Andrew Oxley

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Comparing the anterior nare bacterial community of two discrete human populations using <scp>I</scp> llumina amplicon sequencing. Environmental Microbiology, 2014, 16, 2939-2952.	1.8	177
2	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
3	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
4	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
5	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
6	Comparative evaluation of establishing a human gut microbial community within rodent models. Gut Microbes, 2012, 3, 234-249.	4.3	113
7	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
8	Halophilic archaea in the human intestinal mucosa. Environmental Microbiology, 2010, 12, 2398-2410.	1.8	105
9	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
10	High-Resolution Transcriptomic Analysis of the Adaptive Response of Staphylococcus aureus during Acute and Chronic Phases of Osteomyelitis. MBio, 2014, 5, .	1.8	65
11	Exploring the transcriptome of Staphylococcus aureus in its natural niche. Scientific Reports, 2016, 6, 33174.	1.6	52
12	The microbial community structure of the cotton rat nose. Environmental Microbiology Reports, 2015, 7, 929-935.	1.0	35
13	Exploring the bacterial assemblages along the human nasal passage. Environmental Microbiology, 2016, 18, 2259-2271.	1.8	26
14	Antibiotic-induced alterations and repopulation dynamics of yellowtail kingfish microbiota. Animal Microbiome, 2020, 2, 26.	1.5	23
15	Investigating Both Mucosal Immunity and Microbiota in Response to Gut Enteritis in Yellowtail Kingfish. Microorganisms, 2020, 8, 1267.	1.6	22
16	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
17	Comparison of Helicobacter spp. genetic sequences in wild and captive seals, and gulls. Diseases of Aquatic Organisms, 2005, 65, 99-105.	0.5	11
18	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

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19	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
20	Helicobacter spp. from captive bottlenose dolphins (Tursiops spp.) and polar bears (Ursus maritimus). Veterinary Journal, 2005, 170, 377-380.	0.6	8
21	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
22	Using inÂsitu hybridization to expand the daily egg production method to new fish species. Molecular Ecology Resources, 2017, 17, 1108-1121.	2.2	7