

# Sen-Lin Tang

## List of Publications by Year in descending order

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Version: 2024-02-01

98  
papers

2,925  
citations

147566

31  
h-index

205818

48  
g-index

107  
all docs

107  
docs citations

107  
times ranked

3126  
citing authors

#	ARTICLE	IF	CITATIONS
1	Prevalence, complete genome, and metabolic potentials of a phylogenetically novel cyanobacterial symbiont in the coral-killing sponge, <i>Terpios hoshinota</i> . <i>Environmental Microbiology</i> , 2022, 24, 1308-1325.	1.8	2
2	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.	0.7	8
3	Extra high superoxide dismutase in host tissue is associated with improving bleaching resistance in a thermally adapted <i>Durusdinium trenchii</i> -associating coral. <i>PeerJ</i> , 2022, 10, e12746.	0.9	2
4	A First Insight Into the Heat-Induced Changes in Proteomic Profiles of the Coral Symbiotic Bacterium <i>Endozoicomonas montiporae</i> . <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	0
5	Ocean Currents May Influence the Endolithic Bacterial Composition in Coral Skeletons. <i>Frontiers in Marine Science</i> , 2022, 9, .	1.2	1
6	<i>In Vivo</i> Evidence of Single <sup>13</sup> C and <sup>15</sup> N Isotope- <sup>15</sup> N Labeled Methanotrophic Nitrogen-Fixing Bacterial Cells in Rice Roots. <i>MBio</i> , 2022, 13, .	1.8	4
7	Microbiome Restructuring: Dominant Coral Bacterium <i>Endozoicomonas</i> Species Respond Differentially to Environmental Changes. <i>MSystems</i> , 2022, 7, .	1.7	11
8	Spatiotemporal Changes in the Bacterial Community of the Meromictic Lake Uchum, Siberia. <i>Microbial Ecology</i> , 2021, 81, 357-369.	1.4	6
9	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.	0.5	4
10	The Novel Halovirus Hardycor1, and the Presence of Active (Induced) Proviruses in Four Haloarchaea. <i>Genes</i> , 2021, 12, 149.	1.0	9
11	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.	0.9	8
12	Population differentiation of Rhodobacteraceae along with coral compartments. <i>ISME Journal</i> , 2021, 15, 3286-3302.	4.4	16
13	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, .	1.0	5
14	Salvaging high-quality genomes of microbial species from a meromictic lake using a hybrid sequencing approach. <i>Communications Biology</i> , 2021, 4, 996.	2.0	12
15	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.	3.9	3
16	Detection of Pathogenic and Beneficial Microbes for Roselle Wilt Disease. <i>Frontiers in Microbiology</i> , 2021, 12, 756100.	1.5	2
17	Single-cell genomics-based analysis reveals a vital ecological role of <i>Thiocapsa</i> sp. LSW in the meromictic Lake Shunet, Siberia. <i>Microbial Genomics</i> , 2021, 7, .	1.0	1
18	Locality Effect of Coral-Associated Bacterial Community in the Kuroshio Current From Taiwan to Japan. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	8

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19	Shifting in the Dominant Bacterial Group Endozoicomonas Is Independent of the Dissociation With Coral Symbiont Algae. <i>Frontiers in Microbiology</i> , 2020, 11, 1791.	1.5	16
20	A ubiquitous subcuticular bacterial symbiont of a coral predator, the crown-of-thorns starfish, in the Indo-Pacific. <i>Microbiome</i> , 2020, 8, 123.	4.9	10
21	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, .	1.2	7
22	A Large-Scale Survey of the Bacterial Communities in Lakes of Western Mongolia with Varying Salinity Regimes. <i>Microorganisms</i> , 2020, 8, 1729.	1.6	9
23	Insights into gene regulation of the halovirus His2 infecting <i>Haloarcula hispanica</i> . <i>MicrobiologyOpen</i> , 2020, 9, e1016.	1.2	3
24	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.	2.5	8
25	Terrestrial loads of dissolved organic matter drive inter-annual carbon flux in subtropical lakes during times of drought. <i>Science of the Total Environment</i> , 2020, 717, 137052.	3.9	19
26	Comparative genomics: Dominant coral-bacterium <i>Endozoicomonas acroporae</i> metabolizes dimethylsulfoniopropionate (DMSP). <i>ISME Journal</i> , 2020, 14, 1290-1303.	4.4	96
27	Comparative Genomics of Two New HF1-like Haloviruses. <i>Genes</i> , 2020, 11, 405.	1.0	9
28	Characterization of coral-associated microbial aggregates (CAMAs) within tissues of the coral <i>Acropora hyacinthus</i> . <i>Scientific Reports</i> , 2019, 9, 14662.	1.6	23
29	The Bacteria <i>Endozoicomonas</i> : Community Dynamics, Diversity, Genomes, and Potential Impacts on Corals. , 2019, , 55-67.		6
30	Endolithic Microbes in Coral Skeletons: Algae or Bacteria?. , 2019, , 43-53.		3
31	ENVirT: inference of ecological characteristics of viruses from metagenomic data. <i>BMC Bioinformatics</i> , 2019, 19, 377.	1.2	2
32	Metagenomic, phylogenetic, and functional characterization of predominant endolithic green sulfur bacteria in the coral <i>Isopora palifera</i> . <i>Microbiome</i> , 2019, 7, 3.	4.9	44
33	<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.. <i>Archives of Microbiology</i> , 2018, 200, 473-481.	1.0	17
34	Draft Genome Sequence of <i>Endozoicomonas acroporae</i> Strain Acr-14 <sup>T</sup> , Isolated from <i>Acropora</i> Coral. <i>Genome Announcements</i> , 2018, 6, .	0.8	10
35	Bacterial Community in Water and Air of Two Sub-Alpine Lakes in Taiwan. <i>Microbes and Environments</i> , 2018, 33, 120-126.	0.7	17
36	Outbreak of coral-killing cyanobacteriasponge, <i>Terpios hoshinota</i> , in Taiping Island (Itu Aba), Spratlys, South China Sea. <i>Bulletin of Marine Science</i> , 2018, 94, 1543-1544.	0.4	20

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37	A Newly Designed Primer Revealed High Phylogenetic Diversity of <i>Endozoicomonas</i> in Coral Reefs. <i>Microbes and Environments</i> , 2018, 33, 172-185.	0.7	10
38	The effects of contemporary selection and dispersal limitation on the community assembly of acidophilic microalgae. <i>Journal of Phycology</i> , 2018, 54, 720-733.	1.0	18
39	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.	1.5	11
40	Characterization of Phosphorus in a Toposequence of Subtropical Perhumid Forest Soils Facing a Subalpine Lake. <i>Forests</i> , 2018, 9, 294.	0.9	7
41	Human Body to Water Reservoirs: Estimating Viral Population Characteristics Using High-Throughput Sequencing. , 2018, , 139-155.		0
42	<i>Methanobolus 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.	0.8	13
43	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.	1.3	9
44	Water flow buffers shifts in bacterial community structure in heat-stressed <i>Acropora muricata</i> . <i>Scientific Reports</i> , 2017, 7, 43600.	1.6	19
45	Assessing Species Diversity Using Metavirome Data: Methods and Challenges. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 447-455.	1.9	10
46	CoMet: a workflow using contig coverage and composition for binning a metagenomic sample with high precision. <i>BMC Bioinformatics</i> , 2017, 18, 571.	1.2	15
47	Dynamics of coral-associated bacterial communities acclimated to temperature stress based on recent thermal history. <i>Scientific Reports</i> , 2017, 7, 14933.	1.6	36
48	Long-Term Survey Is Necessary to Reveal Various Shifts of Microbial Composition in Corals. <i>Frontiers in Microbiology</i> , 2017, 8, 1094.	1.5	38
49	Geographical variations in bacterial communities associated with soft coral <i>Scleronephthya gracillimum</i> . <i>PLoS ONE</i> , 2017, 12, e0183663.	1.1	26
50	<i>Endozoicomonas acroporae</i> sp. nov., isolated from <i>Acropora</i> coral. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3791-3797.	0.8	34
51	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.	1.1	9
52	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.	1.5	101
53	Mucus Sugar Content Shapes the Bacterial Community Structure in Thermally Stressed <i>Acropora muricata</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 371.	1.5	86
54	Bacterial Communities of Three Saline Meromictic Lakes in Central Asia. <i>PLoS ONE</i> , 2016, 11, e0150847.	1.1	56

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55	Prevalence of potential nitrogen-fixing, green sulfur bacteria in the skeleton of reef-building coral <i>Solenastrea palifera</i> . <i>Limnology and Oceanography</i> , 2016, 61, 1078-1086.	1.6	59
56	Integrated multi-omics analyses reveal the biochemical mechanisms and phylogenetic relevance of anaerobic androgen biodegradation in the environment. <i>ISME Journal</i> , 2016, 10, 1967-1983.	4.4	48
57	<i>Thalassotalea euphylliae</i> sp. nov., isolated from the torch coral <i>Euphyllia glabrescens</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 5039-5045.	0.8	19
58	Bacterial Community Associated with Organs of Shallow Hydrothermal Vent Crab <i>Xenograpsus testudinatus</i> near Kuishan Island, Taiwan. <i>PLoS ONE</i> , 2016, 11, e0150597.	1.1	16
59	Accurate reconstruction of viral quasispecies spectra through improved estimation of strain richness. <i>BMC Bioinformatics</i> , 2015, 16, S3.	1.2	3
60	Metabolic characteristics of dominant microbes and key rare species from an acidic hot spring in Taiwan revealed by metagenomics. <i>BMC Genomics</i> , 2015, 16, 1029.	1.2	37
61	Analysis of <i>rbcL</i> sequences reveals the global biodiversity, community structure, and biogeographical pattern of thermoacidophilic red algae (Cyanidiales). <i>Journal of Phycology</i> , 2015, 51, 682-694.	1.0	28
62	Changes of soil bacterial communities in bamboo plantations at different elevations. <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	33
63	Prokaryotic assemblages and metagenomes in pelagic zones of the South China Sea. <i>BMC Genomics</i> , 2015, 16, 219.	1.2	33
64	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.	1.3	70
65	Marine Microbial Metagenomics: From Individual to the Environment. <i>International Journal of Molecular Sciences</i> , 2014, 15, 8878-8892.	1.8	31
66	Complete Genome Sequence of the Extremely Halophilic Archaeon <i>Haloarcula hispanica</i> Strain N601. <i>Genome Announcements</i> , 2014, 2, .	0.8	12
67	Changes in the Soil Bacterial Communities in a Cedar Plantation Invaded by Moso Bamboo. <i>Microbial Ecology</i> , 2014, 67, 421-429.	1.4	62
68	Removal of nonylphenol by earthworms and bacterial community change. <i>International Biodeterioration and Biodegradation</i> , 2014, 96, 9-17.	1.9	14
69	<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> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 1334-1339.	0.8	30
70	Microbial and viral metagenomes of a subtropical freshwater reservoir subject to climatic disturbances. <i>ISME Journal</i> , 2013, 7, 2374-2386.	4.4	81
71	Anaerobic and aerobic cleavage of the steroid core ring structure by <i>Steroidobacter denitrificans</i> . <i>Journal of Lipid Research</i> , 2013, 54, 1493-1504.	2.0	48
72	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

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73	PH1: An Archaeovirus of <i>Haloarcula hispanica</i> Related to SH1 and HHIV-2. <i>Archaea</i> , 2013, 2013, 1-17.	2.3	37
74	Unsupervised discovery of microbial population structure within metagenomes using nucleotide base composition. <i>Nucleic Acids Research</i> , 2012, 40, e34-e34.	6.5	58
75	Metabolic stratification driven by surface and subsurface interactions in a terrestrial mud volcano. <i>ISME Journal</i> , 2012, 6, 2280-2290.	4.4	54
76	Diversity and Composition of Sulfate- and Sulfite-Reducing Prokaryotes as Affected by Marine-Freshwater Gradient and Sulfate Availability. <i>Microbial Ecology</i> , 2012, 63, 224-237.	1.4	25
77	Bacteria associated with an encrusting sponge ( <i>Terpios hoshinota</i> ) and the corals partially covered by the sponge. <i>Environmental Microbiology</i> , 2011, 13, 1179-1191.	1.8	31
78	The dynamics of microbial partnerships in the coral <i>Isopora palifera</i> . <i>ISME Journal</i> , 2011, 5, 728-740.	4.4	105
79	Modeling and comparing the organization of circular genomes. <i>Bioinformatics</i> , 2011, 27, 912-918.	1.8	12
80	Bacterial Community Diversity in Undisturbed Perhumid Montane Forest Soils in Taiwan. <i>Microbial Ecology</i> , 2010, 59, 369-378.	1.4	43
81	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.	1.3	7
82	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.	1.4	73
83	Binning sequences using very sparse labels within a metagenome. <i>BMC Bioinformatics</i> , 2008, 9, 215.	1.2	74
84	Genome classification by gene distribution: An overlapping subspace clustering approach. <i>BMC Evolutionary Biology</i> , 2008, 8, 116.	3.2	10
85	Differential expression of lipoprotein genes in <i>Mycoplasma pneumoniae</i> after contact with human lung epithelial cells, and under oxidative and acidic stress. <i>BMC Microbiology</i> , 2008, 8, 124.	1.3	25
86	Questionable 16S ribosomal RNA gene annotations are frequent in completed microbial genomes. <i>Gene</i> , 2008, 416, 44-47.	1.0	13
87	Using Growing Self-Organising Maps to Improve the Binning Process in Environmental Whole-Genome Shotgun Sequencing. <i>Journal of Biomedicine and Biotechnology</i> , 2008, 2008, 1-10.	3.0	50
88	Gene function prediction based on genomic context clustering and discriminative learning: an application to bacteriophages. <i>BMC Bioinformatics</i> , 2007, 8, 56.	1.2	10
89	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.	1.0	109
90	Lipoprotein Multigene Families in <i>Mycoplasma pneumoniae</i> . <i>Journal of Bacteriology</i> , 2006, 188, 5393-5399.	1.0	19

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91	Haloviruses HF1 and HF2: Evidence for a Recent and Large Recombination Event. <i>Journal of Bacteriology</i> , 2004, 186, 2810-2817.	1.0	62
92	Haloarchaeal viruses: how diverse are they?. <i>Research in Microbiology</i> , 2003, 154, 309-313.	1.0	91
93	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.	1.8	80
94	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.	0.8	219
95	HF2: a double-stranded DNA tailed haloarchaeal virus with a mosaic genome. <i>Molecular Microbiology</i> , 2002, 44, 283-296.	1.2	81
96	Role of flagellins from A and B loci in flagella formation of <i>Halobacterium salinarum</i> . <i>Molecular Microbiology</i> , 2000, 35, 69-78.	1.2	48
97	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.. <i>Microbiology (United Kingdom)</i> , 2000, 146, 1061-1069.	0.7	26
98	Population genetics and demography of the coral-killing cyanobacteriosponge, <i>Terpios hoshinota</i> , in the Indo-West Pacific. <i>PeerJ</i> , 0, 10, e13451.	0.9	2