

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	The changing molecular epidemiology of <i>Enterococcus faecium</i> harbouring the van operon at a teaching hospital in Western Australia: A fifteen-year retrospective study. <i>International Journal of Medical Microbiology</i> , 2022, 312, 151546.	3.6	0
2	<i>Apophysomyces Variabilis</i> Infection in Transplant Recipients due to Unrecognized Infection in an Intravenous Drug-Using Donor. <i>Transplantation</i> , 2022, 106, e169-e171.	1.0	4
3	Antimicrobial Resistance in Porcine <i>Enterococci</i> in Australia and the Ramifications for Human Health. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	13
4	Evaluating coverage bias in next-generation sequencing of <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2021, 16, e0253440.	2.5	8
5	Genome-wide association studies reveal candidate genes associated to bacteraemia caused by ST93-IV CA-MRSA. <i>BMC Genomics</i> , 2021, 22, 418.	2.8	0
6	Linezolid-resistant ST872 <i>Enterococcus faecium</i> harbouring <i>optrA</i> and <i>cfr</i> (D) oxazolidinone resistance genes. <i>International Journal of Antimicrobial Agents</i> , 2020, 55, 105831.	2.5	22
7	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
8	Identification and characterisation of fosfomycin resistance in <i>Escherichia coli</i> urinary tract infection isolates from Australia. <i>International Journal of Antimicrobial Agents</i> , 2020, 56, 106121.	2.5	7
9	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
10	Investigation of a <i>Lomentospora prolificans</i> case cluster with whole genome sequencing. <i>Medical Mycology Case Reports</i> , 2020, 29, 1-4.	1.3	6
11	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
12	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
13	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
14	Australian Group on Antimicrobial Resistance (AGAR) Australian <i>Staphylococcus aureus</i> Sepsis Outcome Programme (ASSOP) Annual Report 2018. <i>Communicable Diseases Intelligence</i> (2018), 2020, 44, .	0.7	8
15	Australian Group on Antimicrobial Resistance (AGAR) Australian Enterococcal Sepsis Outcome Programme (AESOP) Annual Report 2018. <i>Communicable Diseases Intelligence</i> (2018), 2020, 44, .	0.7	11
16	Australian Group on Antimicrobial Resistance (AGAR) Australian Enterococcal Sepsis Outcome Programme (AESOP) Annual Report 2019. <i>Communicable Diseases Intelligence</i> (2018), 2020, 44, .	0.7	5
17	Australian Group on Antimicrobial Resistance (AGAR) Australian <i>Staphylococcus aureus</i> Sepsis Outcome Programme (ASSOP) Annual Report 2019. <i>Communicable Diseases Intelligence</i> (2018), 2020, 44, .	0.7	5
18	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

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19	Sulfamethoxazole/trimethoprim resistance overcall by VITEK [®] 2 and BD Phoenix ^{®,†} in community-associated MRSA and MSSA. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 3639-3641.	3.0	5
20	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
21	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
22	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
23	<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
24	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
25	Severe Disease Caused by Community-Associated MRSA ST398 Type V, Australia, 2017. <i>Emerging Infectious Diseases</i> , 2019, 25, 190-192.	4.3	9
26	Australian Group on Antimicrobial Resistance (AGAR) Australian Enterococcal Sepsis Outcome Programme (AESOP) Annual Report 2017. <i>Communicable Diseases Intelligence</i> (2018), 2019, 43, .	0.7	10
27	Australian Group on Antimicrobial Resistance (AGAR) Australian <i>Staphylococcus aureus</i> Sepsis Outcome Programme (ASSOP) Annual Report 2017. <i>Communicable Diseases Intelligence</i> (2018), 2019, 43, .	0.7	10
28	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
29	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
30	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
31	Complete Genome Sequence of a <i>Staphylococcus aureus</i> Sequence Type 612 Isolate from an Australian Horse. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	4
32	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
33	Dissemination and persistence of extended-spectrum cephalosporin-resistance encoding <i>Inc11-bla</i> CTXM-1 plasmid among <i>Escherichia coli</i> in pigs. <i>ISME Journal</i> , 2018, 12, 2352-2362.	9.8	56
34	Characterisation of <i>Staphylococcus felis</i> isolated from cats using whole genome sequencing. <i>Veterinary Microbiology</i> , 2018, 222, 98-104.	1.9	13
35	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
36	Australian Group on Antimicrobial Resistance (AGAR) Australian <i>Staphylococcus aureus</i> Sepsis Outcome Programme (ASSOP) Annual Report 2016. <i>Communicable Diseases Intelligence</i> (2018), 2018, 42, .	0.7	1

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37	Australian Group on Antimicrobial Resistance (AGAR) Australian Enterococcal Sepsis Outcome Programme (AESOP) Annual Report 2015. Communicable Diseases Intelligence (2018), 2018, 42, .	0.7	1
38	Australian Group on Antimicrobial Resistance (AGAR) Australian Enterococcal Sepsis Outcome Programme (AESOP) Annual Report 2016. Communicable Diseases Intelligence (2018), 2018, 42, .	0.7	2
39	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
40	Reverse zoonotic transmission of community-associated MRSA ST1-IV to a dairy cow. International Journal of Antimicrobial Agents, 2017, 50, 125-126.	2.5	13
41	Clonal Expansion of New Penicillin-Resistant Clade of <i>Neisseria meningitidis</i> Serogroup W Clonal Complex 11, Australia. Emerging Infectious Diseases, 2017, 23, 1364-1367.	4.3	30
42	Evolutionary origins of the emergent ST796 clone of vancomycin resistant <i>Enterococcus faecium</i> . PeerJ, 2017, 5, e2916.	2.0	46
43	Molecular Epidemiology of Methicillin-Resistant Staphylococcus aureus Isolated from Australian Veterinarians. PLoS ONE, 2016, 11, e0146034.	2.5	29
44	Isolation and plasmid characterization of carbapenemase (IMP-4) producing Salmonella enterica Typhimurium from cats. Scientific Reports, 2016, 6, 35527.	3.3	68
45	Isolation of <i>mecC</i> MRSA in Australia. Journal of Antimicrobial Chemotherapy, 2016, 71, 2348-2349.	3.0	21
46	Genomic characterization of a novel poxvirus from a flying fox: evidence for a new genus?. Journal of General Virology, 2016, 97, 2363-2375.	2.9	18
47	Mycobacterium chimaera colonisation of heater-cooler units (HCU) in Western Australia, 2015: investigation of possible iatrogenic infection using whole genome sequencing. Eurosurveillance, 2016, 21, .	7.0	20
48	Australian Group on Antimicrobial Resistance Australian Enterococcal Sepsis Outcome Programme annual report, 2014. Communicable Diseases Intelligence, 2016, 40, E236-43.	0.5	6
49	Genomic diversity and adaptation of Salmonella enterica serovar Typhimurium from analysis of six genomes of different phage types. BMC Genomics, 2013, 14, 718.	2.8	34
50	Genetic Relationships of Phage Types and Single Nucleotide Polymorphism Typing of Salmonella enterica Serovar Typhimurium. Journal of Clinical Microbiology, 2012, 50, 727-734.	3.9	23