

Michael W Taylor

List of Publications by Year in descending order

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Version: 2024-02-01

97
papers

11,649
citations

50170

46
h-index

39575

94
g-index

102
all docs

102
docs citations

102
times ranked

10029
citing authors

#	ARTICLE	IF	CITATIONS
1	Sponge-Associated Microorganisms: Evolution, Ecology, and Biotechnological Potential. <i>Microbiology and Molecular Biology Reviews</i> , 2007, 71, 295-347.	2.9	1,254
2	Deciphering the evolution and metabolism of an anammox bacterium from a community genome. <i>Nature</i> , 2006, 440, 790-794.	13.7	1,075
3	Diversity, structure and convergent evolution of the global sponge microbiome. <i>Nature Communications</i> , 2016, 7, 11870.	5.8	594
4	Genomic insights into the marine sponge microbiome. <i>Nature Reviews Microbiology</i> , 2012, 10, 641-654.	13.6	530
5	Marine sponges as microbial fermenters. <i>FEMS Microbiology Ecology</i> , 2006, 55, 167-177.	1.3	521
6	Assessing the complex sponge microbiota: core, variable and species-specific bacterial communities in marine sponges. <i>ISME Journal</i> , 2012, 6, 564-576.	4.4	508
7	Marine sponges and their microbial symbionts: love and other relationships. <i>Environmental Microbiology</i> , 2012, 14, 335-346.	1.8	491
8	Deep sequencing reveals exceptional diversity and modes of transmission for bacterial sponge symbionts. <i>Environmental Microbiology</i> , 2010, 12, 2070-2082.	1.8	394
9	Characterizing the avian gut microbiota: membership, driving influences, and potential function. <i>Frontiers in Microbiology</i> , 2014, 5, 223.	1.5	328
10	Could some coral reefs become sponge reefs as our climate changes?. <i>Global Change Biology</i> , 2013, 19, 2613-2624.	4.2	261
11	Sponge-specific clusters revisited: a comprehensive phylogeny of sponge-associated microorganisms. <i>Environmental Microbiology</i> , 2012, 14, 517-524.	1.8	253
12	Host specificity in marine sponge-associated bacteria, and potential implications for marine microbial diversity. <i>Environmental Microbiology</i> , 2004, 6, 121-130.	1.8	227
13	Wastewater treatment: a model system for microbial ecology. <i>Trends in Biotechnology</i> , 2006, 24, 483-489.	4.9	216
14	Exploring the avian gut microbiota: current trends and future directions. <i>Frontiers in Microbiology</i> , 2015, 6, 673.	1.5	216
15	Comparative Analyses of Vertebrate Gut Microbiomes Reveal Convergence between Birds and Bats. <i>MBio</i> , 2020, 11, .	1.8	204
16	The sponge microbiome project. <i>GigaScience</i> , 2017, 6, 1-7.	3.3	193
17	Evaluating the core microbiota in complex communities: A systematic investigation. <i>Environmental Microbiology</i> , 2017, 19, 1450-1462.	1.8	187
18	The microbiome in threatened species conservation. <i>Biological Conservation</i> , 2019, 229, 85-98.	1.9	185

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19	Bacterial community collapse: a meta-analysis of the sinonasal microbiota in chronic rhinosinusitis. <i>Environmental Microbiology</i> , 2017, 19, 381-392.	1.8	174
20	“Sponge-specific” bacteria are widespread (but rare) in diverse marine environments. <i>ISME Journal</i> , 2013, 7, 438-443.	4.4	161
21	Evaluating variation in human gut microbiota profiles due to DNA extraction method and inter-subject differences. <i>Frontiers in Microbiology</i> , 2015, 6, 130.	1.5	152
22	The nasal microbiota in health and disease: variation within and between subjects. <i>Frontiers in Microbiology</i> , 2015, 9, .	1.5	145
23	Pyrosequencing reveals regional differences in fruit-associated fungal communities. <i>Environmental Microbiology</i> , 2014, 16, 2848-2858.	1.8	143
24	Evidence of microbiota dysbiosis in chronic rhinosinusitis. <i>International Forum of Allergy and Rhinology</i> , 2017, 7, 230-239.	1.5	143
25	Activity profiles for marine sponge-associated bacteria obtained by 16S rRNA vs 16S rRNA gene comparisons. <i>ISME Journal</i> , 2010, 4, 498-508.	4.4	132
26	Diversity and mode of transmission of ammonia-oxidizing archaea in marine sponges. <i>Environmental Microbiology</i> , 2008, 10, 1087-1094.	1.8	127
27	Bacterial community profiles in low microbial abundance sponges. <i>FEMS Microbiology Ecology</i> , 2013, 83, 232-241.	1.3	127
28	Biogeography of bacteria associated with the marine sponge <i>Cymbastela concentrica</i> . <i>Environmental Microbiology</i> , 2005, 7, 419-433.	1.8	124
29	Evaluating the Impact of DNA Extraction Method on the Representation of Human Oral Bacterial and Fungal Communities. <i>PLoS ONE</i> , 2017, 12, e0169877.	1.1	115
30	Chronic Rhinosinusitis and the Evolving Understanding of Microbial Ecology in Chronic Inflammatory Mucosal Disease. <i>Clinical Microbiology Reviews</i> , 2017, 30, 321-348.	5.7	103
31	Evidence for Acyl Homoserine Lactone Signal Production in Bacteria Associated with Marine Sponges. <i>Applied and Environmental Microbiology</i> , 2004, 70, 4387-4389.	1.4	100
32	Successional development of biofilms in moving bed biofilm reactor (MBBR) systems treating municipal wastewater. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 1429-1440.	1.7	99
33	Genomic and phenotypic insights into the ecology of <i>Arthrobacter</i> from Antarctic soils. <i>BMC Genomics</i> , 2015, 16, 36.	1.2	99
34	Thermal stress responses in the bacterial biosphere of the <i>Geobacter</i> carrier reef sponge, <i>Haloploides odorabile</i> . <i>Environmental Microbiology</i> , 2012, 14, 3232-3246.	1.8	93
35	Influence of environmental variation on symbiotic bacterial communities of two temperate sponges. <i>FEMS Microbiology Ecology</i> , 2014, 88, 516-527.	1.3	91
36	Ability of Arkansas LaKast and LaKast Hybrid Rice Bran to Reduce <i>Salmonella Typhimurium</i> in Chicken Cecal Incubations and Effects on Cecal Microbiota. <i>Frontiers in Microbiology</i> , 2015, 9, 134.	1.5	89

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37	â€Candidatus Protochlamydia amoebophilaâ€™™, an endosymbiont of Acanthamoeba spp.. International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 1863-1866.	0.8	88
38	Soaking it up: the complex lives of marine sponges and their microbial associates. ISME Journal, 2007, 1, 187-190.	4.4	86
39	Characterizing the Human Mycobiota: A Comparison of Small Subunit rRNA, ITS1, ITS2, and Large Subunit rRNA Genomic Targets. Frontiers in Microbiology, 2018, 9, 2208.	1.5	79
40	Gut Microbiome of the Critically Endangered New Zealand Parrot, the Kakapo (Strigops habroptilus). PLoS ONE, 2012, 7, e35803.	1.1	75
41	Chloroflexi bacteria are more diverse, abundant, and similar in high than in low microbial abundance sponges. FEMS Microbiology Ecology, 2011, 78, 497-510.	1.3	73
42	Application of Diffusion Growth Chambers for the Cultivation of Marine Sponge-Associated Bacteria. Marine Biotechnology, 2014, 16, 594-603.	1.1	72
43	Sponge-Microbe Associations Survive High Nutrients and Temperatures. PLoS ONE, 2012, 7, e52220.	1.1	72
44	Deep sequencing reveals diversity and community structure of complex microbiota in five Mediterranean sponges. Hydrobiologia, 2012, 687, 341-351.	1.0	68
45	In four shallow and mesophotic tropical reef sponges from Guam the microbial community largely depends on host identity. PeerJ, 2016, 4, e1936.	0.9	62
46	Climate change alterations to ecosystem dominance: how might spongeâ€™dominated reefs function?. Ecology, 2018, 99, 1920-1931.	1.5	56
47	Microbial community dynamics in Inferno Crater Lake, a thermally fluctuating geothermal spring. ISME Journal, 2017, 11, 1158-1167.	4.4	53
48	Molecular Microbiological Profile of Chronic Suppurative Otitis Media. Journal of Clinical Microbiology, 2016, 54, 2538-2546.	1.8	48
49	Inflammatory Endotypes and Microbial Associations in Chronic Rhinosinusitis. Frontiers in Immunology, 2018, 9, 2065.	2.2	48
50	Evolutionary Insights from Sponges. Science, 2007, 316, 1854-1855.	6.0	47
51	Longitudinal study of the bacterial and fungal microbiota in the human sinuses reveals seasonal and annual changes in diversity. Scientific Reports, 2019, 9, 17416.	1.6	44
52	Paired analysis of the microbiota of surface mucus and wholeâ€™tissue specimens in patients with chronic rhinosinusitis. International Forum of Allergy and Rhinology, 2015, 5, 877-883.	1.5	43
53	Oral microbial influences on oral mucositis during radiotherapy treatment of head and neck cancer. Supportive Care in Cancer, 2020, 28, 2683-2691.	1.0	43
54	Influence of Hand Rearing and Bird Age on the Fecal Microbiota of the Critically Endangered Kakapo. Applied and Environmental Microbiology, 2014, 80, 4650-4658.	1.4	42

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55	Microbial and inflammatory-based salivary biomarkers of head and neck squamous cell carcinoma. <i>Clinical and Experimental Dental Research</i> , 2018, 4, 255-262.	0.8	42
56	Temporal molecular and isotopic analysis of active bacterial communities in two New Zealand sponges. <i>FEMS Microbiology Ecology</i> , 2013, 85, 195-205.	1.3	41
57	Integrity of the Human Faecal Microbiota following Long-Term Sample Storage. <i>PLoS ONE</i> , 2016, 11, e0163666.	1.1	41
58	Evaluating methods for the preservation and extraction of DNA and RNA for analysis of microbial communities in marine sponges. <i>Journal of Experimental Marine Biology and Ecology</i> , 2011, 397, 38-43.	0.7	36
59	Phylogeny and genomics of SAUL, an enigmatic bacterial lineage frequently associated with marine sponges. <i>Environmental Microbiology</i> , 2018, 20, 561-576.	1.8	32
60	Genome-Based Comparative Analyses of Antarctic and Temperate Species of <i>Paenibacillus</i> . <i>PLoS ONE</i> , 2014, 9, e108009.	1.1	32
61	Diverse Honeydew-Consuming Fungal Communities Associated with Scale Insects. <i>PLoS ONE</i> , 2013, 8, e70316.	1.1	31
62	<i>Paenibacillus darwinianus</i> sp. nov., isolated from gamma-irradiated Antarctic soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2014, 64, 1406-1411.	0.8	29
63	Diversity of Actinobacteria Associated with the Marine Ascidian <i>Eudistoma toaealensis</i> . <i>Marine Biotechnology</i> , 2015, 17, 377-385.	1.1	28
64	Differentially Regulated Host Proteins Associated with Chronic Rhinosinusitis Are Correlated with the Sinonasal Microbiome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 504.	1.8	25
65	Comparison of Subtyping Approaches and the Underlying Drivers of Microbial Signatures for Chronic Rhinosinusitis. <i>MSphere</i> , 2019, 4, .	1.3	23
66	dsrAB-based analysis of sulphate-reducing bacteria in moving bed biofilm reactor (MBBR) wastewater treatment plants. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 7211-7222.	1.7	20
67	Redefining the sponge-symbiont acquisition paradigm: sponge microbes exhibit chemotaxis towards host-derived compounds. <i>Environmental Microbiology Reports</i> , 2017, 9, 750-755.	1.0	20
68	The effect of medical treatments on the bacterial microbiome in patients with chronic rhinosinusitis: a pilot study. <i>International Forum of Allergy and Rhinology</i> , 2018, 8, 890-899.	1.5	20
69	Antibiotic Treatment for Chronic Rhinosinusitis: Prescription Patterns and Associations With Patient Outcome and the Sinus Microbiota. <i>Frontiers in Microbiology</i> , 2020, 11, 595555.	1.5	20
70	Use of solid-phase extraction to enable enhanced detection of acyl homoserine lactones (AHLs) in environmental samples. <i>Analytical and Bioanalytical Chemistry</i> , 2005, 383, 132-137.	1.9	19
71	Quantifying the impact of storage procedures for faecal bacteriotherapy in the critically endangered New Zealand Parrot, the Kakapo (<i>Strigops habroptilus</i>). <i>Zoo Biology</i> , 2013, 32, 620-625.	0.5	19
72	Detection and quantification of <i>Staphylococcus</i> in chronic rhinosinusitis. <i>International Forum of Allergy and Rhinology</i> , 2019, 9, 1462-1469.	1.5	19

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73	Ultrastructural and molecular characterization of a bacterial symbiosis in the ecologically important scale insect family Coelostomidiidae. <i>FEMS Microbiology Ecology</i> , 2012, 81, 537-546.	1.3	18
74	The sinonasal microbiota, neural signaling, and depression in chronic rhinosinusitis. <i>International Forum of Allergy and Rhinology</i> , 2018, 8, 394-405.	1.5	18
75	Meeting Report: 1st International Symposium on Sponge Microbiology. <i>Marine Biotechnology</i> , 2011, 13, 1057-1061.	1.1	17
76	Primary symbiont of the ancient scale insect family Coelostomidiidae exhibits strict cophylogenetic patterns. <i>Symbiosis</i> , 2013, 61, 77-91.	1.2	16
77	Microbial community structure in the gut of the New Zealand insect Auckland tree weta (<i>Hemideina tjiriki</i>) is robust to anthropogenic dietary and geographic influences. <i>Frontiers in Microbiology</i> , 2017, 8, 2033.	1.5	15
78	The Low-Diversity Fecal Microbiota of the Critically Endangered Kākāpō is Robust to Anthropogenic Dietary and Geographic Influences. <i>Frontiers in Microbiology</i> , 2017, 8, 2033.	1.5	15
79	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
80	Network-guided genomic and metagenomic analysis of the faecal microbiota of the critically endangered kakapo. <i>Scientific Reports</i> , 2018, 8, 8128.	1.6	11
81	Randomised, double-blind, placebo-controlled trial of oral probiotic <i>Streptococcus salivarius</i> M18 on head and neck cancer patients post-radiotherapy: a pilot study. <i>Scientific Reports</i> , 2020, 10, 13201.	1.6	11
82	A Novel Description of the Human Sinus Archaeome During Health and Chronic Rhinosinusitis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 398.	1.8	8
83	Devil in the detail: a closer look at childhood obesity and the gut microbiota. <i>Environmental Microbiology</i> , 2017, 19, 11-12.	1.8	7
84	Characterising clinical <i>Staphylococcus aureus</i> isolates from the sinuses of patients with chronic rhinosinusitis. <i>Scientific Reports</i> , 2021, 11, 21940.	1.6	6
85	Gut microbiota of the threatened takahē: biogeographic patterns and conservation implications. <i>Animal Microbiome</i> , 2022, 4, 11.	1.5	6
86	Embracing the cooperative society to better understand assembly of the gut microbiota. <i>Environmental Microbiology</i> , 2017, 19, 2924-2925.	1.8	5
87	The airway microbiota in children newly diagnosed with bronchiectasis largely retains its diversity. <i>European Respiratory Journal</i> , 2019, 54, 1900704.	3.1	5
88	Multimic analysis identifies natural inpatient temporal variability and changes in response to systemic corticosteroid therapy in chronic rhinosinusitis. <i>Immunity, Inflammation and Disease</i> , 2021, 9, 90-107.	1.3	5
89	Bacterial Signatures of Paediatric Respiratory Disease: An Individual Participant Data Meta-Analysis. <i>Frontiers in Microbiology</i> , 2021, 12, 711134.	1.5	5
90	The New Zealand minds for autism spectrum disorder self-reported cohort. <i>Research in Autism Spectrum Disorders</i> , 2017, 36, 1-7.	0.8	4

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91	Dynamic Upper and Lower Airway Microbiotas in Paediatric Bronchiectasis Exacerbations: A Pilot Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 773496.	1.8	4
92	Isotopic-labelling methods for deciphering the function of uncultured micro-organisms. , 0, , 1-10.		2
93	Impact of explantation techniques on the microbiota of the marine sponge <i>Ecionemia alata</i> . <i>Journal of Experimental Marine Biology and Ecology</i> , 2016, 484, 11-15.	0.7	2
94	Assessing tissue transcription biomarkers of chronic rhinosinusitis: a comparison of sampling methodologies. <i>International Forum of Allergy and Rhinology</i> , 2020, 10, 1057-1064.	1.5	1
95	What Thrives Inside; The World Within the Gut. <i>Frontiers for Young Minds</i> , 2017, 5, .	0.8	0
96	Moving beyond descriptions of diversity: clinical and research implications of bacterial imbalance in chronic rhinosinusitis. <i>Rhinology</i> , 2017, 55, 291-297.	0.7	0
97	Unilateral Intervention in the Sinuses of Rabbits Induces Bilateral Inflammatory and Microbial Changes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 585625.	1.8	0