Anthony M Smith

List of Publications by Year in descending order

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218677 168389 3,029 59 26 53 citations g-index h-index papers 60 60 60 3472 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of Salmonella Typhi identifies inter- and intracontinental transmission events. Nature Genetics, 2015, 47, 632-639.	21.4	403
2	PulseNet International: Vision for the implementation of whole genome sequencing (WGS) for global food-borne disease surveillance. Eurosurveillance, 2017, 22, .	7.0	307
3	Intercontinental dissemination of azithromycin-resistant shigellosis through sexual transmission: a cross-sectional study. Lancet Infectious Diseases, The, 2015, 15, 913-921.	9.1	204
4	Distinct Salmonella Enteritidis lineages associated with enterocolitis in high-income settings and invasive disease in low-income settings. Nature Genetics, 2016, 48, 1211-1217.	21.4	191
5	Outbreak of <i>Listeria monocytogenes </i> in South Africa, 2017â€"2018: Laboratory Activities and Experiences Associated with Whole-Genome Sequencing Analysis of Isolates. Foodborne Pathogens and Disease, 2019, 16, 524-530.	1.8	142
6	Outbreak of Listeriosis in South Africa Associated with Processed Meat. New England Journal of Medicine, 2020, 382, 632-643.	27.0	139
7	Novel Mechanism of Resistance to Oxazolidinones, Macrolides, and Chloramphenicol in Ribosomal Protein L4 of the Pneumococcus. Antimicrobial Agents and Chemotherapy, 2005, 49, 3554-3557.	3.2	138
8	Comparative Genomics of Vibrio cholerae from Haiti, Asia, and Africa. Emerging Infectious Diseases, 2011, 17, 2113-21.	4.3	136
9	Alterations in PBP 1A Essential for High-Level Penicillin Resistance in <i>Streptococcus pneumoniae</i> . Antimicrobial Agents and Chemotherapy, 1998, 42, 1329-1333.	3.2	115
10	Species-wide whole genome sequencing reveals historical global spread and recent local persistence in Shigella flexneri. ELife, 2015, 4, e07335.	6.0	94
11	Characterization of Toxigenic Vibrio cholerae from Haiti, 2010–2011. Emerging Infectious Diseases, 2011, 17, 2122-9.	4.3	85
12	Alterations in MurM, a Cell Wall Muropeptide Branching Enzyme, Increase High-Level Penicillin and Cephalosporin Resistance in Streptococcus pneumoniae. Antimicrobial Agents and Chemotherapy, 2001, 45, 2393-2396.	3.2	78
13	In Vitro Evaluation of the Antimicrobial Activity of Ceftaroline against Cephalosporin-Resistant Isolates of <i>Streptococcus pneumoniae</i> Antimicrobial Agents and Chemotherapy, 2009, 53, 552-556.	3.2	65
14	Rapid Detection of Penicillin-Resistant <i>Streptococcus pneumoniae</i> in Cerebrospinal Fluid by a Seminested-PCR Strategy. Journal of Clinical Microbiology, 1998, 36, 453-457.	3.9	61
15	Emergence of levofloxacin-non-susceptible Streptococcus pneumoniae and treatment for multidrug-resistant tuberculosis in children in South Africa: a cohort observational surveillance study. Lancet, The, 2008, 371, 1108-1113.	13.7	57
16	Three Predominant Clones Identified Within Penicillin-Resistant South African Isolates of Streptococcus pneumoniae. Microbial Drug Resistance, 1997, 3, 385-389.	2.0	48
17	Molecular Surveillance Identifies Multiple Transmissions of Typhoid in West Africa. PLoS Neglected Tropical Diseases, 2016, 10, e0004781.	3.0	46
18	Fluoroquinolone-Resistant Typhoid, South Africa. Emerging Infectious Diseases, 2010, 16, 879-880.	4.3	46

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19	An Outbreak of Foodborne Salmonellosis in Rural KwaZulu-Natal, South Africa. Foodborne Pathogens and Disease, 2011, 8, 693-697.	1.8	40
20	Amino Acid Mutations Essential to Production of an Altered PBP 2X Conferring High-Level β-Lactam Resistance in a Clinical Isolate of Streptococcus pneumoniae. Antimicrobial Agents and Chemotherapy, 2005, 49, 4622-4627.	3.2	37
21	Meningococcal Disease in South Africa, 1999–2002. Emerging Infectious Diseases, 2007, 13, 273-281.	4.3	37
22	Cholera outbreak in South Africa, 2008–2009: Laboratory analysis of Vibrio cholerae O1 strains. Journal of Infectious Diseases, 2013, 208, S39-S45.	4.0	33
23	Telithromycin Resistance in Streptococcus pneumoniae Is Conferred by a Deletion in the Leader Sequence of erm (B) That Increases rRNA Methylation. Antimicrobial Agents and Chemotherapy, 2008, 52, 435-440.	3.2	32
24	Clinical and Microbiological Features of <i>Salmonella</i> Neningitis in a South African Population, 2003â€"2013. Clinical Infectious Diseases, 2015, 61, S272-S282.	5.8	32
25	Non-Penicillin-Binding Protein Mediated High-Level Penicillin and Cephalosporin Resistance in a Hungarian Clone ofStreptococcus pneumoniae. Microbial Drug Resistance, 2000, 6, 105-110.	2.0	29
26	Site-Specific Mutagenesis Analysis of PBP 1A from a Penicillin-Cephalosporin-Resistant Pneumococcal Isolate. Antimicrobial Agents and Chemotherapy, 2003, 47, 387-389.	3.2	28
27	Altered PBP 2A and Its Role in the Development of Penicillin, Cefotaxime, and Ceftriaxone Resistance in a Clinical Isolate of Streptococcus pneumoniae. Antimicrobial Agents and Chemotherapy, 2005, 49, 2002-2007.	3.2	26
28	Emergence of a Pneumococcal Clone with Cephalosporin Resistance and Penicillin Susceptibility. Antimicrobial Agents and Chemotherapy, 2001, 45, 2648-2650.	3.2	25
29	Highly Resistant Cholera Outbreak Strain in Zimbabwe. New England Journal of Medicine, 2020, 383, 687-689.	27.0	25
30	High-Level Telithromycin Resistance in a Clinical Isolate of Streptococcus pneumoniae. Antimicrobial Agents and Chemotherapy, 2007, 51, 1092-1095.	3.2	23
31	Nosocomial Outbreak of Salmonella enterica Serovar Typhimurium Primarily Affecting a Pediatric Ward in South Africa in 2012. Journal of Clinical Microbiology, 2014, 52, 627-631.	3.9	23
32	Application of <i>pbp1A</i> PCR in Identification of Penicillin-Resistant <i>Streptococcus pneumoniae</i> Journal of Clinical Microbiology, 1999, 37, 628-632.	3.9	22
33	Analysis of Penicillin-Binding Protein1band2aGenes fromStreptococcus pneumoniae. Microbial Drug Resistance, 2000, 6, 127-131.	2.0	18
34	Genetic Characterization of Multidrug-Resistant, Extended-Spectrum- \hat{I}^2 -Lactamase-Producing Vibrio cholerae O1 Outbreak Strains, Mpumalanga, South Africa, 2008. Journal of Clinical Microbiology, 2011, 49, 2976-2979.	3.9	18
35	International collaboration tracks typhoid fever cases over two continents from South Africa to Australia. Journal of Medical Microbiology, 2011, 60, 1405-1407.	1.8	16
36	Escherichia coliO104 Associated with Human Diarrhea, South Africa, 2004–2011. Emerging Infectious Diseases, 2012, 18, 1314-7.	4.3	16

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37	Heterogeneous Macrolide Resistance and Gene Conversion in the Pneumococcus. Antimicrobial Agents and Chemotherapy, 2006, 50, 359-361.	3.2	15
38	Surveillance for enterohaemorrhagic Escherichia coli associated with human diarrhoea in South Africa, 2006–2009. Journal of Medical Microbiology, 2011, 60, 681-683.	1.8	14
39	Typhoid Fever in South Africa in an Endemic HIV Setting. PLoS ONE, 2016, 11, e0164939.	2.5	14
40	Plasmid-mediated quinolone resistance in Salmonella from South Africa. Journal of Medical Microbiology, 2009, 58, 1393-1394.	1.8	13
41	Molecular characterization of extended-spectrum β-lactamase-producing Shigella isolates from humans in South Africa, 2003–2009. Journal of Medical Microbiology, 2012, 61, 162-164.	1.8	12
42	The Burden of Typhoid Fever in South Africa: The Potential Impact of Selected Interventions. American Journal of Tropical Medicine and Hygiene, 2018, 99, 55-63.	1.4	12
43	Detailed modelling of a large sample of Herschel sources in the Lockman Hole: identification of cold dust and of lensing candidates through their anomalous SEDsa~ Monthly Notices of the Royal Astronomical Society, 2014, 445, 3848-3861.	4.4	11
44	Comparative Characterization of Vibrio cholerae O1 from Five Sub-Saharan African Countries Using Various Phenotypic and Genotypic Techniques. PLoS ONE, 2015, 10, e0142989.	2.5	11
45	Outbreaks of food-borne diseasea common occurrence but rarely reported. South African Medical Journal, 2007, 97, 1272.	0.6	11
46	Genome Sequence for Shiga Toxin-Producing Escherichia coli O26:H11, Associated with a Cluster of Hemolytic-Uremic Syndrome Cases in South Africa, 2017. Genome Announcements, 2017, 5, .	0.8	10
47	Emergence of <i>Vibrio cholerae</i> O1 Sequence Type 75, South Africa, 2018–2020. Emerging Infectious Diseases, 2021, 27, 2927-2931.	4.3	10
48	GEMS extend understanding of childhood diarrhoea. Lancet, The, 2016, 388, 1252-1254.	13.7	9
49	Development and evaluation of a multiple-locus variable-number tandem-repeats analysis assay for subtyping Salmonella Typhi strains from sub-Saharan Africa. Journal of Medical Microbiology, 2017, 66, 937-945.	1.8	9
50	Whole-genome sequencing to investigate two concurrent outbreaks of Salmonella Enteritidis in South Africa, 2018. Journal of Medical Microbiology, 2020, 69, 1303-1307.	1.8	9
51	Genome Sequences for a Cluster of Human Isolates of <i>Listeria monocytogenes</i> Identified in South Africa in 2015. Genome Announcements, 2016, 4, .	0.8	6
52	Shiga toxin-producing Escherichia coli O26:H11 associated with a cluster of haemolytic uraemic syndrome cases in South Africa, 2017. Access Microbiology, 2019, 1, e000061.	0.5	6
53	Review of molecular subtyping methodologies used to investigate outbreaks due to multidrug-resistant enteric bacterial pathogens in sub-Saharan Africa. African Journal of Laboratory Medicine, 2019, 8, 760.	0.6	6
54	Analysis of a temporal cluster of Shigella boydii isolates in Mpumalanga, South Africa, November to December 2007. Journal of Infection in Developing Countries, 2009, 3, 65-70.	1.2	5

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55	Possible Laboratory Contamination Leads to Incorrect Reporting of Vibrio cholerae O1 and Initiates an Outbreak Response. Journal of Clinical Microbiology, 2012, 50, 480-482.	3.9	4
56	Analysis of Vibrio cholerae isolates from the Northern Cape province of South Africa. Journal of Medical Microbiology, 2009, 58, 151-154.	1.8	3
57	Microbiological characterization of Salmonella enterica serotype Paratyphi, South Africa, 2003–2014. Journal of Medical Microbiology, 2015, 64, 1450-1453.	1.8	3
58	Epidemiological investigation of a typhoid fever outbreak in Sekhukhune District, Limpopo province, South Africa $\hat{a} \in 2017$. Southern African Journal of Infectious Diseases, 2020, 35, 107.	0.5	1
59	Genotypic Diversity and Characterization of Quinolone Resistant Determinants from Enterobacteriaceae in Yaoundé, Cameroon. Open Journal of Medical Microbiology, 2020, 10, 33-45.	0.4	0