Michael W Taylor

List of Publications by Year
in descending order

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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	Gut microbiota of the threatened takahÄ“: biogeographic patterns and conservation implications. Animal Microbiome, 2022, 4, 11.	1.5	6
2	Multiomic analysis identifies natural intrapatient temporal variability and changes in response to systemic corticosteroid therapy in chronic rhinosinusitis. Immunity, Inflammation and Disease, 2021, 9, 90-107.	1.3	5
3	Unilateral Intervention in the Sinuses of Rabbits Induces Bilateral Inflammatory and Microbial Changes. Frontiers in Cellular and Infection Microbiology, 2021, 11, 585625.	1.8	0
4	Characterising clinical Staphylococcus aureus isolates from the sinuses of patients with chronic rhinosinusitis. Scientific Reports, 2021, 11, 21940.	1.6	6
5	Dynamic Upper and Lower Airway Microbiotas in Paediatric Bronchiectasis Exacerbations: A Pilot Study. Frontiers in Cellular and Infection Microbiology, 2021, 11, 773496.	1.8	4
6	Bacterial Signatures of Paediatric Respiratory Disease: An Individual Participant Data Meta-Analysis. Frontiers in Microbiology, 2021, 12, 711134.	1.5	5
7	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
8	Assessing tissue transcription biomarkers of chronic rhinosinusitis: a comparison of sampling methodologies. International Forum of Allergy and Rhinology, 2020, 10, 1057-1064.	1.5	1
9	A Novel Description of the Human Sinus Archaeome During Health and Chronic Rhinosinusitis. Frontiers in Cellular and Infection Microbiology, 2020, 10, 398.	1.8	8
10	Assessing the strength and sensitivity of the core microbiota approach on a highly diverse sponge reef. Environmental Microbiology, 2020, 22, 3985-3999.	1.8	12
11	Randomised, double-blind, placebo-controlled trial of oral probiotic Streptococcus salivarius M18 on head and neck cancer patients post-radiotherapy: a pilot study. Scientific Reports, 2020, 10, 13201.	1.6	11
12	Antibiotic Treatment for Chronic Rhinosinusitis: Prescription Patterns and Associations With Patient Outcome and the Sinus Microbiota. Frontiers in Microbiology, 2020, 11, 595555.	1.5	20
13	Comparative Analyses of Vertebrate Gut Microbiomes Reveal Convergence between Birds and Bats. MBio, 2020, 11, .	1.8	204
14	Detection and quantification of <i>Staphylococcus</i> in chronic rhinosinusitis. International Forum of Allergy and Rhinology, 2019, 9, 1462-1469.	1.5	19
15	The airway microbiota in children newly diagnosed with bronchiectasis largely retains its diversity. European Respiratory Journal, 2019, 54, 1900704.	3.1	5
16	Comparison of Subtyping Approaches and the Underlying Drivers of Microbial Signatures for Chronic Rhinosinusitis. MSphere, 2019, 4, .	1.3	23
17	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
18	The microbiome in threatened species conservation. Biological Conservation, 2019, 229, 85-98.	1.9	185

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19	The sinonasal microbiota, neural signaling, and depression in chronic rhinosinusitis. International Forum of Allergy and Rhinology, 2018, 8, 394-405.	1.5	18
20	The effect of medical treatments on the bacterial microbiome in patients with chronic rhinosinusitis: a pilot study. International Forum of Allergy and Rhinology, 2018, 8, 890-899.	1.5	20
21	Phylogeny and genomics of SAUL, an enigmatic bacterial lineage frequently associated with marine sponges. Environmental Microbiology, 2018, 20, 561-576.	1.8	32
22	Microbial and inflammatoryâ€based salivary biomarkers of head and neck squamous cell carcinoma. Clinical and Experimental Dental Research, 2018, 4, 255-262.	0.8	42
23	Inflammatory Endotypes and Microbial Associations in Chronic Rhinosinusitis. Frontiers in Immunology, 2018, 9, 2065.	2.2	48
24	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
25	Network-guided genomic and metagenomic analysis of the faecal microbiota of the critically endangered kakapo. Scientific Reports, 2018, 8, 8128.	1.6	11
26	Climate change alterations to ecosystem dominance: how might spongeâ€dominated reefs function?. Ecology, 2018, 99, 1920-1931.	1.5	56
27	Microbial community dynamics in Inferno Crater Lake, a thermally fluctuating geothermal spring. ISME Journal, 2017, 11, 1158-1167.	4.4	53
28	Evaluating the core microbiota in complex communities: A systematic investigation. Environmental Microbiology, 2017, 19, 1450-1462.	1.8	187
29	The New Zealand minds for minds autism spectrum disorder self-reported cohort. Research in Autism Spectrum Disorders, 2017, 36, 1-7.	0.8	4
30	Embracing the coâ€operative society to better understand assembly of the gut microbiota. Environmental Microbiology, 2017, 19, 2924-2925.	1.8	5
31	Chronic Rhinosinusitis and the Evolving Understanding of Microbial Ecology in Chronic Inflammatory Mucosal Disease. Clinical Microbiology Reviews, 2017, 30, 321-348.	5.7	103
32	Bacterial community collapse: a metaâ€analysis of the sinonasal microbiota in chronic rhinosinusitis. Environmental Microbiology, 2017, 19, 381-392.	1.8	174
33	The sponge microbiome project. GigaScience, 2017, 6, 1-7.	3.3	193
34	Redefining the spongeâ€symbiont acquisition paradigm: sponge microbes exhibit chemotaxis towards hostâ€derived compounds. Environmental Microbiology Reports, 2017, 9, 750-755.	1.0	20
35	Devil in the detail: a closer look at childhood obesity and the gut microbiota. Environmental Microbiology, 2017, 19, 11-12.	1.8	7
36	Evidence of microbiota dysbiosis in chronic rhinosinusitis. International Forum of Allergy and Rhinology, 2017, 7, 230-239.	1.5	143

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37	What Thrives Inside; The World Within the Gut. Frontiers for Young Minds, 2017, 5, .	0.8	0
38	Moving beyond descriptions of diversity: clinical and research implications of bacterial imbalance in chronic rhinosinusitis. Rhinology, 2017, 55, 291-297.	0.7	0
39	Differentially Regulated Host Proteins Associated with Chronic Rhinosinusitis Are Correlated with the Sinonasal Microbiome. Frontiers in Cellular and Infection Microbiology, 2017, 7, 504.	1.8	25
40	The Low-Diversity Fecal Microbiota of the Critically Endangered KÄ•kÄ•pÅ•Is Robust to Anthropogenic Dietary and Geographic Influences. Frontiers in Microbiology, 2017, 8, 2033.	1.5	15
41	Evaluating the Impact of DNA Extraction Method on the Representation of Human Oral Bacterial and Fungal Communities. PLoS ONE, 2017, 12, e0169877.	1.1	115
42	Integrity of the Human Faecal Microbiota following Long-Term Sample Storage. PLoS ONE, 2016, 11, e0163666.	1.1	41
43	Impact of explantation techniques on the microbiota of the marine sponge Ecionemia alata. Journal of Experimental Marine Biology and Ecology, 2016, 484, 11-15.	0.7	2
44	Molecular Microbiological Profile of Chronic Suppurative Otitis Media. Journal of Clinical Microbiology, 2016, 54, 2538-2546.	1.8	48
45	Diversity, structure and convergent evolution of the global sponge microbiome. Nature Communications, 2016, 7, 11870.	5.8	594
46	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
47	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
48	Exploring the avian gut microbiota: current trends and future directions. Frontiers in Microbiology, 2015, 6, 673.	1.5	216
49	The nasal microbiota in health and disease: variation within and between subjects. Frontiers in Microbiology, 2015, 9, .	1.5	145
50	Evaluating variation in human gut microbiota profiles due to DNA extraction method and inter-subject differences. Frontiers in Microbiology, 2015, 6, 130.	1.5	152
51	Diversity of Actinobacteria Associated with the Marine Ascidian Eudistoma toealensis. Marine Biotechnology, 2015, 17, 377-385.	1.1	28
52	Genomic and phenotypic insights into the ecology of Arthrobacter from Antarctic soils. BMC Genomics, 2015, 16, 36.	1.2	99
53	Microbial community structure in the gut of the New Zealand insect Auckland tree weta (Hemideina) Tj ETQq1 1 0.784314 rgBT /Overlo	1.0	15
54	Ability of Arkansas LaKast and LaKast Hybrid Rice Bran to Reduce Salmonella Typhimurium in Chicken Cecal Incubations and Effects on Cecal Microbiota. Frontiers in Microbiology, 2015, 9, 134.	1.5	89

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55	Characterizing the avian gut microbiota: membership, driving influences, and potential function. Frontiers in Microbiology, 2014, 5, 223.	1.5	328
56	Pyrosequencing reveals regional differences in fruitâ€associated fungal communities. Environmental Microbiology, 2014, 16, 2848-2858.	1.8	143
57	Successional development of biofilms in moving bed biofilm reactor (MBBR) systems treating municipal wastewater. Applied Microbiology and Biotechnology, 2014, 98, 1429-1440.	1.7	99
58	dsrAB-based analysis of sulphate-reducing bacteria in moving bed biofilm reactor (MBBR) wastewater treatment plants. Applied Microbiology and Biotechnology, 2014, 98, 7211-7222.	1.7	20
59	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
60	Application of Diffusion Growth Chambers for the Cultivation of Marine Sponge-Associated Bacteria. Marine Biotechnology, 2014, 16, 594-603.	1.1	72
61	Influence of environmental variation on symbiotic bacterial communities of two temperate sponges. FEMS Microbiology Ecology, 2014, 88, 516-527.	1.3	91
62	Paenibacillus darwinianus sp. nov., isolated from gamma-irradiated Antarctic soil. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 1406-1411.	0.8	29
63	Genome-Based Comparative Analyses of Antarctic and Temperate Species of Paenibacillus. PLoS ONE, 2014, 9, e108009.	1.1	32
64	Bacterial community profiles in low microbial abundance sponges. FEMS Microbiology Ecology, 2013, 83, 232-241.	1.3	127
65	Could some coral reefs become sponge reefs as our climate changes?. Global Change Biology, 2013, 19, 2613-2624.	4.2	261
66	Primary symbiont of the ancient scale insect family Coelostomidiidae exhibits strict cophylogenetic patterns. Symbiosis, 2013, 61, 77-91.	1.2	16
67	Temporal molecular and isotopic analysis of active bacterial communities in two New Zealand sponges. FEMS Microbiology Ecology, 2013, 85, 195-205.	1.3	41
68	Quantifying the impact of storage procedures for faecal bacteriotherapy in the critically endangered New Zealand Parrot, the Kakapo (<i>Strigops habroptilus</i>). Zoo Biology, 2013, 32, 620-625.	0.5	19
69	â€˜Sponge-specificâ€™ bacteria are widespread (but rare) in diverse marine environments. ISME Journal, 2013, 7, 438-443.	4.4	161
70	Diverse Honeydew-Consuming Fungal Communities Associated with Scale Insects. PLoS ONE, 2013, 8, e70316.	1.1	31
71	Assessing the complex sponge microbiota: core, variable and species-specific bacterial communities in marine sponges. ISME Journal, 2012, 6, 564-576.	4.4	508
72	Thermal stress responses in the bacterial biosphere of the <scp>G</scp>reat <scp>B</scp>arrier <scp>R</scp>eef sponge, <i><scp>R</scp>hopaloeides odorabile</i>. Environmental Microbiology, 2012, 14, 3232-3246.	1.8	93

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73	Deep sequencing reveals diversity and community structure of complex microbiota in five Mediterranean sponges. Hydrobiologia, 2012, 687, 341-351.	1.0	68
74	Genomic insights into the marine sponge microbiome. Nature Reviews Microbiology, 2012, 10, 641-654.	13.6	530
75	Ultrastructural and molecular characterization of a bacterial symbiosis in the ecologically important scale insect family Coelostomidiidae. FEMS Microbiology Ecology, 2012, 81, 537-546.	1.3	18
76	Marine sponges and their microbial symbionts: love and other relationships. Environmental Microbiology, 2012, 14, 335-346.	1.8	491
77	Spongeâ€specific clusters revisited: a comprehensive phylogeny of spongeâ€associated microorganisms. Environmental Microbiology, 2012, 14, 517-524.	1.8	253
78	Gut Microbiome of the Critically Endangered New Zealand Parrot, the Kakapo (Strigops habroptilus). PLoS ONE, 2012, 7, e35803.	1.1	75
79	Sponge-Microbe Associations Survive High Nutrients and Temperatures. PLoS ONE, 2012, 7, e52220.	1.1	72
80	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
81	Evaluating methods for the preservation and extraction of DNA and RNA for analysis of microbial communities in marine sponges. Journal of Experimental Marine Biology and Ecology, 2011, 397, 38-43.	0.7	36
82	Meeting Report: 1st International Symposium on Sponge Microbiology. Marine Biotechnology, 2011, 13, 1057-1061.	1.1	17
83	Deep sequencing reveals exceptional diversity and modes of transmission for bacterial sponge symbionts. Environmental Microbiology, 2010, 12, 2070-2082.	1.8	394
84	Activity profiles for marine sponge-associated bacteria obtained by 16S rRNA vs 16S rRNA gene comparisons. ISME Journal, 2010, 4, 498-508.	4.4	132
85	Diversity and mode of transmission of ammoniaâ€oxidizing archaea in marine sponges. Environmental Microbiology, 2008, 10, 1087-1094.	1.8	127
86	Evolutionary Insights from Sponges. Science, 2007, 316, 1854-1855.	6.0	47
87	Sponge-Associated Microorganisms: Evolution, Ecology, and Biotechnological Potential. Microbiology and Molecular Biology Reviews, 2007, 71, 295-347.	2.9	1,254
88	Soaking it up: the complex lives of marine sponges and their microbial associates. ISME Journal, 2007, 1, 187-190.	4.4	86
89	Marine sponges as microbial fermenters. FEMS Microbiology Ecology, 2006, 55, 167-177.	1.3	521
90	Deciphering the evolution and metabolism of an anammox bacterium from a community genome. Nature, 2006, 440, 790-794.	13.7	1,075

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91	Wastewater treatment: a model system for microbial ecology. Trends in Biotechnology, 2006, 24, 483-489.	4.9	216
92	Biogeography of bacteria associated with the marine sponge Cymbastela concentrica. Environmental Microbiology, 2005, 7, 419-433.	1.8	124
93	Use of solid-phase extraction to enable enhanced detection of acyl homoserine lactones (AHLs) in environmental samples. Analytical and Bioanalytical Chemistry, 2005, 383, 132-137.	1.9	19
94	â€˜Candidatus Protochlamydia amoebophilaâ€™, an endosymbiont of Acanthamoeba spp.. International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 1863-1866.	0.8	88
95	Evidence for Acyl Homoserine Lactone Signal Production in Bacteria Associated with Marine Sponges. Applied and Environmental Microbiology, 2004, 70, 4387-4389.	1.4	100
96	Host specificity in marine sponge-associated bacteria, and potential implications for marine microbial diversity. Environmental Microbiology, 2004, 6, 121-130.	1.8	227
97	Isotopic-labelling methods for deciphering the function of uncultured micro-organisms. , 0, , 1-10.		2