

Yann Moalic

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

595
citations

687363

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839539

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21
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docs citations

21
times ranked

1042
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete genome sequence of <i>Thermosulfurimonas marina</i> SU872T, an anaerobic thermophilic chemolithoautotrophic bacterium isolated from a shallow marine hydrothermal vent. <i>Marine Genomics</i> , 2021, 55, 100800.	1.1	2
2	New Insights into the Ecology and Physiology of Methanomassiliicoccales from Terrestrial and Aquatic Environments. <i>Microorganisms</i> , 2021, 9, 30.	3.6	23
3	The Piezo-Hyperthermophilic Archaeon <i>Thermococcus piezophilus</i> Regulates Its Energy Efficiency System to Cope With Large Hydrostatic Pressure Variations. <i>Frontiers in Microbiology</i> , 2021, 12, 730231.	3.5	6
4	RNA processing machineries in Archaea: the 5'â€²-3'â€² exoribonuclease aRNase J of the Î²-CASP family is engaged specifically with the helicase ASH-Ski2 and the 3'â€²-5'â€² exoribonucleolytic RNA exosome machinery. <i>Nucleic Acids Research</i> , 2020, 48, 3832-3847.	14.5	14
5	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	15
6	Development of an Effective 6-Methylpurine Counterselection Marker for Genetic Manipulation in <i>Thermococcus barophilus</i> . <i>Genes</i> , 2018, 9, 77.	2.4	21
7	Relative Abundance and Diversity of Bacterial Methanotrophs at the Oxicâ€”Anoxic Interface of the Congo Deep-Sea Fan. <i>Frontiers in Microbiology</i> , 2017, 8, 715.	3.5	12
8	Learning Ecological Networks from Next-Generation Sequencing Data. <i>Advances in Ecological Research</i> , 2016, , 1-39.	2.7	68
9	Hologenome theory supported by cooccurrence networks of species-specific bacterial communities in siphonous algae (<i>Caulerpa</i>). <i>FEMS Microbiology Ecology</i> , 2015, 91, fiv067.	2.7	55
10	Genetic Manipulations of the Hyperthermophilic Piezophilic Archaeon <i>Thermococcus barophilus</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 2299-2306.	3.1	35
11	Disentangling the Influence of Mutation and Migration in Clonal Seagrasses Using the Genetic Diversity Spectrum for Microsatellites. <i>Journal of Heredity</i> , 2014, 105, 532-541.	2.4	28
12	Scaling of processes shaping the clonal dynamics and genetic mosaic of seagrasses through temporal genetic monitoring. <i>Heredity</i> , 2014, 112, 114-121.	2.6	50
13	Discriminating Micropathogen Lineages and Their Reticulate Evolution through Graph Theory-Based Network Analysis: The Case of <i>Trypanosoma cruzi</i> , the Agent of Chagas Disease. <i>PLoS ONE</i> , 2014, 9, e103213.	2.5	4
14	Biogeography Revisited with Network Theory: Retracing the History of Hydrothermal Vent Communities. <i>Systematic Biology</i> , 2012, 61, 127.	5.6	93
15	Travelling in time with networks: Revealing present day hybridization versus ancestral polymorphism between two species of brown algae, <i>Fucus vesiculosus</i> and <i>F. spiralis</i> . <i>BMC Evolutionary Biology</i> , 2011, 11, 33.	3.2	23
16	The concept of population in clonal organisms: mosaics of temporally colonized patches are forming highly diverse meadows of <i>Zostera marina</i> in Brittany. <i>Molecular Ecology</i> , 2010, 19, no-no.	3.9	82
17	Genome Areas with High Gene Density and CpG Island Neighborhood Strongly Attract Porcine Endogenous Retrovirus for Integration and Favor the Formation of Hot Spots. <i>Journal of Virology</i> , 2009, 83, 1920-1929.	3.4	19
18	Porcine Endogenous Retrovirus Integration Sites in the Human Genome: Features in Common with Those of Murine Leukemia Virus. <i>Journal of Virology</i> , 2006, 80, 10980-10988.	3.4	45