

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	Differential priority effects impact taxonomy and functionality of host-associated microbiomes. <i>Molecular Ecology</i> , 2023, 32, 6278-6293.	2.0	6
2	Bacterial controlled mitigation of dysbiosis in a seaweed disease. <i>ISME Journal</i> , 2022, 16, 378-387.	4.4	21
3	Rare genera differentiate urban green space soil bacterial communities in three cities across the world. <i>Access Microbiology</i> , 2022, 4, 000320.	0.2	2
4	Comparative metabolomic analysis reveals shared and unique chemical interactions in sponge holobionts. <i>Microbiome</i> , 2022, 10, 22.	4.9	11
5	Community in microbial stress response and differential metabolic interactions revealed by time-series analysis of sponge symbionts. <i>Environmental Microbiology</i> , 2022, 24, 2299-2314.	1.8	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.	2.7	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.	1.8	6
8	Bacterial contamination of intravitreal needles by the ocular surface microbiome. <i>Ocular Surface</i> , 2021, 19, 169-175.	2.2	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.	4.4	24
10	Coral Probiotics: Premise, Promise, Prospects. <i>Annual Review of Animal Biosciences</i> , 2021, 9, 265-288.	3.6	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.	1.3	5
12	A genomic view of the microbiome of coral reef demosponges. <i>ISME Journal</i> , 2021, 15, 1641-1654.	4.4	67
13	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
14	Characterization of a novel roseophage and the morphological and transcriptional response of the sponge symbiont <i>Ruegeria</i> AU67 to infection. <i>Environmental Microbiology</i> , 2021, 23, 2532-2549.	1.8	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, .	1.3	13
16	Comparative analysis of ocular surface tissue microbiome in human, mouse, rabbit, and guinea pig. <i>Experimental Eye Research</i> , 2021, 207, 108609.	1.2	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, .	1.3	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.	1.6	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.	1.8	12
20	<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
21	Does sociality drive diversity and composition of airway microbiota in cetaceans?. <i>Environmental Microbiology Reports</i> , 2020, 12, 324-333.	1.0	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.	2.2	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.	1.4	43
24	Comparative Genomics Reveals Ecological and Evolutionary Insights into Sponge-Associated <i>Thaumarchaeota</i> . <i>MSystems</i> , 2019, 4, .	1.7	59
25	Measuring continuous compositional change using decline and decay in zeta diversity. <i>Ecology</i> , 2019, 100, e02832.	1.5	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, .	1.3	10
27	A horizon scan of priorities for coastal marine microbiome research. <i>Nature Ecology and Evolution</i> , 2019, 3, 1509-1520.	3.4	77
28	Changes in the metabolic potential of the sponge microbiome under ocean acidification. <i>Nature Communications</i> , 2019, 10, 4134.	5.8	55
29	The effect of oxidative treatment on soluble compounds from Australian coal. <i>Fuel</i> , 2019, 257, 116071.	3.4	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.	0.4	12
31	Microbial indicators of environmental perturbations in coral reef ecosystems. <i>Microbiome</i> , 2019, 7, 94.	4.9	126
32	<i>Phaeobacter inhibens</i> controls bacterial community assembly on a marine diatom. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	24
33	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
34	Modularity and predicted functions of the global sponge-microbiome network. <i>Nature Communications</i> , 2019, 10, 992.	5.8	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.	1.2	101
36	Relating Urban Biodiversity to Human Health With the "Holobiont"™ Concept. <i>Frontiers in Microbiology</i> , 2019, 10, 550.	1.5	64

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37	Gut Microbiota in Children With Cystic Fibrosis: A Taxonomic and Functional Dysbiosis. <i>Scientific Reports</i> , 2019, 9, 18593.	1.6	84
38	Fluorescence in situ hybridization (FISH) and cell sorting of living bacteria. <i>Scientific Reports</i> , 2019, 9, 18618.	1.6	71
39	Biogeography of the human ocular microbiota. <i>Ocular Surface</i> , 2019, 17, 111-118.	2.2	80
40	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
41	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
42	Detecting signatures of a sponge-associated lifestyle in bacterial genomes. <i>Environmental Microbiology Reports</i> , 2018, 10, 433-443.	1.0	10
43	Below-ground processes control the success of an invasive seaweed. <i>Journal of Ecology</i> , 2018, 106, 2082-2095.	1.9	20
44	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
45	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
46	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
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. <i>Journal of Global Antimicrobial Resistance</i> , 2018, 14, 166-168.	0.9	0
49	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
50	Binning_refiner: improving genome bins through the combination of different binning programs. <i>Bioinformatics</i> , 2017, 33, 1873-1875.	1.8	75
51	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
52	Integrated metabolism in sponge-microbe symbiosis revealed by genome-centered metatranscriptomics. <i>ISME Journal</i> , 2017, 11, 1651-1666.	4.4	118
53	Expression of eukaryotic-like protein in the microbiome of sponges. <i>Molecular Ecology</i> , 2017, 26, 1432-1451.	2.0	55
54	The sponge microbiome project. <i>GigaScience</i> , 2017, 6, 1-7.	3.3	193

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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	Temporal Stability and Composition of the Ocular Surface Microbiome. <i>Scientific Reports</i> , 2017, 7, 9880.	1.6	172
57	Predicting the HMA-LMA Status in Marine Sponges by Machine Learning. <i>Frontiers in Microbiology</i> , 2017, 8, 752.	1.5	175
58	HgtSIM: a simulator for horizontal gene transfer (HGT) in microbial communities. <i>PeerJ</i> , 2017, 5, e4015.	0.9	10
59	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
60	A Combination of Biocharâ€“Mineral Complexes and Compost Improves Soil Bacterial Processes, Soil Quality, and Plant Properties. <i>Frontiers in Microbiology</i> , 2016, 7, 372.	1.5	73
61	Sample Processing Impacts the Viability and Cultivability of the Sponge Microbiome. <i>Frontiers in Microbiology</i> , 2016, 7, 499.	1.5	49
62	Multiple opportunistic pathogens can cause a bleaching disease in the red seaweed <i>Delisea pulchra</i> . <i>Environmental Microbiology</i> , 2016, 18, 3962-3975.	1.8	113
63	Partitioning of functional and taxonomic diversity in surface-associated microbial communities. <i>Environmental Microbiology</i> , 2016, 18, 4391-4402.	1.8	55
64	The Sponge Hologenome. <i>MBio</i> , 2016, 7, e00135-16.	1.8	269
65	Evolution and function of eukaryotic-like proteins from sponge symbionts. <i>Molecular Ecology</i> , 2016, 25, 5242-5253.	2.0	80
66	Diversity, structure and convergent evolution of the global sponge microbiome. <i>Nature Communications</i> , 2016, 7, 11870.	5.8	594
67	Disrupted progression of the intestinal microbiota with age in children with cystic fibrosis. <i>Scientific Reports</i> , 2016, 6, 24857.	1.6	85
68	Continental-scale variation in seaweed host-associated bacterial communities is a function of host condition, not geography. <i>Environmental Microbiology</i> , 2015, 17, 4078-4088.	1.8	160
69	The Electrochemical Properties of Biochars and How They Affect Soil Redox Properties and Processes. <i>Agronomy</i> , 2015, 5, 322-340.	1.3	122
70	Editorial for: Microbial symbiosis of marine sessile hosts- diversity and function. <i>Frontiers in Microbiology</i> , 2015, 6, 585.	1.5	7
71	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
72	High-Resolution and Specific Detection of Bacteria on Complex Surfaces Using Nanoparticle Probes and Electron Microscopy. <i>PLoS ONE</i> , 2015, 10, e0126404.	1.1	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, .	1.3	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.	1.5	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.	1.5	49
76	Biogeographic variation in the microbiome of the ecologically important sponge, <i>Carteriospongia foliascens</i> . <i>PeerJ</i> , 2015, 3, e1435.	0.9	42
77	Ankyrin repeat proteins from sponge symbionts modulate amoebal phagocytosis. <i>Molecular Ecology</i> , 2014, 23, 1635-1645.	2.0	124
78	Bacterial pathogens, virulence mechanism and host defence in marine macroalgae. <i>Environmental Microbiology</i> , 2014, 16, 925-938.	1.8	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.	1.1	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.	1.2	310
81	The seaweed holobiont: understanding seaweed-bacteria interactions. <i>FEMS Microbiology Reviews</i> , 2013, 37, 462-476.	3.9	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.	4.4	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.	1.1	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.	3.3	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.	4.4	143
86	GemSIM: general, error-model based simulator of next-generation sequencing data. <i>BMC Genomics</i> , 2012, 13, 74.	1.2	143
87	Metaproteogenomic analysis of a community of sponge symbionts. <i>ISME Journal</i> , 2012, 6, 1515-1525.	4.4	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.	3.3	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.	2.2	82

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91	An experimental model for the spatial structuring and selection of bacterial communities. <i>Journal of Microbiological Methods</i> , 2011, 87, 165-168.	0.7	2
92	Genomes and Virulence Factors of Novel Bacterial Pathogens Causing Bleaching Disease in the Marine Red Alga <i>Delisea pulchra</i> . <i>PLoS ONE</i> , 2011, 6, e27387.	1.1	95
93	Functional genomic analysis of an uncultured $\hat{\Gamma}$ -proteobacterium in the sponge <i>Cymbastela concentrica</i> . <i>ISME Journal</i> , 2011, 5, 427-435.	4.4	58
94	Composition, uniqueness and variability of the epiphytic bacterial community of the green alga <i>Ulva australis</i> . <i>ISME Journal</i> , 2011, 5, 590-600.	4.4	361
95	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
96	Variability and abundance of the epiphytic bacterial community associated with a green marine <i>Ulvacean</i> alga. <i>ISME Journal</i> , 2010, 4, 301-311.	4.4	172
97	Functional genomic signatures of sponge bacteria reveal unique and shared features of symbiosis. <i>ISME Journal</i> , 2010, 4, 1557-1567.	4.4	278
98	Selective Extraction of Bacterial DNA from the Surfaces of Macroalgae. <i>Applied and Environmental Microbiology</i> , 2009, 75, 252-256.	1.4	55
99	Analysis of the <i>Pseudoalteromonas tunicata</i> Genome Reveals Properties of a Surface-Associated Life Style in the Marine Environment. <i>PLoS ONE</i> , 2008, 3, e3252.	1.1	126
100	Cold Adaptation of Archaeal Elongation Factor 2 (EF-2) Proteins. <i>Current Protein and Peptide Science</i> , 2002, 3, 223-230.	0.7	22
101	Phylogenetic relationship and antifouling activity of bacterial epiphytes from the marine alga <i>Ulva lactuca</i> . Brief report. <i>Environmental Microbiology</i> , 2000, 2, 343-347.	1.8	137
102	Cold stress response in Archaea. <i>Extremophiles</i> , 2000, 4, 321-331.	0.9	115
103	Archaeal cold-adapted proteins: structural and evolutionary analysis of the elongation factor 2 proteins from psychophilic, mesophilic and thermophilic methanogens 1. <i>FEBS Letters</i> , 1998, 439, 281-286.	1.3	48