Andrew Oxley

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Dead or alive: microbial viability treatment reveals both active and inactive bacterial constituents in the fish gut microbiota. Journal of Applied Microbiology, 2021, 131, 2528-2538.	1.4	8
2	A microbial sea of possibilities: current knowledge and prospects for an improved understanding of the fish microbiome. Reviews in Aquaculture, 2020, 12, 1101-1134.	4.6	117
3	Antibiotic-induced alterations and repopulation dynamics of yellowtail kingfish microbiota. Animal Microbiome, 2020, 2, 26.	1.5	23
4	Investigating Both Mucosal Immunity and Microbiota in Response to Gut Enteritis in Yellowtail Kingfish. Microorganisms, 2020, 8, 1267.	1.6	22
5	The active bacterial assemblages of the upper GI tract in individuals with and without <i>Helicobacter</i> infection. Gut, 2018, 67, 216-225.	6.1	151
6	Using inÂsitu hybridization to expand the daily egg production method to new fish species. Molecular Ecology Resources, 2017, 17, 1108-1121.	2.2	7
7	The Inner Workings of the Outer Surface: Skin and Gill Microbiota as Indicators of Changing Gut Health in Yellowtail Kingfish. Frontiers in Microbiology, 2017, 8, 2664.	1.5	126
8	Exploring the bacterial assemblages along the human nasal passage. Environmental Microbiology, 2016, 18, 2259-2271.	1.8	26
9	Exploring the transcriptome of Staphylococcus aureus in its natural niche. Scientific Reports, 2016, 6, 33174.	1.6	52
10	The microbial community structure of the cotton rat nose. Environmental Microbiology Reports, 2015, 7, 929-935.	1.0	35
11	Application of a Novel "Pan-Genome―Based Strategy for Assigning RNAseq Transcript Reads to Staphylococcus aureus Strains. PLoS ONE, 2015, 10, e0145861.	1.1	9
12	High-Resolution Transcriptomic Analysis of the Adaptive Response of Staphylococcus aureus during Acute and Chronic Phases of Osteomyelitis. MBio, 2014, 5, .	1.8	65
13	Comparing the anterior nare bacterial community of two discrete human populations using <scp>I</scp> Ilumina amplicon sequencing. Environmental Microbiology, 2014, 16, 2939-2952.	1.8	177
14	Comparative evaluation of establishing a human gut microbial community within rodent models. Gut Microbes, 2012, 3, 234-249.	4.3	113
15	The abundance of nitrogen cycle genes amoA and nifH depends on land-uses and soil types in South-Eastern Australia. Soil Biology and Biochemistry, 2010, 42, 1774-1783.	4.2	127
16	Halophilic archaea in the human intestinal mucosa. Environmental Microbiology, 2010, 12, 2398-2410.	1.8	105
17	Gordonibacter pamelaeae gen. nov., sp. nov., a new member of the Coriobacteriaceae isolated from a patient with Crohn's disease, and reclassification of Eggerthella hongkongensis Lau et al. 2006 as Paraeggerthella hongkongensis gen. nov., comb. nov International Journal of Systematic and Evolutionary Microbiology. 2009. 59. 1405-1415.	0.8	84
18	Helicobacter spp. from captive bottlenose dolphins (Tursiops spp.) and polar bears (Ursus maritimus). Veterinary Journal, 2005, 170, 377-380.	0.6	8

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19	Comparison of Helicobacter spp. genetic sequences in wild and captive seals, and gulls. Diseases of Aquatic Organisms, 2005, 65, 99-105.	0.5	11
20	Species of the Family Helicobacteraceae Detected in an Australian Sea Lion (Neophoca cinerea) with Chronic Gastritis. Journal of Clinical Microbiology, 2004, 42, 3505-3512.	1.8	21
21	Fecal shedding of Helicobacter spp. by co-housed Australian sea lions (Neophoca cinerea) and Australian fur seals (Arctocephalus pusillus doriferus). Veterinary Microbiology, 2004, 101, 235-243.	0.8	8
22	Bacterial flora from the gut of the wild and cultured banana prawn, Penaeus merguiensis. Journal of Applied Microbiology, 2002, 93, 214-223.	1.4	112