

Kento Tominaga

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9949815/publications.pdf>

Version: 2024-02-01

14
papers

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citing authors

#	ARTICLE	IF	CITATIONS
1	Year-round dynamics of amplicon sequence variant communities differ among eukaryotes, <i>Imitervirales</i> and prokaryotes in a coastal ecosystem. <i>FEMS Microbiology Ecology</i> , 2022, 97, .	2.7	3
2	Taxonomic and functional characterization of the rumen microbiome of Japanese Black cattle revealed by 16S rRNA gene amplicon and metagenome shotgun sequencing. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	9
3	Diel cycling of the cosmopolitan abundant Pelagibacter virus 37: one of the most abundant viruses on earth. <i>Environmental Microbiology Reports</i> , 2020, 12, 214-219.	2.4	8
4	In silico Prediction of Virus-Host Interactions for Marine Bacteroidetes With the Use of Metagenome-Assembled Genomes. <i>Frontiers in Microbiology</i> , 2020, 11, 738.	3.5	20
5	Differential Responses of a Coastal Prokaryotic Community to Phytoplanktonic Organic Matter Derived from Cellular Components and Exudates. <i>Microbes and Environments</i> , 2020, 35, n/a.	1.6	7
6	An Optimized Metabarcoding Method for Mimiviridae. <i>Microorganisms</i> , 2020, 8, 506.	3.6	6
7	Calcium salts of long-chain fatty acids from linseed oil decrease methane production by altering the rumen microbiome in vitro. <i>PLoS ONE</i> , 2020, 15, e0242158.	2.5	12
8	Predetermined clockwork microbial worlds: Current understanding of aquatic microbial diel response from model systems to complex environments. <i>Advances in Applied Microbiology</i> , 2020, 113, 163-191.	2.4	2
9	Title is missing!. , 2020, 15, e0242158.		0
10	Title is missing!. , 2020, 15, e0242158.		0
11	Title is missing!. , 2020, 15, e0242158.		0
12	Title is missing!. , 2020, 15, e0242158.		0
13	Cooccurrence of Broad- and Narrow-Host-Range Viruses Infecting the Bloom-Forming Toxic Cyanobacterium <i>Microcystis aeruginosa</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	15
14	Systematic identification of synthetic lethal mutations with reduced-genome <i>Escherichia coli</i> : synthetic genetic interactions among <i>yoaA</i> , <i>xthA</i> and <i>holC</i> related to survival from MMS exposure. <i>Genes and Genetic Systems</i> , 2016, 91, 183-188.	0.7	8