

Michelle Sait

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

2,934
citations

567281

15
h-index

345221

36
g-index

38
all docs

38
docs citations

38
times ranked

4451
citing authors

#	ARTICLE	IF	CITATIONS
1	Lab-in-a-van: Rapid SARS-CoV-2 testing response with a mobile laboratory. <i>EBioMedicine</i> , 2022, 79, 103983.	6.1	4
2	Multi-site implementation of whole genome sequencing for hospital infection control: A prospective genomic epidemiological analysis. <i>The Lancet Regional Health - Western Pacific</i> , 2022, 23, 100446.	2.9	6
3	Search and Contain: Impact of an Integrated Genomic and Epidemiological Surveillance and Response Program for Control of Carbapenemase-producing <i>Enterobacterales</i> . <i>Clinical Infectious Diseases</i> , 2021, 73, e3912-e3920.	5.8	12
4	Optimal preparation of SARS-CoV-2 viral transport medium for culture. <i>Virology Journal</i> , 2021, 18, 53.	3.4	15
5	Reflex Detection of Ciprofloxacin Resistance in <i>Neisseria gonorrhoeae</i> by Use of the SpeeDx ResistancePlus GC Assay. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	3.9	13
6	Multi-site assessment of rapid, point-of-care antigen testing for the diagnosis of SARS-CoV-2 infection in a low-prevalence setting: A validation and implementation study. <i>The Lancet Regional Health - Western Pacific</i> , 2021, 9, 100115.	2.9	29
7	Adding saliva testing to oropharyngeal and deep nasal swab testing increases PCR detection of SARS-CoV-2 in primary care and children. <i>Medical Journal of Australia</i> , 2021, 215, 273-278.	1.7	8
8	Defective Severe Acute Respiratory Syndrome Coronavirus 2 Immune Responses in an Immunocompromised Individual With Prolonged Viral Replication. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab359.	0.9	5
9	Efficacy of Two <i>Chlamydia abortus</i> Subcellular Vaccines in a Pregnant Ewe Challenge Model for Ovine Enzootic Abortion. <i>Vaccines</i> , 2021, 9, 898.	4.4	7
10	Genomics-informed responses in the elimination of COVID-19 in Victoria, Australia: an observational, genomic epidemiological study. <i>Lancet Public Health</i> , The, 2021, 6, e547-e556.	10.0	53
11	COVID-19: Integrating genomic and epidemiological data to inform public health interventions and policy in Tasmania, Australia. <i>Western Pacific Surveillance and Response Journal: WPSAR</i> , 2021, 12, 93-101.	0.6	2
12	Tracking the COVID-19 pandemic in Australia using genomics. <i>Nature Communications</i> , 2020, 11, 4376.	12.8	152
13	Viral Genomics to Inform Infection-control Response in Occupational Coronavirus Disease 2019 (COVID-19) Transmission. <i>Clinical Infectious Diseases</i> , 2020, 73, e1881-e1884.	5.8	3
14	Validation of a single-step, single-tube reverse transcription loop-mediated isothermal amplification assay for rapid detection of SARS-CoV-2 RNA. <i>Journal of Medical Microbiology</i> , 2020, 69, 1169-1178.	1.8	61
15	Genomics for Molecular Epidemiology and Detecting Transmission of Carbapenemase-Producing <i>Enterobacterales</i> in Victoria, Australia, 2012 to 2016. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	56
16	Risk Factors for Asymptomatic Enteric Pathogen Detection Among Men Who Have Sex With Men. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz326.	0.9	14
17	Recent trends in invasive group A <i>Streptococcus</i> disease in Victoria. <i>Communicable Diseases Intelligence</i> (2018), 2019, 43, .	0.7	3
18	Incorporating Whole-Genome Sequencing into Public Health Surveillance: Lessons from Prospective Sequencing of <i>Salmonella</i> Typhimurium in Australia. <i>Foodborne Pathogens and Disease</i> , 2018, 15, 161-167.	1.8	24

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19	Genomic evidence that the live <i>Chlamydia abortus</i> vaccine strain 1B is not attenuated and has the potential to cause disease. <i>Vaccine</i> , 2018, 36, 3593-3598.	3.8	25
20	Translating genomics into practice for real-time surveillance and response to carbapenemase-producing <i>Enterobacteriaceae</i> : evidence from a complex multi-institutional KPC outbreak. <i>PeerJ</i> , 2018, 6, e4210.	2.0	66
21	Pathogenic outcome following experimental infection of sheep with <i>Chlamydia abortus</i> variant strains LLG and POS. <i>PLoS ONE</i> , 2017, 12, e0177653.	2.5	13
22	Genome sequencing and comparative analysis of three <i>Chlamydia pecorum</i> strains associated with different pathogenic outcomes. <i>BMC Genomics</i> , 2014, 15, 23.	2.8	39
23	Genome Sequence of <i>Lawsonia intracellularis</i> Strain N343, Isolated from a Sow with Hemorrhagic Proliferative Enteropathy. <i>Genome Announcements</i> , 2013, 1, .	0.8	17
24	Genome Sequence of <i>Chlamydia psittaci</i> Strain 01DC12 Originating from Swine. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
25	Expression patterns of five polymorphic membrane proteins during the <i>Chlamydia abortus</i> developmental cycle. <i>Veterinary Microbiology</i> , 2012, 160, 525-529.	1.9	11
26	Processing of <i>Chlamydia abortus</i> Polymorphic Membrane Protein 18D during the Chlamydial Developmental Cycle. <i>PLoS ONE</i> , 2012, 7, e49190.	2.5	15
27	Genomic and Experimental Evidence Suggests that <i>Verrucomicrobium spinosum</i> Interacts with Eukaryotes. <i>Frontiers in Microbiology</i> , 2011, 2, 211.	3.5	19
28	Genetic variability of <i>Chlamydophila abortus</i> strains assessed by PCR-RFLP analysis of polymorphic membrane protein-encoding genes. <i>Veterinary Microbiology</i> , 2011, 151, 284-290.	1.9	9
29	Molecular detection of <i>Chlamydia</i> -like organisms in cattle drinking water. <i>Veterinary Microbiology</i> , 2011, 152, 196-199.	1.9	16
30	Genome Sequence of the <i>Chlamydophila abortus</i> Variant Strain LLG. <i>Journal of Bacteriology</i> , 2011, 193, 4276-4277.	2.2	13
31	Identification, sequencing and molecular analysis of Chp4, a novel chlamydiophage of <i>Chlamydophila abortus</i> belonging to the family Microviridae. <i>Journal of General Virology</i> , 2011, 92, 1733-1737.	2.9	14
32	Three Genomes from the Phylum <i>Acidobacteria</i> Provide Insight into the Lifestyles of These Microorganisms in Soils. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2046-2056.	3.1	804
33	Effect of pH on Isolation and Distribution of Members of Subdivision 1 of the Phylum <i>Acidobacteria</i> Occurring in Soil. <i>Applied and Environmental Microbiology</i> , 2006, 72, 1852-1857.	3.1	206
34	Detection and Cultivation of Soil <i>Verrucomicrobia</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 8402-8410.	3.1	142
35	Improved Culturability of Soil Bacteria and Isolation in Pure Culture of Novel Members of the Divisions <i>Acidobacteria</i> , <i>Actinobacteria</i> , <i>Proteobacteria</i> , and <i>Verrucomicrobia</i> . <i>Applied and Environmental Microbiology</i> , 2002, 68, 2391-2396.	3.1	631
36	Cultivation of globally distributed soil bacteria from phylogenetic lineages previously only detected in cultivation-independent surveys. <i>Environmental Microbiology</i> , 2002, 4, 654-666.	3.8	408

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37	Recent trends in invasive group A Streptococcus disease in Victoria. Communicable Diseases Intelligence (2018), 0, 43, .	0.7	12
38	Genomic Characterisation Reveals a Dominant Lineage of SARS-CoV-2 in Papua New Guinea. Virus Evolution, 0, , .	4.9	0