

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
g-index

47
all docs

47
docs citations

47
times ranked

3217
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary dynamics of <i>Clostridium difficile</i> over short and long time scales. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7527-7532.	7.1	346
2	A New Pneumococcal Capsule Type, 10D, is the 100th Serotype and Has a Large <i>cps</i> Fragment from an Oral Streptococcus. MBio, 2020, 11, .	4.1	219
3	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. EBioMedicine, 2019, 43, 338-346.	6.1	168
4	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. Lancet Infectious Diseases, The, 2019, 19, 759-769.	9.1	165
5	Antigenic diversity is generated by distinct evolutionary mechanisms in African trypanosome species. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3416-3421.	7.1	137
6	Comparative Genomics of Vancomycin-Resistant Staphylococcus aureus Strains and Their Positions within the Clade Most Commonly Associated with Methicillin-Resistant S. aureus Hospital-Acquired Infection in the United States. MBio, 2012, 3, .	4.1	125
7	Arginine-deprivation-induced oxidative damage sterilizes <i>Mycobacterium tuberculosis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 9779-9784.	7.1	97
8	Genome sequence of Staphylococcus lugdunensis N920143 allows identification of putative colonization and virulence factors. FEMS Microbiology Letters, 2011, 322, 60-67.	1.8	90
9	A Conserved Acetyl Esterase Domain Targets Diverse Bacteriophages to the Vi Capsular Receptor of <i>Salmonella enterica</i> Serovar Typhi. Journal of Bacteriology, 2010, 192, 5746-5754.	2.2	79
10	Defining the Estimated Core Genome of Bacterial Populations Using a Bayesian Decision Model. PLoS Computational Biology, 2014, 10, e1003788.	3.2	72
11	SeroBA: rapid high-throughput serotyping of Streptococcus pneumoniae from whole genome sequence data. Microbial Genomics, 2018, 4, .	2.0	68
12	Genomic analyses of pneumococci reveal a wide diversity of bacteriocins including pneumocyclacin, a novel circular bacteriocin. BMC Genomics, 2015, 16, 554.	2.8	67
13	Pneumococcal prophages are diverse, but not without structure or history. Scientific Reports, 2017, 7, 42976.	3.3	62
14	Diverse Streptococcus pneumoniae Strains Drive a Mucosal-Associated Invariant T-Cell Response Through Major Histocompatibility Complex class II-Related Molecule-Dependent and Cytokine-Driven Pathways. Journal of Infectious Diseases, 2018, 217, 988-999.	4.0	59
15	Genomics Reveals the Worldwide Distribution of Multidrug-Resistant Serotype 6E Pneumococci. Journal of Clinical Microbiology, 2015, 53, 2271-2285.	3.9	44
16	Putatively novel serotypes and the potential for reduced vaccine effectiveness: capsular locus diversity revealed among 5405 pneumococcal genomes. Microbial Genomics, 2016, 2, 000090.	2.0	41
17	Evidence of antimicrobial resistance-conferring genetic elements among pneumococci isolated prior to 1974. BMC Genomics, 2013, 14, 500.	2.8	40
18	Genome Sequencing Reveals a Large and Diverse Repertoire of Antimicrobial Peptides. Frontiers in Microbiology, 2018, 9, 2012.	3.5	34

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19	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
20	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
21	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
22	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
23	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
24	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
25	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
26	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
27	Putative novel <i>cps</i> loci in a large global collection of pneumococci. <i>Microbial Genomics</i> , 2019, 5, .	2.0	14
28	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
29	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
30	Comparative genomic analyses of the <i>Taylorellae</i> . <i>Veterinary Microbiology</i> , 2012, 159, 195-203.	1.9	9
31	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
32	Population structure and transmission of <i>Mycobacterium bovis</i> in Ethiopia. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
33	Relationships among streptococci from the <i>mitis</i> group, misidentified as <i>Streptococcus pneumoniae</i> . <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2020, 39, 1865-1878.	2.9	7
34	Genomic and temporal analyses of <i>Mycobacterium bovis</i> in southern Brazil. <i>Microbial Genomics</i> , 2021, 7, .	2.0	7
35	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
36	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