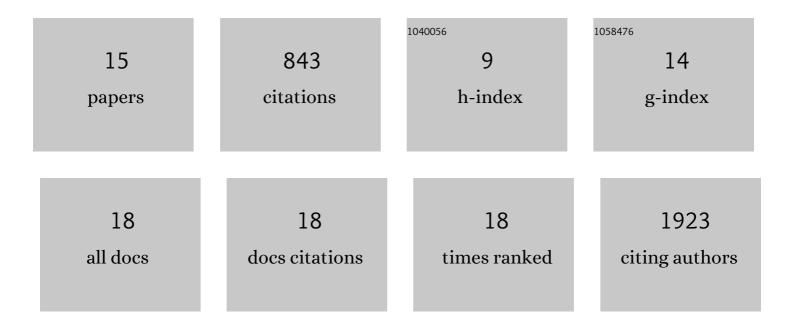
Mailie L Gall

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/965748/publications.pdf Version: 2024-02-01



MALLIE L CALL

#	Article	IF	CITATIONS
1	Revealing COVID-19 transmission in Australia by SARS-CoV-2 genome sequencing and agent-based modeling. Nature Medicine, 2020, 26, 1398-1404.	30.7	283
2	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2 with grinch. Wellcome Open Research, 2021, 6, 121.	1.8	129
3	An emergent clade of SARS-CoV-2 linked to returned travellers from Iran. Virus Evolution, 2020, 6, veaa027.	4.9	119
4	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2. Wellcome Open Research, 2021, 6, 121.	1.8	115
5	Co-infection with SARS-CoV-2 Omicron and Delta variants revealed by genomic surveillance. Nature Communications, 2022, 13, 2745.	12.8	64
6	From pole to pole: the potential for the Arctic seastar <i>Asterias amurensis</i> to invade a warming Southern Ocean. Global Change Biology, 2016, 22, 3874-3887.	9.5	35
7	Diet-induced shifts in the crown-of-thorns (Acanthaster sp.) larval microbiome. Marine Biology, 2018, 165, 1.	1.5	28
8	Effects of marine heatwave conditions across the metamorphic transition to the juvenile sea urchin (Heliocidaris erythrogramma). Marine Pollution Bulletin, 2021, 163, 111914.	5.0	13
9	A biomonitor as a measure of an ecologically-significant fraction of metals in an industrialized harbour. Journal of Environmental Monitoring, 2012, 14, 830.	2.1	12
10	Staying in place and moving in space: contrasting larval thermal sensitivity explains distributional changes of sympatric sea urchin species to habitat warming. Global Change Biology, 2022, , .	9.5	9
11	Differential tolerance to copper, but no evidence of population-level genetic differences in a widely-dispersing native barnacle. Ecotoxicology, 2013, 22, 929-937.	2.4	7
12	Documenting elimination of co-circulating COVID-19 clusters using genomics in New South Wales, Australia. BMC Research Notes, 2021, 14, 415.	1.4	4
13	SARS-CoV-2 Within-Host and in vitro Genomic Variability and Sub-Genomic RNA Levels Indicate Differences in Viral Expression Between Clinical Cohorts and in vitro Culture. Frontiers in Microbiology, 2022, 13, .	3.5	4
14	Added Value of Genomic Surveillance of Virulence Factors in Shiga Toxin-Producing Escherichia coli in New South Wales, Australia. Frontiers in Microbiology, 2021, 12, 713724.	3.5	2
15	Characterisation of thirteen polymorphic microsatellite markers for the red sea urchin Heliocidaris tuberculata (Lamarck, 1816) developed using a 454-sequencing approach. Conservation Genetics Resources, 2014, 6, 237-239.	0.8	0