

Andries J Van Tonder

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

2,235
citations

331670

21
h-index

330143

37
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47
all docs

47
docs citations

47
times ranked

3217
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic Insights Into the Mechanism of Carbapenem Resistance Dissemination in Enterobacterales From a Tertiary Public Health Setting in South Asia. <i>Clinical Infectious Diseases</i> , 2023, 76, 119-133.	5.8	6
2	International links between <i>Streptococcus pneumoniae</i> vaccine serotype 4 sequence type (ST) 801 in Northern European shipyard outbreaks of invasive pneumococcal disease. <i>Vaccine</i> , 2022, 40, 1054-1060.	3.8	4
3	Population structure and transmission of <i>Mycobacterium bovis</i> in Ethiopia. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
4	Genomic and temporal analyses of <i>Mycobacterium bovis</i> in southern Brazil. <i>Microbial Genomics</i> , 2021, 7, .	2.0	7
5	Predicted structural mimicry of spike receptor-binding motifs from highly pathogenic human coronaviruses. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3938-3953.	4.1	25
6	Inferring <i>Mycobacterium bovis</i> transmission between cattle and badgers using isolates from the Randomised Badger Culling Trial. <i>PLoS Pathogens</i> , 2021, 17, e1010075.	4.7	20
7	A mosaic tetracycline resistance gene <i>tet(S/M)</i> detected in an MDR pneumococcal CC230 lineage that underwent capsular switching in South Africa. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 512-520.	3.0	12
8	Relationships among streptococci from the mitis group, misidentified as <i>Streptococcus pneumoniae</i> . <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2020, 39, 1865-1878.	2.9	7
9	A New Pneumococcal Capsule Type, 10D, is the 100th Serotype and Has a Large <i>cps</i> Fragment from an Oral <i>Streptococcus</i> . <i>MBio</i> , 2020, 11, .	4.1	219
10	Visualizing variation within Global Pneumococcal Sequence Clusters (GPSCs) and country population snapshots to contextualize pneumococcal isolates. <i>Microbial Genomics</i> , 2020, 6, .	2.0	25
11	Vaccination of Icelandic Children with the 10-Valent Pneumococcal Vaccine Leads to a Significant Herd Effect among Adults in Iceland. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	16
12	Pneumococcal lineages associated with serotype replacement and antibiotic resistance in childhood invasive pneumococcal disease in the post-PCV13 era: an international whole-genome sequencing study. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 759-769.	9.1	165
13	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. <i>EBioMedicine</i> , 2019, 43, 338-346.	6.1	168
14	Genomic Analyses of >3,100 Nasopharyngeal Pneumococci Revealed Significant Differences Between Pneumococci Recovered in Four Different Geographical Regions. <i>Frontiers in Microbiology</i> , 2019, 10, 317.	3.5	9
15	Molecular epidemiology and whole genome sequencing analysis of clinical <i>Mycobacterium bovis</i> from Ghana. <i>PLoS ONE</i> , 2019, 14, e0209395.	2.5	20
16	Putative novel <i>cps</i> loci in a large global collection of pneumococci. <i>Microbial Genomics</i> , 2019, 5, .	2.0	14
17	Effect of Vaccination on Pneumococci Isolated from the Nasopharynx of Healthy Children and the Middle Ear of Children with Otitis Media in Iceland. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	26
18	Genome Sequencing Reveals a Large and Diverse Repertoire of Antimicrobial Peptides. <i>Frontiers in Microbiology</i> , 2018, 9, 2012.	3.5	34

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19	Diverse <i>Streptococcus pneumoniae</i> Strains Drive a Mucosal-Associated Invariant T-Cell Response Through Major Histocompatibility Complex class II-Related Molecule-Dependent and Cytokine-Driven Pathways. <i>Journal of Infectious Diseases</i> , 2018, 217, 988-999.	4.0	59
20	Global Distribution of Invasive Serotype 35D <i>Streptococcus pneumoniae</i> Isolates following Introduction of 13-Valent Pneumococcal Conjugate Vaccine. <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	12
21	Arginine-deprivation-induced oxidative damage sterilizes <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 9779-9784.	7.1	97
22	SeroBA: rapid high-throughput serotyping of <i>Streptococcus pneumoniae</i> from whole genome sequence data. <i>Microbial Genomics</i> , 2018, 4, .	2.0	68
23	Pneumococcal prophages are diverse, but not without structure or history. <i>Scientific Reports</i> , 2017, 7, 42976.	3.3	62
24	Putatively novel serotypes and the potential for reduced vaccine effectiveness: capsular locus diversity revealed among 5405 pneumococcal genomes. <i>Microbial Genomics</i> , 2016, 2, 000090.	2.0	41
25	Genomics Reveals the Worldwide Distribution of Multidrug-Resistant Serotype 6E Pneumococci. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2271-2285.	3.9	44
26	Genomic analyses of pneumococci reveal a wide diversity of bacteriocins including pneumocyclin, a novel circular bacteriocin. <i>BMC Genomics</i> , 2015, 16, 554.	2.8	67
27	Genome Sequences of Three <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar <i>Infantis</i> Strains from Healthy Broiler Chicks in Hungary and in the United Kingdom. <i>Genome Announcements</i> , 2015, 3, .	0.8	31
28	Defining the Estimated Core Genome of Bacterial Populations Using a Bayesian Decision Model. <i>PLoS Computational Biology</i> , 2014, 10, e1003788.	3.2	72
29	Evidence of antimicrobial resistance-conferring genetic elements among pneumococci isolated prior to 1974. <i>BMC Genomics</i> , 2013, 14, 500.	2.8	40
30	Comparative Genomics of Vancomycin-Resistant <i>Staphylococcus aureus</i> Strains and Their Positions within the Clade Most Commonly Associated with Methicillin-Resistant <i>S. aureus</i> Hospital-Acquired Infection in the United States. <i>MBio</i> , 2012, 3, .	4.1	125
31	Antigenic diversity is generated by distinct evolutionary mechanisms in African trypanosome species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 3416-3421.	7.1	137
32	Comparative genomic analyses of the <i>Taylorellae</i> . <i>Veterinary Microbiology</i> , 2012, 159, 195-203.	1.9	9
33	Lineage-specific Virulence Determinants of <i>Haemophilus influenzae</i> Biogroup <i>aegyptius</i> . <i>Emerging Infectious Diseases</i> , 2012, 18, 449-457.	4.3	22
34	Genome sequence of <i>Staphylococcus lugdunensis</i> N920143 allows identification of putative colonization and virulence factors. <i>FEMS Microbiology Letters</i> , 2011, 322, 60-67.	1.8	90
35	A Conserved Acetyl Esterase Domain Targets Diverse Bacteriophages to the Vi Capsular Receptor of <i>Salmonella enterica</i> Serovar Typhi. <i>Journal of Bacteriology</i> , 2010, 192, 5746-5754.	2.2	79
36	Evolutionary dynamics of <i>Clostridium difficile</i> over short and long time scales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 7527-7532.	7.1	346