

# 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	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
2	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
3	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
4	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
5	Tracking the COVID-19 pandemic in Australia using genomics. <i>Nature Communications</i> , 2020, 11, 4376.	12.8	152
6	Detection and Cultivation of Soil <i>Verrucomicrobia</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 8402-8410.	3.1	142
7	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
8	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
9	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
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	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
12	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
13	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
14	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
15	Genomic and Experimental Evidence Suggests that <i>Verrucomicrobium spinosum</i> Interacts with Eukaryotes. <i>Frontiers in Microbiology</i> , 2011, 2, 211.	3.5	19
16	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
17	Molecular detection of <i>Chlamydia</i> -like organisms in cattle drinking water. <i>Veterinary Microbiology</i> , 2011, 152, 196-199.	1.9	16
18	Optimal preparation of SARS-CoV-2 viral transport medium for culture. <i>Virology Journal</i> , 2021, 18, 53.	3.4	15

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19	Processing of Chlamydia abortus Polymorphic Membrane Protein 18D during the Chlamydial Developmental Cycle. PLoS ONE, 2012, 7, e49190.	2.5	15
20	Identification, sequencing and molecular analysis of Chp4, a novel chlamydiophage of Chlamydophila abortus belonging to the family Microviridae. Journal of General Virology, 2011, 92, 1733-1737.	2.9	14
21	Risk Factors for Asymptomatic Enteric Pathogen Detection Among Men Who Have Sex With Men. Open Forum Infectious Diseases, 2019, 6, ofz326.	0.9	14
22	Genome Sequence of the Chlamydophila abortus Variant Strain LLG. Journal of Bacteriology, 2011, 193, 4276-4277.	2.2	13
23	Pathogenic outcome following experimental infection of sheep with Chlamydia abortus variant strains LLG and POS. PLoS ONE, 2017, 12, e0177653.	2.5	13
24	Reflex Detection of Ciprofloxacin Resistance in Neisseria gonorrhoeae by Use of the SpeeDx ResistancePlus GC Assay. Journal of Clinical Microbiology, 2021, 59, .	3.9	13
25	Search and Contain: Impact of an Integrated Genomic and Epidemiological Surveillance and Response Program for Control of Carbapenemase-producing <i>Enterobacterales</i>. Clinical Infectious Diseases, 2021, 73, e3912-e3920.	5.8	12
26	Recent trends in invasive group A Streptococcus disease in Victoria. Communicable Diseases Intelligence (2018), 0, 43, .	0.7	12
27	Expression patterns of five polymorphic membrane proteins during the Chlamydia abortus developmental cycle. Veterinary Microbiology, 2012, 160, 525-529.	1.9	11
28	Genetic variability of Chlamydophila abortus strains assessed by PCR-RFLP analysis of polymorphic membrane protein-encoding genes. Veterinary Microbiology, 2011, 151, 284-290.	1.9	9
29	Adding saliva testing to oropharyngeal and deep nasal swab testing increases PCR detection of SARS-CoV-2 in primary care and children. Medical Journal of Australia, 2021, 215, 273-278.	1.7	8
30	Genome Sequence of Chlamydia psittaci Strain 01DC12 Originating from Swine. Genome Announcements, 2013, 1, .	0.8	7
31	Efficacy of Two Chlamydia abortus Subcellular Vaccines in a Pregnant Ewe Challenge Model for Ovine Enzootic Abortion. Vaccines, 2021, 9, 898.	4.4	7
32	Multi-site implementation of whole genome sequencing for hospital infection control: A prospective genomic epidemiological analysis. The Lancet Regional Health - Western Pacific, 2022, 23, 100446.	2.9	6
33	Defective Severe Acute Respiratory Syndrome Coronavirus 2 Immune Responses in an Immunocompromised Individual With Prolonged Viral Replication. Open Forum Infectious Diseases, 2021, 8, ofab359.	0.9	5
34	Lab-in-a-van: Rapid SARS-CoV-2 testing response with a mobile laboratory. EBioMedicine, 2022, 79, 103983.	6.1	4
35	Viral Genomics to Inform Infection-control Response in Occupational Coronavirus Disease 2019 (COVID-19) Transmission. Clinical Infectious Diseases, 2020, 73, e1881-e1884.	5.8	3
36	Recent trends in invasive group A Streptococcus disease in Victoria. Communicable Diseases Intelligence (2018), 2019, 43, .	0.7	3

#	ARTICLE	IF	CITATIONS
37	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
38	Genomic Characterisation Reveals a Dominant Lineage of SARS-CoV-2 in Papua New Guinea. <i>Virus Evolution</i> , 0, , .	4.9	0