

Torsten Thomas

List of Publications by Year in descending order

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Version: 2024-02-01

103
papers

9,895
citations

38720

50
h-index

38368

95
g-index

109
all docs

109
docs citations

109
times ranked

9547
citing authors

#	ARTICLE	IF	CITATIONS
1	Bacterial community assembly based on functional genes rather than species. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14288-14293.	3.3	768
2	Metagenomics - a guide from sampling to data analysis. Microbial Informatics and Experimentation, 2012, 2, 3.	7.6	680
3	Diversity, structure and convergent evolution of the global sponge microbiome. Nature Communications, 2016, 7, 11870.	5.8	594
4	The seaweed holobiont: understanding seaweed-bacteria interactions. FEMS Microbiology Reviews, 2013, 37, 462-476.	3.9	560
5	Composition, uniqueness and variability of the epiphytic bacterial community of the green alga <i>Ulva australis</i> . ISME Journal, 2011, 5, 590-600.	4.4	361
6	Functional equivalence and evolutionary convergence in complex communities of microbial sponge symbionts. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1878-87.	3.3	361
7	Shifting paradigms: development of high-efficiency biochar fertilizers based on nano-structures and soluble components. Carbon Management, 2013, 4, 323-343.	1.2	310
8	Functional genomic signatures of sponge bacteria reveal unique and shared features of symbiosis. ISME Journal, 2010, 4, 1557-1567.	4.4	278
9	The Sponge Hologenome. MBio, 2016, 7, e00135-16.	1.8	269
10	Marine microbial symbiosis heats up: the phylogenetic and functional response of a sponge holobiont to thermal stress. ISME Journal, 2013, 7, 991-1002.	4.4	266
11	The sponge microbiome project. GigaScience, 2017, 6, 1-7.	3.3	193
12	Predicting the HMA-LMA Status in Marine Sponges by Machine Learning. Frontiers in Microbiology, 2017, 8, 752.	1.5	175
13	Variability and abundance of the epiphytic bacterial community associated with a green marine <i>Ulvacean</i> alga. ISME Journal, 2010, 4, 301-311.	4.4	172
14	Temporal Stability and Composition of the Ocular Surface Microbiome. Scientific Reports, 2017, 7, 9880.	1.6	172
15	Continental-scale variation in seaweed host-associated bacterial communities is a function of host condition, not geography. Environmental Microbiology, 2015, 17, 4078-4088.	1.8	160
16	<i>Phaeobacter gallaeciensis</i> genomes from globally opposite locations reveal high similarity of adaptation to surface life. ISME Journal, 2012, 6, 2229-2244.	4.4	143
17	GemSIM: general, error-model based simulator of next-generation sequencing data. BMC Genomics, 2012, 13, 74.	1.2	143
18	Phylogenetic relationship and antifouling activity of bacterial epiphytes from the marine alga <i>Ulva lactuca</i> . Brief report. Environmental Microbiology, 2000, 2, 343-347.	1.8	137

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19	Metaproteogenomic analysis of a community of sponge symbionts. ISME Journal, 2012, 6, 1515-1525.	4.4	131
20	Microbial indicators of environmental perturbations in coral reef ecosystems. Microbiome, 2019, 7, 94.	4.9	126
21	Analysis of the <i>Pseudoalteromonas tunicata</i> Genome Reveals Properties of a Surface-Associated Life Style in the Marine Environment. PLoS ONE, 2008, 3, e3252.	1.1	126
22	Ankyrin repeat proteins from sponge symbionts modulate amoebal phagocytosis. Molecular Ecology, 2014, 23, 1635-1645.	2.0	124
23	The Electrochemical Properties of Biochars and How They Affect Soil Redox Properties and Processes. Agronomy, 2015, 5, 322-340.	1.3	122
24	Integrated metabolism in sponge-microbe symbiosis revealed by genome-centered metatranscriptomics. ISME Journal, 2017, 11, 1651-1666.	4.4	118
25	Cold stress response in Archaea. Extremophiles, 2000, 4, 321-331.	0.9	115
26	Bacterial pathogens, virulence mechanism and host defence in marine macroalgae. Environmental Microbiology, 2014, 16, 925-938.	1.8	114
27	Multiple opportunistic pathogens can cause a bleaching disease in the red seaweed <i>Delisea pulchra</i> . Environmental Microbiology, 2016, 18, 3962-3975.	1.8	113
28	Coral Probiotics: Premise, Promise, Prospects. Annual Review of Animal Biosciences, 2021, 9, 265-288.	3.6	113
29	Community Structure and Functional Gene Profile of Bacteria on Healthy and Diseased Thalli of the Red Seaweed <i>Delisea pulchra</i> . PLoS ONE, 2012, 7, e50854.	1.1	112
30	A comprehensive analysis of the microbial communities of healthy and diseased marine macroalgae and the detection of known and potential bacterial pathogens. Frontiers in Microbiology, 2015, 6, 146.	1.5	102
31	Future climate change is predicted to affect the microbiome and condition of habitat-forming kelp. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20181887.	1.2	101
32	Genomes and Virulence Factors of Novel Bacterial Pathogens Causing Bleaching Disease in the Marine Red Alga <i>Delisea pulchra</i> . PLoS ONE, 2011, 6, e27387.	1.1	95
33	Modularity and predicted functions of the global sponge-microbiome network. Nature Communications, 2019, 10, 992.	5.8	94
34	Disrupted progression of the intestinal microbiota with age in children with cystic fibrosis. Scientific Reports, 2016, 6, 24857.	1.6	85
35	Gut Microbiota in Children With Cystic Fibrosis: A Taxonomic and Functional Dysbiosis. Scientific Reports, 2019, 9, 18593.	1.6	84
36	Identification of the Antibacterial Compound Produced by the Marine Epiphytic Bacterium <i>Pseudovibrio</i> sp. D323 and Related Sponge-Associated Bacteria. Marine Drugs, 2011, 9, 1391-1402.	2.2	82

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37	Evolution and function of eukaryotic-like proteins from sponge symbionts. <i>Molecular Ecology</i> , 2016, 25, 5242-5253.	2.0	80
38	Biogeography of the human ocular microbiota. <i>Ocular Surface</i> , 2019, 17, 111-118.	2.2	80
39	A horizon scan of priorities for coastal marine microbiome research. <i>Nature Ecology and Evolution</i> , 2019, 3, 1509-1520.	3.4	77
40	Binning_refiner: improving genome bins through the combination of different binning programs. <i>Bioinformatics</i> , 2017, 33, 1873-1875.	1.8	75
41	A Combination of Biochar-Mineral Complexes and Compost Improves Soil Bacterial Processes, Soil Quality, and Plant Properties. <i>Frontiers in Microbiology</i> , 2016, 7, 372.	1.5	73
42	Functional biogeography and host specificity of bacterial communities associated with the Marine Green Alga <i>Ulva</i> spp.. <i>Molecular Ecology</i> , 2018, 27, 1952-1965.	2.0	71
43	Fluorescence in situ hybridization (FISH) and cell sorting of living bacteria. <i>Scientific Reports</i> , 2019, 9, 18618.	1.6	71
44	Measuring continuous compositional change using decline and decay in zeta diversity. <i>Ecology</i> , 2019, 100, e02832.	1.5	69
45	MetaCHIP: community-level horizontal gene transfer identification through the combination of best-match and phylogenetic approaches. <i>Microbiome</i> , 2019, 7, 36.	4.9	69
46	A genomic view of the microbiome of coral reef demosponges. <i>ISME Journal</i> , 2021, 15, 1641-1654.	4.4	67
47	Relating Urban Biodiversity to Human Health With the "Holobiont" Concept. <i>Frontiers in Microbiology</i> , 2019, 10, 550.	1.5	64
48	Comparative Genomics Reveals Ecological and Evolutionary Insights into Sponge-Associated Thaumarchaeota. <i>MSystems</i> , 2019, 4, .	1.7	59
49	Functional genomic analysis of an uncultured γ -proteobacterium in the sponge <i>Cymbastela concentrica</i> . <i>ISME Journal</i> , 2011, 5, 427-435.	4.4	58
50	Long-term succession in a coal seam microbiome during <i>in situ</i> biostimulation of coalbed-methane generation. <i>ISME Journal</i> , 2019, 13, 632-650.	4.4	57
51	Selective Extraction of Bacterial DNA from the Surfaces of Macroalgae. <i>Applied and Environmental Microbiology</i> , 2009, 75, 252-256.	1.4	55
52	Partitioning of functional and taxonomic diversity in surface-associated microbial communities. <i>Environmental Microbiology</i> , 2016, 18, 4391-4402.	1.8	55
53	Expression of eukaryotic-like protein in the microbiome of sponges. <i>Molecular Ecology</i> , 2017, 26, 1432-1451.	2.0	55
54	Changes in the metabolic potential of the sponge microbiome under ocean acidification. <i>Nature Communications</i> , 2019, 10, 4134.	5.8	55

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55	Microbial communities in marine sediments modify success of an invasive macrophyte. <i>Scientific Reports</i> , 2017, 7, 9845.	1.6	52
56	Identification and Visualization of a Distinct Microbiome in Ocular Surface Conjunctival Tissue. , 2018, 59, 4268.		52
57	Expanding our Understanding of the Seaweed Holobiont: RNA Viruses of the Red Alga <i>Delisea pulchra</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 1489.	1.5	49
58	Sample Processing Impacts the Viability and Cultivability of the Sponge Microbiome. <i>Frontiers in Microbiology</i> , 2016, 7, 499.	1.5	49
59	Archaeal cold-adapted proteins: structural and evolutionary analysis of the elongation factor 2 proteins from psychrophilic, mesophilic and thermophilic methanogens 1. <i>FEBS Letters</i> , 1998, 439, 281-286.	1.3	48
60	Genotype to phenotype: Diet-by-mitochondrial DNA haplotype interactions drive metabolic flexibility and organismal fitness. <i>PLoS Genetics</i> , 2018, 14, e1007735.	1.5	46
61	Carrageenans from the Red Seaweed <i>Sarconema filiforme</i> Attenuate Symptoms of Diet-Induced Metabolic Syndrome in Rats. <i>Marine Drugs</i> , 2020, 18, 97.	2.2	45
62	Revegetation of urban green space rewilds soil microbiotas with implications for human health and urban design. <i>Restoration Ecology</i> , 2020, 28, S322.	1.4	43
63	Coal-Packed Methane Biofilter for Mitigation of Green House Gas Emissions from Coal Mine Ventilation Air. <i>PLoS ONE</i> , 2014, 9, e94641.	1.1	43
64	Microbial community function in the bleaching disease of the marine macroalgae <i>Delisea pulchra</i> . <i>Environmental Microbiology</i> , 2017, 19, 3012-3024.	1.8	42
65	Biogeographic variation in the microbiome of the ecologically important sponge, <i>Carteriospongia foliascens</i> . <i>PeerJ</i> , 2015, 3, e1435.	0.9	42
66	Antidiatom and antibacterial activity of epiphytic bacteria isolated from <i>Ulva lactuca</i> in tropical waters. <i>World Journal of Microbiology and Biotechnology</i> , 2011, 27, 1543-1549.	1.7	34
67	Contribution of horizontal gene transfer to the functionality of microbial biofilm on a macroalgae. <i>ISME Journal</i> , 2021, 15, 807-817.	4.4	28
68	A glutathione peroxidase (GpoA) plays a role in the pathogenicity of <i>Nautella italica</i> strain R11 towards the red alga <i>Delisea pulchra</i> . <i>FEMS Microbiology Ecology</i> , 2015, 91, .	1.3	24
69	<i>Phaeobacter inhibens</i> controls bacterial community assembly on a marine diatom. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	24
70	Phylogeny resolved, metabolism revealed: functional radiation within a widespread and divergent clade of sponge symbionts. <i>ISME Journal</i> , 2021, 15, 503-519.	4.4	24
71	Cold Adaptation of Archaeal Elongation Factor 2 (EF-2) Proteins. <i>Current Protein and Peptide Science</i> , 2002, 3, 223-230.	0.7	22
72	The effects of warming and ocean acidification on growth, photosynthesis, and bacterial communities for the marine invasive macroalga <i>Caulerpa taxifolia</i> . <i>Limnology and Oceanography</i> , 2018, 63, 459-471.	1.6	22

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73	Bacterial controlled mitigation of dysbiosis in a seaweed disease. <i>ISME Journal</i> , 2022, 16, 378-387.	4.4	21
74	Below-ground processes control the success of an invasive seaweed. <i>Journal of Ecology</i> , 2018, 106, 2082-2095.	1.9	20
75	<i>Caulerpa lentillifera</i> (Sea Grapes) Improves Cardiovascular and Metabolic Health of Rats with Diet-Induced Metabolic Syndrome. <i>Metabolites</i> , 2020, 10, 500.	1.3	20
76	VarR controls colonization and virulence in the marine macroalgal pathogen <i>Nautella italica</i> R11. <i>Frontiers in Microbiology</i> , 2015, 6, 1130.	1.5	19
77	Effects of Temperature Stress and Aquarium Conditions on the Red Macroalga <i>Delisea pulchra</i> and its Associated Microbial Community. <i>Frontiers in Microbiology</i> , 2016, 7, 161.	1.5	18
78	Effects of different C/N ratios on bacterial compositions and processes in an organically managed soil. <i>Biology and Fertility of Soils</i> , 2018, 54, 137-147.	2.3	15
79	Respiratory microbiota of humpback whales may be reduced in diversity and richness the longer they fast. <i>Scientific Reports</i> , 2020, 10, 12645.	1.6	15
80	Novel ssDNA Viruses Detected in the Virome of Bleached, Habitat-Forming Kelp <i>Ecklonia radiata</i> . <i>Frontiers in Marine Science</i> , 2018, 4, .	1.2	14
81	The surface bacterial community of an Australian kelp shows cross-continental variation and relative stability within regions. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	13
82	Complete genome sequences of pooled genomic DNA from 10 marine bacteria using PacBio long-read sequencing. <i>Marine Genomics</i> , 2019, 48, 100687.	0.4	12
83	Assessing the strength and sensitivity of the core microbiota approach on a highly diverse sponge reef. <i>Environmental Microbiology</i> , 2020, 22, 3985-3999.	1.8	12
84	Comparative metabolomic analysis reveals shared and unique chemical interactions in sponge holobionts. <i>Microbiome</i> , 2022, 10, 22.	4.9	11
85	Detecting signatures of a sponge-associated lifestyle in bacterial genomes. <i>Environmental Microbiology Reports</i> , 2018, 10, 433-443.	1.0	10
86	Interannual comparison of core taxa and community composition of the blow microbiota from East Australian humpback whales. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	10
87	HgtSIM: a simulator for horizontal gene transfer (HGT) in microbial communities. <i>PeerJ</i> , 2017, 5, e4015.	0.9	10
88	The effect of oxidative treatment on soluble compounds from Australian coal. <i>Fuel</i> , 2019, 257, 116071.	3.4	8
89	Bacterial contamination of intravitreal needles by the ocular surface microbiome. <i>Ocular Surface</i> , 2021, 19, 169-175.	2.2	8
90	Editorial for: Microbial symbiosis of marine sessile hosts- diversity and function. <i>Frontiers in Microbiology</i> , 2015, 6, 585.	1.5	7

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91	High-Resolution and Specific Detection of Bacteria on Complex Surfaces Using Nanoparticle Probes and Electron Microscopy. PLoS ONE, 2015, 10, e0126404.	1.1	7
92	Comparative analysis of ocular surface tissue microbiome in human, mouse, rabbit, and guinea pig. Experimental Eye Research, 2021, 207, 108609.	1.2	7
93	Stress response of the marine sponge <i>Scopalina</i> sp.. Can microbial community composition predict sponge disease?. FEMS Microbiology Ecology, 2021, 97, .	1.3	7
94	Differential priority effects impact taxonomy and functionality of host-associated microbiomes. Molecular Ecology, 2023, 32, 6278-6293.	2.0	6
95	MarkerMAG: linking metagenome-assembled genomes (MAGs) with 16S rRNA marker genes using paired-end short reads. Bioinformatics, 2022, 38, 3684-3688.	1.8	6
96	Does sociality drive diversity and composition of airway microbiota in cetaceans?. Environmental Microbiology Reports, 2020, 12, 324-333.	1.0	5
97	Highly abundant core taxa in the blow within and across captive bottlenose dolphins provide evidence for a temporally stable airway microbiota. BMC Microbiology, 2021, 21, 20.	1.3	5
98	Community in microbial stress response and differential metabolic interactions revealed by time-series analysis of sponge symbionts. Environmental Microbiology, 2022, 24, 2299-2314.	1.8	5
99	Characterization of a novel roseophage and the morphological and transcriptional response of the sponge symbiont <i>Ruegeria</i> AU67 to infection. Environmental Microbiology, 2021, 23, 2532-2549.	1.8	4
100	An experimental model for the spatial structuring and selection of bacterial communities. Journal of Microbiological Methods, 2011, 87, 165-168.	0.7	2
101	Rare genera differentiate urban green space soil bacterial communities in three cities across the world. Access Microbiology, 2022, 4, 000320.	0.2	2
102	Spatial compositional turnover varies with trophic level and body size in marine assemblages of micro- and macroorganisms. Global Ecology and Biogeography, 2022, 31, 1556-1570.	2.7	2
103	Detection of carbapenem-resistant bacteria in the public area of a hospital. Journal of Global Antimicrobial Resistance, 2018, 14, 166-168.	0.9	0