

# Grant A Hill-Cawthorne

## List of Publications by Year in descending order

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Version: 2024-02-01

62  
papers

3,030  
citations

218381

26  
h-index

168136

53  
g-index

73  
all docs

73  
docs citations

73  
times ranked

4898  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluation of the rate, pattern and appropriateness of antibiotic prescription in a cohort of pilgrims suffering from upper respiratory tract infection during the 2018 Hajj season. Access Microbiology, 2022, 4, .	0.2	4
2	Travel-Related Antimicrobial Resistance: A Systematic Review. Tropical Medicine and Infectious Disease, 2021, 6, 11.	0.9	51
3	Health Risks, Preventive Behaviours and Respiratory Illnesses at the 2019 Arbaeen: Implications for COVID-19 and Other Pandemics. International Journal of Environmental Research and Public Health, 2021, 18, 3287.	1.2	7
4	Functional analysis of colonization factor antigen I positive enterotoxigenic Escherichia coli identifies genes implicated in survival in water and host colonization. Microbial Genomics, 2021, 7, .	1.0	2
5	The Rise of Antimicrobial Resistance in Mass Gatherings. , 2021, , 1199-1214.		0
6	Arbaeen public health concerns: A pilot cross-sectional survey. Travel Medicine and Infectious Disease, 2020, 35, 101546.	1.5	10
7	Extensive Homoplasmy but No Evidence of Convergent Evolution of Repeat Numbers at MIRU Loci in Modern Mycobacterium tuberculosis Lineages. Frontiers in Public Health, 2020, 8, 455.	1.3	2
8	Human Movement and Transmission of Antimicrobial-Resistant Bacteria. Handbook of Environmental Chemistry, 2020, , 311-344.	0.2	2
9	Genomic characterisation of Salmonella enterica serovar Wangata isolates obtained from different sources reveals low genomic diversity. PLoS ONE, 2020, 15, e0229697.	1.1	2
10	The Contribution of Wastewater to the Transmission of Antimicrobial Resistance in the Environment: Implications of Mass Gathering Settings. Tropical Medicine and Infectious Disease, 2020, 5, 33.	0.9	92
11	Pilot Survey of Knowledge, Attitudes and Perceptions of Hajj Deployed Health Care Workers on Antibiotics and Antibiotic Prescriptions for Upper Respiratory Tract Infections: Results from Two Hajj Seasons. Tropical Medicine and Infectious Disease, 2020, 5, 18.	0.9	12
12	A Brief History of Ebolavirus Disease: Paving the Way Forward by Learning from the Previous Outbreaks. Infectious Disorders - Drug Targets, 2020, 20, 259-266.	0.4	6
13	The Rise of Antimicrobial Resistance in Mass Gatherings. , 2020, , 1-16.		1
14	A One Health investigation of <i>Salmonella enterica</i> serovar Wangata in north-eastern New South Wales, Australia, 2016–2017. Epidemiology and Infection, 2019, 147, e150.	1.0	13
15	Respiratory syncytial virus in the Western Pacific Region: a systematic review and meta-analysis. Journal of Global Health, 2019, 9, 020431.	1.2	17
16	Molecular epidemiology of respiratory syncytial virus. Reviews in Medical Virology, 2018, 28, e1968.	3.9	60
17	Genome-wide analysis of multi- and extensively drug-resistant Mycobacterium tuberculosis. Nature Genetics, 2018, 50, 307-316.	9.4	271
18	Opportunities and challenges to improving antibiotic prescribing practices through a One Health approach: results of a comparative survey of doctors, dentists and veterinarians in Australia. BMJ Open, 2018, 8, e020439.	0.8	41

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19	Population monitoring for drug-resistant tuberculosis: is genomics the answer?. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 592-594.	4.6	0
20	Hajj – Beyond traveller's diarrhea. <i>Travel Medicine and Infectious Disease</i> , 2018, 21, 80-81.	1.5	5
21	Diversity of Salmonella serotypes from humans, food, domestic animals and wildlife in New South Wales, Australia. <i>BMC Infectious Diseases</i> , 2018, 18, 623.	1.3	46
22	Multi-clonal evolution of multi-drug-resistant/extensively drug-resistant Mycobacterium tuberculosis in a high-prevalence setting of Papua New Guinea for over three decades. <i>Microbial Genomics</i> , 2018, 4, .	1.0	33
23	Genomic characterization of NDM-1 and 5, and OXA-181 carbapenemases in uropathogenic Escherichia coli isolates from Riyadh, Saudi Arabia. <i>PLoS ONE</i> , 2018, 13, e0201613.	1.1	34
24	A planetary health approach to emerging infections in Australia. <i>Lancet</i> , The, 2017, 389, 1293.	6.3	4
25	Refugees and antimicrobial resistance: A systematic review. <i>Travel Medicine and Infectious Disease</i> , 2017, 15, 23-28.	1.5	43
26	Refugees and antimicrobial resistance - Response. <i>Travel Medicine and Infectious Disease</i> , 2017, 17, 63.	1.5	1
27	Enteric Infections Circulating during Hajj Seasons, 2011–2013. <i>Emerging Infectious Diseases</i> , 2017, 23, .	2.0	33
28	Whole Genome Sequencing Demonstrates Limited Transmission within Identified Mycobacterium tuberculosis Clusters in New South Wales, Australia. <i>PLoS ONE</i> , 2016, 11, e0163612.	1.1	44
29	Mycobacterium tuberculosis whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. <i>BMC Medicine</i> , 2016, 14, 31.	2.3	102
30	Hajj vaccinations – facts, challenges, and hope. <i>International Journal of Infectious Diseases</i> , 2016, 47, 29-37.	1.5	18
31	Transmission of multi-drug resistant tuberculosis in Mongolia is driven by Beijing strains of Mycobacterium tuberculosis resistant to all first-line drugs. <i>Tuberculosis</i> , 2016, 101, 49-53.	0.8	12
32	Mycobacterium tuberculosis components expressed during chronic infection of the lung contribute to long-term control of pulmonary tuberculosis in mice. <i>Npj Vaccines</i> , 2016, 1, 16012.	2.9	24
33	Genomic and Phenotypic Analyses Reveal the Emergence of an Atypical Salmonella enterica Serovar Senftenberg Variant in China. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2014-2022.	1.8	14
34	Genotype heterogeneity of Mycobacterium tuberculosis within geospatial hotspots suggests foci of imported infection in Sydney, Australia. <i>Infection, Genetics and Evolution</i> , 2016, 40, 346-351.	1.0	10
35	Identifying Likely Transmission Pathways within a 10-Year Community Outbreak of Tuberculosis by High-Depth Whole Genome Sequencing. <i>PLoS ONE</i> , 2016, 11, e0150550.	1.1	24
36	Future directions for public health research in emerging infectious diseases. <i>Public Health Research and Practice</i> , 2016, 26, .	0.7	17

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37	Genomic expression catalogue of a global collection of BCG vaccine strains show evidence for highly diverged metabolic and cell-wall adaptations. <i>Scientific Reports</i> , 2015, 5, 15443.	1.6	78
38	Rapid determination of anti-tuberculosis drug resistance from whole-genome sequences. <i>Genome Medicine</i> , 2015, 7, 51.	3.6	323
39	Genomic diversity of drug-resistant <i>Mycobacterium tuberculosis</i> isolates in Lisbon Portugal: Towards tuberculosis genomic epidemiology. <i>International Journal of Mycobacteriology</i> , 2015, 4, 27-28.	0.3	0
40	Whole genome sequencing-based characterization of extensively drug resistant (XDR) strains of <i>Mycobacterium tuberculosis</i> from Pakistan. <i>International Journal of Mycobacteriology</i> , 2015, 4, 11-12.	0.3	1
41	Characterization of genomic variations in SNPs of PE_PGRS genes reveals deletions and insertions in extensively drug resistant (XDR) <i>M. tuberculosis</i> strains from Pakistan. <i>International Journal of Mycobacteriology</i> , 2015, 4, 73-79.	0.3	3
42	Cost-Effectiveness Analysis of Alternative Antiviral Strategies for the Treatment of HBeAg-Positive and HBeAg-Negative Chronic Hepatitis B in the United Kingdom. <i>Value in Health</i> , 2015, 18, 800-809.	0.1	18
43	Spatiotemporal evidence for cross-border spread of MDR-TB along the Trans-Siberian Railway line. <i>International Journal of Tuberculosis and Lung Disease</i> , 2015, 19, 1376-1382.	0.6	19
44	It Is Not All about Single Nucleotide Polymorphisms: Comparison of Mobile Genetic Elements and Deletions in <i>Listeria monocytogenes</i> Genomes Links Cases of Hospital-Acquired Listeriosis to the Environmental Source. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3492-3500.	1.8	24
45	Genomic Epidemiology of <i>Clostridium botulinum</i> Isolates from Temporally Related Cases of Infant Botulism in New South Wales, Australia. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2846-2853.	1.8	9
46	Alemtuzumab treatment of multiple sclerosis: long-term safety and efficacy. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2015, 86, 208-215.	0.9	208
47	Whole Genome Sequencing Based Characterization of Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Isolates from Pakistan. <i>PLoS ONE</i> , 2015, 10, e0117771.	1.1	59
48	Vulnerability, hysteria and fear “conquering” Ebola virus. <i>Medical Journal of Australia</i> , 2014, 201, 320-321.	0.8	5
49	Added value of whole-genome sequencing for management of highly drug-resistant TB. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 70, 1198-202.	1.3	36
50	The Population Structure of <i>Vibrio cholerae</i> from the Chandigarh Region of Northern India. <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2981.	1.3	21
51	Unraveling <i>Mycobacterium tuberculosis</i> genomic diversity and evolution in Lisbon, Portugal, a highly drug resistant setting. <i>BMC Genomics</i> , 2014, 15, 991.	1.2	52
52	PolyTB: A genomic variation map for <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2014, 94, 346-354.	0.8	79
53	Recombinations in Staphylococcal Cassette Chromosome mec Elements Compromise the Molecular Detection of Methicillin Resistance in <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2014, 9, e101419.	1.1	50
54	Knowledge, Attitude and Practice (KAP) Survey Concerning Antimicrobial Use among Australian Hajj Pilgrims. <i>Infectious Disorders - Drug Targets</i> , 2014, 14, 125-132.	0.4	31

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55	Care of the dying patient in the community. <i>BMJ</i> , The, 2013, 347, f4085-f4085.	3.0	23
56	Human autoimmunity after lymphocyte depletion is caused by homeostatic T-cell proliferation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20200-20205.	3.3	185
57	Comparative Genomics of the Apicomplexan Parasites <i>Toxoplasma gondii</i> and <i>Neospora caninum</i> : <i>Coccidia</i> Differing in Host Range and Transmission Strategy. <i>PLoS Pathogens</i> , 2012, 8, e1002567.	2.1	206
58	Long term lymphocyte reconstitution after alemtuzumab treatment of multiple sclerosis. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2012, 83, 298-304.	0.9	171
59	A Novel Strategy To Reduce the Immunogenicity of Biological Therapies. <i>Journal of Immunology</i> , 2010, 185, 763-768.	0.4	65
60	Oseltamivir-Resistant Pandemic (H1N1) 2009 in Patient with Impaired Immune System. <i>Emerging Infectious Diseases</i> , 2010, 16, 1185-1186.	2.0	11
61	Genes related to sex steroids, neural growth, and social emotional behavior are associated with autistic traits, empathy, and Asperger syndrome. <i>Autism Research</i> , 2009, 2, 157-177.	2.1	290
62	Technical Section: Technical notes & tips. <i>Annals of the Royal College of Surgeons of England</i> , 2008, 90, 425-436.	0.3	0