

Anthony Underwood

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

3,737
citations

201385

27
h-index

182168

51
g-index

65
all docs

65
docs citations

65
times ranked

6525
citing authors

#	ARTICLE	IF	CITATIONS
1	Hospital admission and emergency care attendance risk for SARS-CoV-2 delta (B.1.617.2) compared with alpha (B.1.1.7) variants of concern: a cohort study. <i>Lancet Infectious Diseases</i> , The, 2022, 22, 35-42.	4.6	612
2	Circulation of Third-Generation Cephalosporin Resistant <i>Salmonella</i> Typhi in Mumbai, India. <i>Clinical Infectious Diseases</i> , 2022, 74, 2234-2237.	2.9	14
3	Train-the-Trainer as an Effective Approach to Building Global Networks of Experts in Genomic Surveillance of Antimicrobial Resistance (AMR). <i>Clinical Infectious Diseases</i> , 2021, 73, S283-S289.	2.9	8
4	Clones and Clusters of Antimicrobial-Resistant <i>Klebsiella</i> From Southwestern Nigeria. <i>Clinical Infectious Diseases</i> , 2021, 73, S308-S315.	2.9	26
5	Good Financial Grant Practice: A Tool for Developing and Demonstrating Institutional Financial and Grant Management Capacity in Global Health. <i>Clinical Infectious Diseases</i> , 2021, 73, S275-S282.	2.9	3
6	Complexity of Genomic Epidemiology of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Isolates in Colombia Urges the Reinforcement of Whole Genome Sequencing-Based Surveillance Programs. <i>Clinical Infectious Diseases</i> , 2021, 73, S290-S299.	2.9	22
7	Rapid Genomic Characterization and Global Surveillance of <i>Klebsiella</i> Using Pathogenwatch. <i>Clinical Infectious Diseases</i> , 2021, 73, S325-S335.	2.9	47
8	Integrating Scalable Genome Sequencing Into Microbiology Laboratories for Routine Antimicrobial Resistance Surveillance. <i>Clinical Infectious Diseases</i> , 2021, 73, S258-S266.	2.9	14
9	Genome Sequencing Identifies Previously Unrecognized <i>Klebsiella pneumoniae</i> Outbreaks in Neonatal Intensive Care Units in the Philippines. <i>Clinical Infectious Diseases</i> , 2021, 73, S316-S324.	2.9	12
10	Implementing Whole-Genome Sequencing for Ongoing Surveillance of Antimicrobial Resistance: Exemplifying Insights Into <i>Klebsiella pneumoniae</i> . <i>Clinical Infectious Diseases</i> , 2021, 73, S255-S257.	2.9	7
11	A community-driven resource for genomic epidemiology and antimicrobial resistance prediction of <i>Neisseria gonorrhoeae</i> at Pathogenwatch. <i>Genome Medicine</i> , 2021, 13, 61.	3.6	63
12	A global resource for genomic predictions of antimicrobial resistance and surveillance of <i>Salmonella</i> Typhi at pathogenwatch. <i>Nature Communications</i> , 2021, 12, 2879.	5.8	56
13	CLIMB-COVID: continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance. <i>Genome Biology</i> , 2021, 22, 196.	3.8	53
14	Assignment of epidemiological lineages in an emerging pandemic using the pangolin tool. <i>Virus Evolution</i> , 2021, 7, veab064.	2.2	774
15	OUP accepted manuscript. <i>Clinical Infectious Diseases</i> , 2021, 73, S267-S274.	2.9	12
16	High-Resolution Genomic Profiling of Carbapenem-Resistant <i>Klebsiella pneumoniae</i> Isolates: A Multicentric Retrospective Indian Study. <i>Clinical Infectious Diseases</i> , 2021, 73, S300-S307.	2.9	30
17	Sustained transmission of high-level azithromycin-resistant <i>Neisseria gonorrhoeae</i> in England: an observational study. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 573-581.	4.6	99
18	SnapperDB: a database solution for routine sequencing analysis of bacterial isolates. <i>Bioinformatics</i> , 2018, 34, 3028-3029.	1.8	164

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19	Final report of ENGAGE – Establishing Next Generation sequencing Ability for Genomic analysis in Europe. EFSA Supporting Publications, 2018, 15, 1431E.	0.3	14
20	Enhanced nasopharyngeal infection and shedding associated with an epidemic lineage of <i>emm</i> 3 group A <i>Streptococcus</i> . <i>Virulence</i> , 2017, 8, 1390-1400.	1.8	17
21	Genome analysis following a national increase in Scarlet Fever in England 2014. <i>BMC Genomics</i> , 2017, 18, 224.	1.2	65
22	BugMat and FindNeighbour: command line and server applications for investigating bacterial relatedness. <i>BMC Bioinformatics</i> , 2017, 18, 477.	1.2	16
23	Integration of Genomic and Other Epidemiologic Data to Investigate and Control a Cross-Institutional Outbreak of <i>Streptococcus pyogenes</i> . <i>Emerging Infectious Diseases</i> , 2016, 22, 973-980.	2.0	18
24	Multiple major disease-associated clones of <i>Legionella pneumophila</i> have emerged recently and independently. <i>Genome Research</i> , 2016, 26, 1555-1564.	2.4	72
25	Evaluation of an Optimal Epidemiological Typing Scheme for <i>Legionella pneumophila</i> with Whole-Genome Sequence Data Using Validation Guidelines. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2135-2148.	1.8	46
26	Emergence of a novel lineage containing a prophage in <i>emm</i> /M3 group A <i>Streptococcus</i> associated with upsurge in invasive disease in the UK. <i>Microbial Genomics</i> , 2016, 2, e000059.	1.0	29
27	Genomic determination of minimum multi-locus sequence typing schemas to represent the genomic phylogeny of <i>Mycoplasma hominis</i> . <i>BMC Genomics</i> , 2016, 17, 964.	1.2	10
28	MOST: a modified MLST typing tool based on short read sequencing. <i>PeerJ</i> , 2016, 4, e2308.	0.9	105
29	Whole-Genome Sequencing and Epidemiological Analysis Do Not Provide Evidence for Cross-transmission of <i>Mycobacterium abscessus</i> in a Cohort of Pediatric Cystic Fibrosis Patients. <i>Clinical Infectious Diseases</i> , 2015, 60, 1007-16.	2.9	81
30	High-Resolution Analysis by Whole-Genome Sequencing of an International Lineage (Sequence Type 111) of <i>Pseudomonas aeruginosa</i> Associated with Metallo-Carbapenemases in the United Kingdom. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2622-2631.	1.8	50
31	Whole-Genome Sequencing for National Surveillance of Shiga Toxin–Producing <i>Escherichia coli</i> O157. <i>Clinical Infectious Diseases</i> , 2015, 61, 305-312.	2.9	181
32	Metaproteomics Analysis Reveals the Adaptation Process for the Chicken Gut Microbiota. <i>Applied and Environmental Microbiology</i> , 2014, 80, 478-485.	1.4	65
33	An Investigation of the Diversity of Strains of Enteroaggregative <i>Escherichia coli</i> Isolated from Cases Associated with a Large Multi-Pathogen Foodborne Outbreak in the UK. <i>PLoS ONE</i> , 2014, 9, e98103.	1.1	41
34	Enteraggregative <i>Escherichia coli</i> Have Evolved Independently as Distinct Complexes within the <i>E. coli</i> Population with Varying Ability to Cause Disease. <i>PLoS ONE</i> , 2014, 9, e112967.	1.1	17
35	Clusters of genetically similar isolates of <i>Pseudomonas aeruginosa</i> from multiple hospitals in the UK. <i>Journal of Medical Microbiology</i> , 2013, 62, 988-1000.	0.7	47
36	snp-search: simple processing, manipulation and searching of SNPs from high-throughput sequencing. <i>BMC Bioinformatics</i> , 2013, 14, 326.	1.2	5

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37	Evolutionary Dynamics of Local Pandemic H1N1/2009 Influenza Virus Lineages Revealed by Whole-Genome Analysis. <i>Journal of Virology</i> , 2012, 86, 11-18.	1.5	101
38	Non-culture detection of <i>Streptococcus agalactiae</i> (Lancefield group B <i>Streptococcus</i>) in clinical samples by real-time PCR. <i>Journal of Medical Microbiology</i> , 2012, 61, 1086-1090.	0.7	18
39	Multiple-locus variable-number tandem-repeat analysis of <i>Streptococcus pneumoniae</i> and comparison with multiple loci sequence typing. <i>BMC Microbiology</i> , 2012, 12, 241.	1.3	13
40	Evolutionary Pathways of the Pandemic Influenza A (H1N1) 2009 in the UK. <i>PLoS ONE</i> , 2011, 6, e23779.	1.1	34
41	Whole-genome comparison of two <i>Acinetobacter baumannii</i> isolates from a single patient, where resistance developed during tigecycline therapy. <i>Journal of Antimicrobial Chemotherapy</i> , 2011, 66, 1499-1503.	1.3	96
42	Call for a Quality Standard for Sequence-Based Assays in Clinical Microbiology: Necessity for Quality Assessment of Sequences Used in Microbial Identification and Typing. <i>Journal of Clinical Microbiology</i> , 2011, 49, 23-26.	1.8	20
43	The Impact of Pandemic Influenza H1N1 on Health-Related Quality of Life: A Prospective Population-Based Study. <i>PLoS ONE</i> , 2011, 6, e17030.	1.1	75
44	Complete Nucleotide Sequences of Plasmids pEK204, pEK499, and pEK516, Encoding CTX-M Enzymes in Three Major <i>Escherichia coli</i> Lineages from the United Kingdom, All Belonging to the International O25:H4-ST131 Clone. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 4472-4482.	1.4	256
45	Mathematical Modelling of <i>Mycobacterium tuberculosis</i> VNTR Loci Estimates a Very Slow Mutation Rate for the Repeats. <i>Journal of Molecular Evolution</i> , 2008, 66, 565-574.	0.8	30
46	VNTRDB: a bacterial variable number tandem repeat locus database. <i>Nucleic Acids Research</i> , 2007, 35, D416-D421.	6.5	33
47	Evolutionary clues from comparative analysis of <i>Mycobacterium tuberculosis</i> variable-number tandem repeat sequences within genetic families. <i>Infection, Genetics and Evolution</i> , 2007, 7, 239-246.	1.0	5
48	Evolution of short sequence repeats in <i>Mycobacterium tuberculosis</i> . <i>FEMS Microbiology Letters</i> , 2006, 256, 340-346.	0.7	23
49	A virulence-associated gene microarray: a tool for investigation of the evolution and pathogenic potential of <i>Staphylococcus aureus</i> . <i>Microbiology (United Kingdom)</i> , 2004, 150, 3763-3771.	0.7	40
50	The Secreted Larval Acidic Proteins (SLAPs) of <i>Onchocerca</i> spp. are encoded by orthologues of the alt gene family of <i>Brugia malayi</i> and have host protective potential. <i>Molecular and Biochemical Parasitology</i> , 2004, 134, 213-224.	0.5	36
51	Identification of a molecular marker for the Y chromosome of <i>Brugia malayi</i> . <i>Molecular and Biochemical Parasitology</i> , 1999, 99, 1-10.	0.5	20