

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

218677

26
h-index

168389

53
g-index

73
all docs

73
docs citations

73
times ranked

4898
citing authors

#	ARTICLE	IF	CITATIONS
1	Rapid determination of anti-tuberculosis drug resistance from whole-genome sequences. <i>Genome Medicine</i> , 2015, 7, 51.	8.2	323
2	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.	3.8	290
3	Genome-wide analysis of multi- and extensively drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2018, 50, 307-316.	21.4	271
4	Alemtuzumab treatment of multiple sclerosis: long-term safety and efficacy. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2015, 86, 208-215.	1.9	208
5	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.	4.7	206
6	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.	7.1	185
7	Long term lymphocyte reconstitution after alemtuzumab treatment of multiple sclerosis. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2012, 83, 298-304.	1.9	171
8	<i>Mycobacterium tuberculosis</i> whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. <i>BMC Medicine</i> , 2016, 14, 31.	5.5	102
9	The Contribution of Wastewater to the Transmission of Antimicrobial Resistance in the Environment: Implications of Mass Gathering Settings. <i>Tropical Medicine and Infectious Disease</i> , 2020, 5, 33.	2.3	92
10	PolyTB: A genomic variation map for <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2014, 94, 346-354.	1.9	79
11	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.	3.3	78
12	A Novel Strategy To Reduce the Immunogenicity of Biological Therapies. <i>Journal of Immunology</i> , 2010, 185, 763-768.	0.8	65
13	Molecular epidemiology of respiratory syncytial virus. <i>Reviews in Medical Virology</i> , 2018, 28, e1968.	8.3	60
14	Whole Genome Sequencing Based Characterization of Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Isolates from Pakistan. <i>PLoS ONE</i> , 2015, 10, e0117771.	2.5	59
15	Unraveling <i>Mycobacterium tuberculosis</i> genomic diversity and evolution in Lisbon, Portugal, a highly drug resistant setting. <i>BMC Genomics</i> , 2014, 15, 991.	2.8	52
16	Travel-Related Antimicrobial Resistance: A Systematic Review. <i>Tropical Medicine and Infectious Disease</i> , 2021, 6, 11.	2.3	51
17	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.	2.5	50
18	Diversity of <i>Salmonella</i> serotypes from humans, food, domestic animals and wildlife in New South Wales, Australia. <i>BMC Infectious Diseases</i> , 2018, 18, 623.	2.9	46

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19	Whole Genome Sequencing Demonstrates Limited Transmission within Identified Mycobacterium tuberculosis Clusters in New South Wales, Australia. PLoS ONE, 2016, 11, e0163612.	2.5	44
20	Refugees and antimicrobial resistance: A systematic review. Travel Medicine and Infectious Disease, 2017, 15, 23-28.	3.0	43
21	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.	1.9	41
22	Added value of whole-genome sequencing for management of highly drug-resistant TB. Journal of Antimicrobial Chemotherapy, 2014, 70, 1198-202.	3.0	36
23	Genomic characterization of NDM-1 and 5, and OXA-181 carbapenemases in uropathogenic Escherichia coli isolates from Riyadh, Saudi Arabia. PLoS ONE, 2018, 13, e0201613.	2.5	34
24	Enteric Infections Circulating during Hajj Seasons, 2011-2013. Emerging Infectious Diseases, 2017, 23, .	4.3	33
25	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. Microbial Genomics, 2018, 4, .	2.0	33
26	Knowledge, Attitude and Practice (KAP) Survey Concerning Antimicrobial Use among Australian Hajj Pilgrims. Infectious Disorders - Drug Targets, 2014, 14, 125-132.	0.8	31
27	It Is Not All about Single Nucleotide Polymorphisms: Comparison of Mobile Genetic Elements and Deletions in Listeria monocytogenes Genomes Links Cases of Hospital-Acquired Listeriosis to the Environmental Source. Journal of Clinical Microbiology, 2015, 53, 3492-3500.	3.9	24
28	Mycobacterium tuberculosis components expressed during chronic infection of the lung contribute to long-term control of pulmonary tuberculosis in mice. Npj Vaccines, 2016, 1, 16012.	6.0	24
29	Identifying Likely Transmission Pathways within a 10-Year Community Outbreak of Tuberculosis by High-Depth Whole Genome Sequencing. PLoS ONE, 2016, 11, e0150550.	2.5	24
30	Care of the dying patient in the community. BMJ, The, 2013, 347, f4085-f4085.	6.0	23
31	The Population Structure of Vibrio cholerae from the Chandigarh Region of Northern India. PLoS Neglected Tropical Diseases, 2014, 8, e2981.	3.0	21
32	Spatiotemporal evidence for cross-border spread of MDR-TB along the Trans-Siberian Railway line. International Journal of Tuberculosis and Lung Disease, 2015, 19, 1376-1382.	1.2	19
33	Cost-Effectiveness Analysis of Alternative Antiviral Strategies for the Treatment of HBeAg-Positive and HBeAg-Negative Chronic Hepatitis B in the United Kingdom. Value in Health, 2015, 18, 800-809.	0.3	18
34	Hajj vaccinations—facts, challenges, and hope. International Journal of Infectious Diseases, 2016, 47, 29-37.	3.3	18
35	Respiratory syncytial virus in the Western Pacific Region: a systematic review and meta-analysis. Journal of Global Health, 2019, 9, 020431.	2.7	17
36	Future directions for public health research in emerging infectious diseases. Public Health Research and Practice, 2016, 26, .	1.5	17

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37	Genomic and Phenotypic Analyses Reveal the Emergence of an Atypical <i>Salmonella enterica</i> Serovar Senftenberg Variant in China. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2014-2022.	3.9	14
38	A One Health investigation of <i>Salmonella enterica</i> serovar Wangata in north-eastern New South Wales, Australia, 2016–2017. <i>Epidemiology and Infection</i> , 2019, 147, e150.	2.1	13
39	Transmission of multi-drug resistant tuberculosis in Mongolia is driven by Beijing strains of <i>Mycobacterium tuberculosis</i> resistant to all first-line drugs. <i>Tuberculosis</i> , 2016, 101, 49-53.	1.9	12
40	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. <i>Tropical Medicine and Infectious Disease</i> , 2020, 5, 18.	2.3	12
41	Oseltamivir-Resistant Pandemic (H1N1) 2009 in Patient with Impaired Immune System. <i>Emerging Infectious Diseases</i> , 2010, 16, 1185-1186.	4.3	11
42	Genotype heterogeneity of <i>Mycobacterium tuberculosis</i> within geospatial hotspots suggests foci of imported infection in Sydney, Australia. <i>Infection, Genetics and Evolution</i> , 2016, 40, 346-351.	2.3	10
43	Arbaeen public health concerns: A pilot cross-sectional survey. <i>Travel Medicine and Infectious Disease</i> , 2020, 35, 101546.	3.0	10
44	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.	3.9	9
45	Health Risks, Preventive Behaviours and Respiratory Illnesses at the 2019 Arbaeen: Implications for COVID-19 and Other Pandemics. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 3287.	2.6	7
46	A Brief History of Ebolavirus Disease: Paving the Way Forward by Learning from the Previous Outbreaks. <i>Infectious Disorders - Drug Targets</i> , 2020, 20, 259-266.	0.8	6
47	Vulnerability, hysteria and fear “conquering Ebola virus. <i>Medical Journal of Australia</i> , 2014, 201, 320-321.	1.7	5
48	Hajj “Beyond traveller's diarrhea. <i>Travel Medicine and Infectious Disease</i> , 2018, 21, 80-81.	3.0	5
49	A planetary health approach to emerging infections in Australia. <i>Lancet, The</i> , 2017, 389, 1293.	13.7	4
50	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. <i>Access Microbiology</i> , 2022, 4, .	0.5	4
51	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.	0.6	3
52	Extensive Homoplasmy but No Evidence of Convergent Evolution of Repeat Numbers at MIRU Loci in Modern <i>Mycobacterium tuberculosis</i> Lineages. <i>Frontiers in Public Health</i> , 2020, 8, 455.	2.7	2
53	Human Movement and Transmission of Antimicrobial-Resistant Bacteria. <i>Handbook of Environmental Chemistry</i> , 2020, , 311-344.	0.4	2
54	Genomic characterisation of <i>Salmonella enterica</i> serovar Wangata isolates obtained from different sources reveals low genomic diversity. <i>PLoS ONE</i> , 2020, 15, e0229697.	2.5	2

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55	Functional analysis of colonization factor antigen I positive enterotoxigenic Escherichia coli identifies genes implicated in survival in water and host colonization. <i>Microbial Genomics</i> , 2021, 7, .	2.0	2
56	Whole genome sequencing-based characterization of extensively drug resistant (XDR) strains of Mycobacterium tuberculosis from Pakistan. <i>International Journal of Mycobacteriology</i> , 2015, 4, 11-12.	0.6	1
57	Refugees and antimicrobial resistance - Response. <i>Travel Medicine and Infectious Disease</i> , 2017, 17, 63.	3.0	1
58	The Rise of Antimicrobial Resistance in Mass Gatherings. , 2020, , 1-16.		1
59	Genomic diversity of drug-resistant Mycobacterium tuberculosis isolates in Lisbon Portugal: Towards tuberculosis genomic epidemiology. <i>International Journal of Mycobacteriology</i> , 2015, 4, 27-28.	0.6	0
60	Population monitoring for drug-resistant tuberculosis: is genomics the answer?. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 592-594.	9.1	0
61	The Rise of Antimicrobial Resistance in Mass Gatherings. , 2021, , 1199-1214.		0
62	Technical Section: Technical notes & tips. <i>Annals of the Royal College of Surgeons of England</i> , 2008, 90, 425-436.	0.6	0