH1 and HHIV-2. Archaea, 2013, 2013, 1-17.	2.3	37
28	Metabolic characteristics of dominant microbes and key rare species from an acidic hot spring in Taiwan revealed by metagenomics. BMC Genomics, 2015, 16, 1029.	2.8	37
29	Dynamics of coral-associated bacterial communities acclimated to temperature stress based on recent thermal history. Scientific Reports, 2017, 7, 14933.	3.3	36
30	<i>Endozoicomonas acroporae</i> sp. nov., isolated from <i>Acropora</i> coral. International Journal of Systematic and Evolutionary Microbiology, 2017, 67, 3791-3797.	1.7	34
31	Changes of soil bacterial communities in bamboo plantations at different elevations. FEMS Microbiology Ecology, 2015, 91, .	2.7	33
32	Prokaryotic assemblages and metagenomes in pelagic zones of the South China Sea. BMC Genomics, 2015, 16, 219.	2.8	33
33	Bacteria associated with an encrusting sponge (<i>Terpios hoshinota</i>) and the corals partially covered by the sponge. Environmental Microbiology, 2011, 13, 1179-1191.	3.8	31
34	Marine Microbial Metagenomics: From Individual to the Environment. International Journal of Molecular Sciences, 2014, 15, 8878-8892.	4.1	31
35	<i>Aliidiomarina shirensis</i> sp. nov., a halophilic bacterium isolated from Shira Lake in Khakasia, southern Siberia, and a proposal to transfer <i>Idiomarina maris</i> to the genus <i>Aliidiomarina</i> . International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 1334-1339.	1.7	30
36	Analysis of <i>rbcL</i> sequences reveals the global biodiversity, community structure, and biogeographical pattern of thermoacidophilic red algae (Cyanidiales). Journal of Phycology, 2015, 51, 682-694.	2.3	28

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37	Geographical variations in bacterial communities associated with soft coral <i>Scleronephthya gracillimum</i> . PLoS ONE, 2017, 12, e0183663.	2.5	26
38	2-Oxoacid dehydrogenase multienzyme complexes in the halophilic Archaea? Gene sequences and protein structural predictions The GenBank accession number for the sequence reported in this paper is AF068743.. Microbiology (United Kingdom), 2000, 146, 1061-1069.	1.8	26
39	Differential expression of lipoprotein genes in <i>Mycoplasma pneumoniae</i> after contact with human lung epithelial cells, and under oxidative and acidic stress. BMC Microbiology, 2008, 8, 124.	3.3	25
40	Diversity and Composition of Sulfate- and Sulfite-Reducing Prokaryotes as Affected by Marine-Freshwater Gradient and Sulfate Availability. Microbial Ecology, 2012, 63, 224-237.	2.8	25
41	Characterization of coral-associated microbial aggregates (CAMAs) within tissues of the coral <i>Acropora hyacinthus</i> . Scientific Reports, 2019, 9, 14662.	3.3	23
42	Outbreak of coral-killing cyanobacteriasponge, <i>Terpios hoshinota</i> , in Taiping Island (Itu Aba), Spratlys, South China Sea. Bulletin of Marine Science, 2018, 94, 1543-1544.	0.8	20
43	Lipoprotein Multigene Families in <i>Mycoplasma pneumoniae</i> . Journal of Bacteriology, 2006, 188, 5393-5399.	2.2	19
44	Water flow buffers shifts in bacterial community structure in heat-stressed <i>Acropora muricata</i> . Scientific Reports, 2017, 7, 43600.	3.3	19
45	Terrestrial loads of dissolved organic matter drive inter-annual carbon flux in subtropical lakes during times of drought. Science of the Total Environment, 2020, 717, 137052.	8.0	19
46	<i>Thalassotalea euphylliae</i> sp. nov., isolated from the torch coral <i>Euphyllia glabrescens</i> . International Journal of Systematic and Evolutionary Microbiology, 2016, 66, 5039-5045.	1.7	19
47	The effects of contemporary selection and dispersal limitation on the community assembly of acidophilic microalgae. Journal of Phycology, 2018, 54, 720-733.	2.3	18
48	<i>Coralloluteibacterium stylophorae</i> gen. nov., sp. nov., a new member of the family Lysobacteraceae isolated from the reef-building coral <i>Stylophora</i> sp.. Archives of Microbiology, 2018, 200, 473-481.	2.2	17
49	Bacterial Community in Water and Air of Two Sub-Alpine Lakes in Taiwan. Microbes and Environments, 2018, 33, 120-126.	1.6	17
50	Shifting in the Dominant Bacterial Group <i>Endozoicomonas</i> Is Independent of the Dissociation With Coral Symbiont Algae. Frontiers in Microbiology, 2020, 11, 1791.	3.5	16
51	Population differentiation of Rhodobacteraceae along with coral compartments. ISME Journal, 2021, 15, 3286-3302.	9.8	16
52	Bacterial Community Associated with Organs of Shallow Hydrothermal Vent Crab <i>Xenograpsus testudinatus</i> near Kuishan Island, Taiwan. PLoS ONE, 2016, 11, e0150597.	2.5	16
53	CoMet: a workflow using contig coverage and composition for binning a metagenomic sample with high precision. BMC Bioinformatics, 2017, 18, 571.	2.6	15
54	Removal of nonylphenol by earthworms and bacterial community change. International Biodeterioration and Biodegradation, 2014, 96, 9-17.	3.9	14

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55	Questionable 16S ribosomal RNA gene annotations are frequent in completed microbial genomes. <i>Gene</i> , 2008, 416, 44-47.	2.2	13
56	<i>Methanolobus psychrotolerans</i> sp. nov., a psychrotolerant methanoarchaeon isolated from a saline meromictic lake in Siberia. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1378-1383.	1.7	13
57	Modeling and comparing the organization of circular genomes. <i>Bioinformatics</i> , 2011, 27, 912-918.	4.1	12
58	Complete Genome Sequence of <i>Simiduia agarivorans</i> SA1 T , a Marine Bacterium Able To Degrade a Variety of Polysaccharides. <i>Genome Announcements</i> , 2013, 1, .	0.8	12
59	Complete Genome Sequence of the Extremely Halophilic Archaeon <i>Haloarcula hispanica</i> Strain N601. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
60	Salvaging high-quality genomes of microbial species from a meromictic lake using a hybrid sequencing approach. <i>Communications Biology</i> , 2021, 4, 996.	4.4	12
61	Comprehensive Insights Into Composition, Metabolic Potentials, and Interactions Among Archaeal, Bacterial, and Viral Assemblages in Meromictic Lake Shunet in Siberia. <i>Frontiers in Microbiology</i> , 2018, 9, 1763.	3.5	11
62	Microbiome Restructuring: Dominant Coral Bacterium <i>Endozoicomonas</i> Species Respond Differentially to Environmental Changes. <i>MSystems</i> , 2022, 7, .	3.8	11
63	Gene function prediction based on genomic context clustering and discriminative learning: an application to bacteriophages. <i>BMC Bioinformatics</i> , 2007, 8, S6.	2.6	10
64	Genome classification by gene distribution: An overlapping subspace clustering approach. <i>BMC Evolutionary Biology</i> , 2008, 8, 116.	3.2	10
65	Assessing Species Diversity Using Metavirome Data: Methods and Challenges. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 447-455.	4.1	10
66	Draft Genome Sequence of <i>Endozoicomonas acroporae</i> Strain Acr-14 ^T , Isolated from <i>Acropora</i> Coral. <i>Genome Announcements</i> , 2018, 6, .	0.8	10
67	A Newly Designed Primer Revealed High Phylogenetic Diversity of <i>Endozoicomonas</i> in Coral Reefs. <i>Microbes and Environments</i> , 2018, 33, 172-185.	1.6	10
68	A ubiquitous subcuticular bacterial symbiont of a coral predator, the crown-of-thorns starfish, in the Indo-Pacific. <i>Microbiome</i> , 2020, 8, 123.	11.1	10
69	Absence of winter and spring monsoon changes water level and rapidly shifts metabolism in a subtropical lake. <i>Inland Waters</i> , 2016, 6, 436-448.	2.2	9
70	Vertical distribution of physical–chemical features of water and bottom sediments in four saline lakes of the Khangai mountain region, Western Mongolia. <i>Environmental Earth Sciences</i> , 2017, 76, 1.	2.7	9
71	A Large-Scale Survey of the Bacterial Communities in Lakes of Western Mongolia with Varying Salinity Regimes. <i>Microorganisms</i> , 2020, 8, 1729.	3.6	9
72	Comparative Genomics of Two New HF1-like Haloviruses. <i>Genes</i> , 2020, 11, 405.	2.4	9

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73	The Novel Halovirus Hardycor1, and the Presence of Active (Induced) Proviruses in Four Haloarchaea. <i>Genes</i> , 2021, 12, 149.	2.4	9
74	Locality Effect of Coral-Associated Bacterial Community in the Kuroshio Current From Taiwan to Japan. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	2.2	8
75	Metagenomic sequencing reveals altered bacterial abundance during coral-sponge interaction: Insights into the invasive process of coral-killing sponge <i>Terpios hoshinota</i> . <i>Microbiological Research</i> , 2020, 240, 126553.	5.3	8
76	Monthly progression rates of the coral-killing sponge <i>Terpios hoshinota</i> in Sesoko Island, Okinawa, Japan. <i>Coral Reefs</i> , 2021, 40, 973-981.	2.2	8
77	Four-Year Field Survey of Black Band Disease and Skeletal Growth Anomalies in Encrusting <i>Montipora</i> spp. Corals around Sesoko Island, Okinawa. <i>Diversity</i> , 2022, 14, 32.	1.7	8
78	Gene functionality's influence on the second codon: A large-scale survey of second codon composition in three domains. <i>Genomics</i> , 2010, 96, 92-101.	2.9	7
79	Characterization of Phosphorus in a Toposequence of Subtropical Perhumid Forest Soils Facing a Subalpine Lake. <i>Forests</i> , 2018, 9, 294.	2.1	7
80	Effects of Ocean Acidification on Coral Endolithic Bacterial Communities in <i>Isopora palifera</i> and <i>Porites lobata</i> . <i>Frontiers in Marine Science</i> , 2020, 7, .	2.5	7
81	The Bacteria Endozoicomonas: Community Dynamics, Diversity, Genomes, and Potential Impacts on Corals. , 2019, , 55-67.		6
82	Spatiotemporal Changes in the Bacterial Community of the Meromictic Lake Uchum, Siberia. <i>Microbial Ecology</i> , 2021, 81, 357-369.	2.8	6
83	Potential syntrophic relationship between coral-associated <i>Prosthecochloris</i> and its companion sulfate-reducing bacterium unveiled by genomic analysis. <i>Microbial Genomics</i> , 2021, 7, .	2.0	5
84	Spatial and cross-seasonal patterns of coral diseases in reefs of Taiwan: high prevalence and regional variation. <i>Diseases of Aquatic Organisms</i> , 2021, 146, 145-156.	1.0	4
85	<i>In Vivo</i> Evidence of Single ¹³ C and ¹⁵ N Isotope-Labelled Methanotrophic Nitrogen-Fixing Bacterial Cells in Rice Roots. <i>MBio</i> , 2022, 13, .	4.1	4
86	Accurate reconstruction of viral quasispecies spectra through improved estimation of strain richness. <i>BMC Bioinformatics</i> , 2015, 16, S3.	2.6	3
87	Endolithic Microbes in Coral Skeletons: Algae or Bacteria?. , 2019, , 43-53.		3
88	Insights into gene regulation of the halovirus His2 infecting <i>Haloarcula hispanica</i> . <i>MicrobiologyOpen</i> , 2020, 9, e1016.	3.0	3
89	Aquatic microbial community is partially functionally redundant: Insights from an in situ reciprocal transplant experiment. <i>Science of the Total Environment</i> , 2021, 786, 147433.	8.0	3
90	ENViT: inference of ecological characteristics of viruses from metagenomic data. <i>BMC Bioinformatics</i> , 2019, 19, 377.	2.6	2

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91	Prevalence, complete genome, and metabolic potentials of a phylogenetically novel cyanobacterial symbiont in the coral-killing sponge, <i>Terpios hoshinota</i> . Environmental Microbiology, 2022, 24, 1308-1325.	3.8	2
92	Detection of Pathogenic and Beneficial Microbes for Roselle Wilt Disease. Frontiers in Microbiology, 2021, 12, 756100.	3.5	2
93	Extra high superoxide dismutase in host tissue is associated with improving bleaching resistance in <i>œthermal adapted</i> and <i>Durusdinium trenchii</i> -associating coral. PeerJ, 2022, 10, e12746.	2.0	2
94	Population genetics and demography of the coral-killing cyanobacteriosponge, <i>Terpios hoshinota</i> , in the Indo-West Pacific. PeerJ, 0, 10, e13451.	2.0	2
95	Ocean Currents May Influence the Endolithic Bacterial Composition in Coral Skeletons. Frontiers in Marine Science, 2022, 9, .	2.5	1
96	Single-cell genomics-based analysis reveals a vital ecological role of <i>Thiocapsa</i> sp. LSW in the meromictic Lake Shunet, Siberia. Microbial Genomics, 2021, 7, .	2.0	1
97	Human Body to Water Reservoirs: Estimating Viral Population Characteristics Using High-Throughput Sequencing. , 2018, , 139-155.		0
98	A First Insight Into the Heat-Induced Changes in Proteomic Profiles of the Coral Symbiotic Bacterium <i>Endozoicomonas montiporae</i> . Frontiers in Marine Science, 2022, 9, .	2.5	0