

# Stanley Pang

## List of Publications by Year in descending order

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50  
papers

898  
citations

471509

17  
h-index

526287

27  
g-index

53  
all docs

53  
docs citations

53  
times ranked

1478  
citing authors

#	ARTICLE	IF	CITATIONS
1	Antimicrobial-resistant CC17 <i>Enterococcus faecium</i> : The past, the present and the future. <i>Journal of Global Antimicrobial Resistance</i> , 2019, 16, 36-47.	2.2	106
2	Isolation and plasmid characterization of carbapenemase (IMP-4) producing <i>Salmonella enterica</i> Typhimurium from cats. <i>Scientific Reports</i> , 2016, 6, 35527.	3.3	68
3	Dissemination and persistence of extended-spectrum cephalosporin-resistance encoding <i>Incl1-bla<sub>CTXM-1</sub></i> plasmid among <i>Escherichia coli</i> in pigs. <i>ISME Journal</i> , 2018, 12, 2352-2362.	9.8	56
4	Evolutionary origins of the emergent ST796 clone of vancomycin resistant <i>Enterococcus faecium</i> . <i>PeerJ</i> , 2017, 5, e2916.	2.0	46
5	Clonal diversity and geographic distribution of methicillin-resistant <i>Staphylococcus pseudintermedius</i> from Australian animals: Discovery of novel sequence types. <i>Veterinary Microbiology</i> , 2018, 213, 58-65.	1.9	45
6	<i>Candida auris</i> Sternal Osteomyelitis in a Man from Kenya Visiting Australia, 2015. <i>Emerging Infectious Diseases</i> , 2019, 25, 192-194.	4.3	41
7	Genomic diversity and adaptation of <i>Salmonella enterica</i> serovar Typhimurium from analysis of six genomes of different phage types. <i>BMC Genomics</i> , 2013, 14, 718.	2.8	34
8	Molecular Characterization of Methicillin-Resistant <i>Staphylococcus aureus</i> Isolated from Australian Animals and Veterinarians. <i>Microbial Drug Resistance</i> , 2018, 24, 203-212.	2.0	33
9	Clonal Expansion of New Penicillin-Resistant Clade of <i>Neisseria meningitidis</i> Serogroup W Clonal Complex 11, Australia. <i>Emerging Infectious Diseases</i> , 2017, 23, 1364-1367.	4.3	30
10	Molecular Epidemiology of Methicillin-Resistant <i>Staphylococcus aureus</i> Isolated from Australian Veterinarians. <i>PLoS ONE</i> , 2016, 11, e0146034.	2.5	29
11	Genomic characterization of coagulase-negative staphylococci including methicillin-resistant <i>Staphylococcus sciuri</i> causing bovine mastitis. <i>Veterinary Microbiology</i> , 2018, 219, 17-22.	1.9	29
12	Genetic Relationships of Phage Types and Single Nucleotide Polymorphism Typing of <i>Salmonella enterica</i> Serovar Typhimurium. <i>Journal of Clinical Microbiology</i> , 2012, 50, 727-734.	3.9	23
13	Linezolid-resistant ST872 <i>Enterococcus faecium</i> harbouring <i>optrA</i> and <i>cfr (D)</i> oxazolidinone resistance genes. <i>International Journal of Antimicrobial Agents</i> , 2020, 55, 105831.	2.5	22
14	Isolation of <i>mecC</i> MRSA in Australia. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2348-2349.	3.0	21
15	Characterization of Staphylococcal Cassette Chromosome <i>mec</i> Elements from Methicillin-Resistant <i>Staphylococcus pseudintermedius</i> Infections in Australian Animals. <i>MSphere</i> , 2018, 3, .	2.9	20
16	<i>Mycobacterium chimaera</i> colonisation of heater-cooler units (HCU) in Western Australia, 2015: investigation of possible iatrogenic infection using whole genome sequencing. <i>Eurosurveillance</i> , 2016, 21, .	7.0	20
17	Misidentification of <i>Staphylococcus aureus</i> by the Cepheid Xpert MRSA/SA BC Assay Due to Deletions in the <i>spa</i> Gene. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	18
18	Genomic characterization of a novel poxvirus from a flying fox: evidence for a new genus?. <i>Journal of General Virology</i> , 2016, 97, 2363-2375.	2.9	18

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19	Prevalence and antimicrobial resistance of MRSA across different pig age groups in an intensive pig production system in Australia. <i>Zoonoses and Public Health</i> , 2020, 67, 576-586.	2.2	14
20	A three-year whole genome sequencing perspective of <i>Enterococcus faecium</i> sepsis in Australia. <i>PLoS ONE</i> , 2020, 15, e0228781.	2.5	14
21	Reverse zoonotic transmission of community-associated MRSA ST1-IV to a dairy cow. <i>International Journal of Antimicrobial Agents</i> , 2017, 50, 125-126.	2.5	13
22	Characterisation of <i>Staphylococcus felis</i> isolated from cats using whole genome sequencing. <i>Veterinary Microbiology</i> , 2018, 222, 98-104.	1.9	13
23	Antimicrobial Resistance in Porcine Enterococci in Australia and the Ramifications for Human Health. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	13
24	Peptidyl-Prolyl Isomerase <i>ppiB</i> Is Essential for Proteome Homeostasis and Virulence in <i>Burkholderia pseudomallei</i> . <i>Infection and Immunity</i> , 2019, 87, .	2.2	12
25	Molecular characterization and evolution of the first outbreak of vancomycin-resistant <i>Enterococcus faecium</i> in Western Australia. <i>International Journal of Antimicrobial Agents</i> , 2019, 53, 814-819.	2.5	12
26	Antimicrobial resistance and genomic insights into bovine mastitis-associated <i>Staphylococcus aureus</i> in Australia. <i>Veterinary Microbiology</i> , 2020, 250, 108850.	1.9	11
27	Australian Group on Antimicrobial Resistance (AGAR) Australian Enterococcal Sepsis Outcome Programme (AESOP) Annual Report 2018. <i>Communicable Diseases Intelligence (2018)</i> , 2020, 44, .	0.7	11
28	A multicentre outbreak of ST45 MRSA containing deletions in the <i>spa</i> gene in New South Wales, Australia. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1112-1116.	3.0	10
29	Australian Group on Antimicrobial Resistance (AGAR) Australian Enterococcal Sepsis Outcome Programme (AESOP) Annual Report 2017. <i>Communicable Diseases Intelligence (2018)</i> , 2019, 43, .	0.7	10
30	Australian Group on Antimicrobial Resistance (AGAR) Australian <i>Staphylococcus aureus</i> Sepsis Outcome Programme (ASSOP) Annual Report 2017. <i>Communicable Diseases Intelligence (2018)</i> , 2019, 43, .	0.7	10
31	Multiple introductions of methicillin-resistant <i>Staphylococcus aureus</i> ST612 into Western Australia associated both with human and equine reservoirs. <i>International Journal of Antimicrobial Agents</i> , 2019, 54, 681-685.	2.5	9
32	Severe Disease Caused by Community-Associated MRSA ST398 Type V, Australia, 2017. <i>Emerging Infectious Diseases</i> , 2019, 25, 190-192.	4.3	9
33	Progress towards a coordinated, national paediatric antimicrobial resistance surveillance programme: <i>Staphylococcus aureus</i> , enterococcal and Gram-negative bacteraemia in Australia. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 1639-1644.	3.0	9
34	Evaluating coverage bias in next-generation sequencing of <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2021, 16, e0253440.	2.5	8
35	Australian Group on Antimicrobial Resistance (AGAR) Australian <i>Staphylococcus aureus</i> Sepsis Outcome Programme (ASSOP) Annual Report 2018. <i>Communicable Diseases Intelligence (2018)</i> , 2020, 44, .	0.7	8
36	Genomic and Epidemiological Evidence of a Dominant Panton-Valentine Leucocidin-Positive Methicillin Resistant <i>Staphylococcus aureus</i> Lineage in Sri Lanka and Presence Among Isolates From the United Kingdom and Australia. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 123.	3.9	7

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37	Identification and characterisation of fosfomycin resistance in Escherichia coli urinary tract infection isolates from Australia. International Journal of Antimicrobial Agents, 2020, 56, 106121.	2.5	7
38	Investigation of a Lomentospora prolificans case cluster with whole genome sequencing. Medical Mycology Case Reports, 2020, 29, 1-4.	1.3	6
39	Australian Group on Antimicrobial Resistance Australian Enterococcal Sepsis Outcome Programme annual report, 2014. Communicable Diseases Intelligence, 2016, 40, E236-43.	0.5	6
40	Sulfamethoxazole/trimethoprim resistance overcall by VITEK® 2 and BD Phoenix®, in community-associated MRSA and MSSA. Journal of Antimicrobial Chemotherapy, 2019, 74, 3639-3641.	3.0	5
41	Australian Group on Antimicrobial Resistance (AGAR) Australian Enterococcal Sepsis Outcome Programme (AESOP) Annual Report 2019. Communicable Diseases Intelligence (2018), 2020, 44, .	0.7	5
42	Australian Group on Antimicrobial Resistance (AGAR) Australian Staphylococcus aureus Sepsis Outcome Programme (ASSOP) Annual Report 2019. Communicable Diseases Intelligence (2018), 2020, 44, .	0.7	5
43	Complete Genome Sequence of a Staphylococcus aureus Sequence Type 612 Isolate from an Australian Horse. Microbiology Resource Announcements, 2018, 7, .	0.6	4
44	Apophysomyces Variabilis Infection in Transplant Recipients due to Unrecognized Infection in an Intravenous Drug-Using Donor. Transplantation, 2022, 106, e169-e171.	1.0	4
45	Australian Group on Antimicrobial Resistance (AGAR) Australian Enterococcal Sepsis Outcome Programme (AESOP) Annual Report 2016. Communicable Diseases Intelligence (2018), 2018, 42, .	0.7	2
46	Australian Group on Antimicrobial Resistance (AGAR) Australian Staphylococcus aureus Sepsis Outcome Programme (ASSOP) Annual Report 2016. Communicable Diseases Intelligence (2018), 2018, 42, .	0.7	1
47	Australian Group on Antimicrobial Resistance (AGAR) Australian Enterococcal Sepsis Outcome Programme (AESOP) Annual Report 2015. Communicable Diseases Intelligence (2018), 2018, 42, .	0.7	1
48	Genome-wide association studies reveal candidate genes associated to bacteraemia caused by ST93-IV CA-MRSA. BMC Genomics, 2021, 22, 418.	2.8	0
49	The changing molecular epidemiology of Enterococcus faecium harbouring the van operon at a teaching hospital in Western Australia: A fifteen-year retrospective study. International Journal of Medical Microbiology, 2022, 312, 151546.	3.6	0
50	Australian Group on Antimicrobial Resistance (AGAR) Australian Staphylococcus aureus Sepsis Outcome Programme (ASSOP) Annual Report 2015. Communicable Diseases Intelligence (2018), 2018, 42, .	0.7	0