

Torsten Thomas

List of Publications by Year in descending order

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Version: 2024-02-01

103
papers

9,895
citations

38742

50
h-index

38395

95
g-index

109
all docs

109
docs citations

109
times ranked

9547
citing authors

#	ARTICLE	IF	CITATIONS
1	Differential priority effects impact taxonomy and functionality of host-associated microbiomes. <i>Molecular Ecology</i> , 2023, 32, 6278-6293.	3.9	6
2	Bacterial controlled mitigation of dysbiosis in a seaweed disease. <i>ISME Journal</i> , 2022, 16, 378-387.	9.8	21
3	Rare genera differentiate urban green space soil bacterial communities in three cities across the world. <i>Access Microbiology</i> , 2022, 4, 000320.	0.5	2
4	Comparative metabolomic analysis reveals shared and unique chemical interactions in sponge holobionts. <i>Microbiome</i> , 2022, 10, 22.	11.1	11
5	Communality in microbial stress response and differential metabolic interactions revealed by time-series analysis of sponge symbionts. <i>Environmental Microbiology</i> , 2022, 24, 2299-2314.	3.8	5
6	Spatial compositional turnover varies with trophic level and body size in marine assemblages of micro- and macroorganisms. <i>Global Ecology and Biogeography</i> , 2022, 31, 1556-1570.	5.8	2
7	MarkerMAG: linking metagenome-assembled genomes (MAGs) with 16S rRNA marker genes using paired-end short reads. <i>Bioinformatics</i> , 2022, 38, 3684-3688.	4.1	6
8	Bacterial contamination of intravitreal needles by the ocular surface microbiome. <i>Ocular Surface</i> , 2021, 19, 169-175.	4.4	8
9	Phylogeny resolved, metabolism revealed: functional radiation within a widespread and divergent clade of sponge symbionts. <i>ISME Journal</i> , 2021, 15, 503-519.	9.8	24
10	Coral Probiotics: Premise, Promise, Prospects. <i>Annual Review of Animal Biosciences</i> , 2021, 9, 265-288.	7.4	113
11	Highly abundant core taxa in the blow within and across captive bottlenose dolphins provide evidence for a temporally stable airway microbiota. <i>BMC Microbiology</i> , 2021, 21, 20.	3.3	5
12	A genomic view of the microbiome of coral reef demosponges. <i>ISME Journal</i> , 2021, 15, 1641-1654.	9.8	67
13	Contribution of horizontal gene transfer to the functionality of microbial biofilm on a macroalgae. <i>ISME Journal</i> , 2021, 15, 807-817.	9.8	28
14	Characterization of a novel roseophage and the morphological and transcriptional response of the sponge symbiont <i>Ruegeria</i> sp. AU67 to infection. <i>Environmental Microbiology</i> , 2021, 23, 2532-2549.	3.8	4
15	The surface bacterial community of an Australian kelp shows cross-continental variation and relative stability within regions. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	13
16	Comparative analysis of ocular surface tissue microbiome in human, mouse, rabbit, and guinea pig. <i>Experimental Eye Research</i> , 2021, 207, 108609.	2.6	7
17	Stress response of the marine sponge <i>Scopalina</i> sp.. Can microbial community composition predict sponge disease?. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	7
18	Respiratory microbiota of humpback whales may be reduced in diversity and richness the longer they fast. <i>Scientific Reports</i> , 2020, 10, 12645.	3.3	15

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19	Assessing the strength and sensitivity of the core microbiota approach on a highly diverse sponge reef. <i>Environmental Microbiology</i> , 2020, 22, 3985-3999.	3.8	12
20	Caulerpa lentillifera (Sea Grapes) Improves Cardiovascular and Metabolic Health of Rats with Diet-Induced Metabolic Syndrome. <i>Metabolites</i> , 2020, 10, 500.	2.9	20
21	Does sociality drive diversity and composition of airway microbiota in cetaceans?. <i>Environmental Microbiology Reports</i> , 2020, 12, 324-333.	2.4	5
22	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.	4.6	45
23	Revegetation of urban green space rewilds soil microbiotas with implications for human health and urban design. <i>Restoration Ecology</i> , 2020, 28, S322.	2.9	43
24	Comparative Genomics Reveals Ecological and Evolutionary Insights into Sponge-Associated <i>Thaumarchaeota</i> . <i>MSystems</i> , 2019, 4, .	3.8	59
25	Measuring continuous compositional change using decline and decay in zeta diversity. <i>Ecology</i> , 2019, 100, e02832.	3.2	69
26	Interannual comparison of core taxa and community composition of the blow microbiota from East Australian humpback whales. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	10
27	A horizon scan of priorities for coastal marine microbiome research. <i>Nature Ecology and Evolution</i> , 2019, 3, 1509-1520.	7.8	77
28	Changes in the metabolic potential of the sponge microbiome under ocean acidification. <i>Nature Communications</i> , 2019, 10, 4134.	12.8	55
29	The effect of oxidative treatment on soluble compounds from Australian coal. <i>Fuel</i> , 2019, 257, 116071.	6.4	8
30	Complete genome sequences of pooled genomic DNA from 10 marine bacteria using PacBio long-read sequencing. <i>Marine Genomics</i> , 2019, 48, 100687.	1.1	12
31	Microbial indicators of environmental perturbations in coral reef ecosystems. <i>Microbiome</i> , 2019, 7, 94.	11.1	126
32	Phaeobacter inhibens controls bacterial community assembly on a marine diatom. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	24
33	MetaCHIP: community-level horizontal gene transfer identification through the combination of best-match and phylogenetic approaches. <i>Microbiome</i> , 2019, 7, 36.	11.1	69
34	Modularity and predicted functions of the global sponge-microbiome network. <i>Nature Communications</i> , 2019, 10, 992.	12.8	94
35	Future climate change is predicted to affect the microbiome and condition of habitat-forming kelp. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20181887.	2.6	101
36	Relating Urban Biodiversity to Human Health With the "Holobiont" Concept. <i>Frontiers in Microbiology</i> , 2019, 10, 550.	3.5	64

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37	Gut Microbiota in Children With Cystic Fibrosis: A Taxonomic and Functional Dysbiosis. Scientific Reports, 2019, 9, 18593.	3.3	84
38	Fluorescence in situ hybridization (FISH) and cell sorting of living bacteria. Scientific Reports, 2019, 9, 18618.	3.3	71
39	Biogeography of the human ocular microbiota. Ocular Surface, 2019, 17, 111-118.	4.4	80
40	Long-term succession in a coal seam microbiome during <i>in situ</i> biostimulation of coalbed-methane generation. ISME Journal, 2019, 13, 632-650.	9.8	57
41	Functional biogeography and host specificity of bacterial communities associated with the Marine Green Alga <i>Ulva</i> spp.. Molecular Ecology, 2018, 27, 1952-1965.	3.9	71
42	Detecting signatures of a sponge-associated lifestyle in bacterial genomes. Environmental Microbiology Reports, 2018, 10, 433-443.	2.4	10
43	Below-ground processes control the success of an invasive seaweed. Journal of Ecology, 2018, 106, 2082-2095.	4.0	20
44	The effects of warming and ocean acidification on growth, photosynthesis, and bacterial communities for the marine invasive macroalga <i>Caulerpa taxifolia</i> . Limnology and Oceanography, 2018, 63, 459-471.	3.1	22
45	Effects of different C/N ratios on bacterial compositions and processes in an organically managed soil. Biology and Fertility of Soils, 2018, 54, 137-147.	4.3	15
46	Genotype to phenotype: Diet-by-mitochondrial DNA haplotype interactions drive metabolic flexibility and organismal fitness. PLoS Genetics, 2018, 14, e1007735.	3.5	46
47	Identification and Visualization of a Distinct Microbiome in Ocular Surface Conjunctival Tissue. , 2018, 59, 4268.		52
48	Detection of carbapenem-resistant bacteria in the public area of a hospital. Journal of Global Antimicrobial Resistance, 2018, 14, 166-168.	2.2	0
49	Novel ssDNA Viruses Detected in the Virome of Bleached, Habitat-Forming Kelp <i>Ecklonia radiata</i> . Frontiers in Marine Science, 2018, 4, .	2.5	14
50	Binning_refiner: improving genome bins through the combination of different binning programs. Bioinformatics, 2017, 33, 1873-1875.	4.1	75
51	Microbial community function in the bleaching disease of the marine macroalgae <i>Delisea pulchra</i> . Environmental Microbiology, 2017, 19, 3012-3024.	3.8	42
52	Integrated metabolism in sponge-microbe symbiosis revealed by genome-centered metatranscriptomics. ISME Journal, 2017, 11, 1651-1666.	9.8	118
53	Expression of eukaryotic-like protein in the microbiome of sponges. Molecular Ecology, 2017, 26, 1432-1451.	3.9	55
54	The sponge microbiome project. GigaScience, 2017, 6, 1-7.	6.4	193

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55	Microbial communities in marine sediments modify success of an invasive macrophyte. Scientific Reports, 2017, 7, 9845.	3.3	52
56	Temporal Stability and Composition of the Ocular Surface Microbiome. Scientific Reports, 2017, 7, 9880.	3.3	172
57	Predicting the HMA-LMA Status in Marine Sponges by Machine Learning. Frontiers in Microbiology, 2017, 8, 752.	3.5	175
58	HgtSIM: a simulator for horizontal gene transfer (HGT) in microbial communities. PeerJ, 2017, 5, e4015.	2.0	10
59	Effects of Temperature Stress and Aquarium Conditions on the Red Macroalga <i>Delisea pulchra</i> and its Associated Microbial Community. Frontiers in Microbiology, 2016, 7, 161.	3.5	18
60	A Combination of Biocharâ€“Mineral Complexes and Compost Improves Soil Bacterial Processes, Soil Quality, and Plant Properties. Frontiers in Microbiology, 2016, 7, 372.	3.5	73
61	Sample Processing Impacts the Viability and Cultivability of the Sponge Microbiome. Frontiers in Microbiology, 2016, 7, 499.	3.5	49
62	Multiple opportunistic pathogens can cause a bleaching disease in the red seaweed <i>Delisea pulchra</i> . Environmental Microbiology, 2016, 18, 3962-3975.	3.8	113
63	Partitioning of functional and taxonomic diversity in surface-associated microbial communities. Environmental Microbiology, 2016, 18, 4391-4402.	3.8	55
64	The Sponge Hologenome. MBio, 2016, 7, e00135-16.	4.1	269
65	Evolution and function of eukaryotic-like proteins from sponge symbionts. Molecular Ecology, 2016, 25, 5242-5253.	3.9	80
66	Diversity, structure and convergent evolution of the global sponge microbiome. Nature Communications, 2016, 7, 11870.	12.8	594
67	Disrupted progression of the intestinal microbiota with age in children with cystic fibrosis. Scientific Reports, 2016, 6, 24857.	3.3	85
68	Continental-scale variation in seaweed host-associated bacterial communities is a function of host condition, not geography. Environmental Microbiology, 2015, 17, 4078-4088.	3.8	160
69	The Electrochemical Properties of Biochars and How They Affect Soil Redox Properties and Processes. Agronomy, 2015, 5, 322-340.	3.0	122
70	Editorial for: Microbial symbiosis of marine sessile hosts- diversity and function. Frontiers in Microbiology, 2015, 6, 585.	3.5	7
71	VarR controls colonization and virulence in the marine macroalgal pathogen <i>Nautella italica</i> R11. Frontiers in Microbiology, 2015, 6, 1130.	3.5	19
72	High-Resolution and Specific Detection of Bacteria on Complex Surfaces Using Nanoparticle Probes and Electron Microscopy. PLoS ONE, 2015, 10, e0126404.	2.5	7

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73	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, .	2.7	24
74	A comprehensive analysis of the microbial communities of healthy and diseased marine macroalgae and the detection of known and potential bacterial pathogens. <i>Frontiers in Microbiology</i> , 2015, 6, 146.	3.5	102
75	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.	3.5	49
76	Biogeographic variation in the microbiome of the ecologically important sponge, <i>Carteriospongia foliascens</i> . <i>PeerJ</i> , 2015, 3, e1435.	2.0	42
77	Ankyrin repeat proteins from sponge symbionts modulate amoebal phagocytosis. <i>Molecular Ecology</i> , 2014, 23, 1635-1645.	3.9	124
78	Bacterial pathogens, virulence mechanism and host defence in marine macroalgae. <i>Environmental Microbiology</i> , 2014, 16, 925-938.	3.8	114
79	Coal-Packed Methane Biofilter for Mitigation of Green House Gas Emissions from Coal Mine Ventilation Air. <i>PLoS ONE</i> , 2014, 9, e94641.	2.5	43
80	Shifting paradigms: development of high-efficiency biochar fertilizers based on nano-structures and soluble components. <i>Carbon Management</i> , 2013, 4, 323-343.	2.4	310
81	The seaweed holobiont: understanding seaweed-bacteria interactions. <i>FEMS Microbiology Reviews</i> , 2013, 37, 462-476.	8.6	560
82	Marine microbial symbiosis heats up: the phylogenetic and functional response of a sponge holobiont to thermal stress. <i>ISME Journal</i> , 2013, 7, 991-1002.	9.8	266
83	Community Structure and Functional Gene Profile of Bacteria on Healthy and Diseased Thalli of the Red Seaweed <i>Delisea pulchra</i> . <i>PLoS ONE</i> , 2012, 7, e50854.	2.5	112
84	Functional equivalence and evolutionary convergence in complex communities of microbial sponge symbionts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1878-87.	7.1	361
85	<i>Phaeobacter gallaeciensis</i> genomes from globally opposite locations reveal high similarity of adaptation to surface life. <i>ISME Journal</i> , 2012, 6, 2229-2244.	9.8	143
86	GemSIM: general, error-model based simulator of next-generation sequencing data. <i>BMC Genomics</i> , 2012, 13, 74.	2.8	143
87	Metaproteogenomic analysis of a community of sponge symbionts. <i>ISME Journal</i> , 2012, 6, 1515-1525.	9.8	131
88	Metagenomics - a guide from sampling to data analysis. <i>Microbial Informatics and Experimentation</i> , 2012, 2, 3.	7.6	680
89	Bacterial community assembly based on functional genes rather than species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14288-14293.	7.1	768
90	Identification of the Antibacterial Compound Produced by the Marine Epiphytic Bacterium <i>Pseudovibrio</i> sp. D323 and Related Sponge-Associated Bacteria. <i>Marine Drugs</i> , 2011, 9, 1391-1402.	4.6	82

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91	An experimental model for the spatial structuring and selection of bacterial communities. Journal of Microbiological Methods, 2011, 87, 165-168.	1.6	2
92	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.	2.5	95
93	Functional genomic analysis of an uncultured β -proteobacterium in the sponge <i>Cymbastela concentrica</i> . ISME Journal, 2011, 5, 427-435.	9.8	58
94	Composition, uniqueness and variability of the epiphytic bacterial community of the green alga <i>Ulva australis</i> . ISME Journal, 2011, 5, 590-600.	9.8	361
95	Antidiatom and antibacterial activity of epiphytic bacteria isolated from <i>Ulva lactuca</i> in tropical waters. World Journal of Microbiology and Biotechnology, 2011, 27, 1543-1549.	3.6	34
96	Variability and abundance of the epiphytic bacterial community associated with a green marine <i>Ulvacean</i> alga. ISME Journal, 2010, 4, 301-311.	9.8	172
97	Functional genomic signatures of sponge bacteria reveal unique and shared features of symbiosis. ISME Journal, 2010, 4, 1557-1567.	9.8	278
98	Selective Extraction of Bacterial DNA from the Surfaces of Macroalgae. Applied and Environmental Microbiology, 2009, 75, 252-256.	3.1	55
99	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.	2.5	126
100	Cold Adaptation of Archaeal Elongation Factor 2 (EF-2) Proteins. Current Protein and Peptide Science, 2002, 3, 223-230.	1.4	22
101	Phylogenetic relationship and antifouling activity of bacterial epiphytes from the marine alga <i>Ulva lactuca</i> . Brief report. Environmental Microbiology, 2000, 2, 343-347.	3.8	137
102	Cold stress response in Archaea. Extremophiles, 2000, 4, 321-331.	2.3	115
103	Archaeal cold-adapted proteins: structural and evolutionary analysis of the elongation factor 2 proteins from psychophilic, mesophilic and thermophilic methanogens 1. FEBS Letters, 1998, 439, 281-286.	2.8	48