Matthew J Ellington

List of Publications by Year
in descending order

32 papers	3,732 citations	361413 20 h-index	434195 31 g-index
33 all docs	33 docs citations	33 times ranked	5244 citing authors

#	Article	IF	Citations
1	Rapid Whole-Genome Sequencing for Investigation of a Neonatal MRSA Outbreak. New England Journal of Medicine, 2012, 366, 2267-2275.	27.0	609
2	Multiplex PCR for rapid detection of genes encoding CTX-M extended-spectrum Î²-lactamases. Journal of Antimicrobial Chemotherapy, 2006, 57, 154-155.	3.0	546
3	Routine Use of Microbial Whole Genome Sequencing in Diagnostic and Public Health Microbiology. PLoS Pathogens, 2012, 8, e1002824.	4.7	450
4	Molecular mechanisms disrupting porin expression in ertapenem-resistant Klebsiella and Enterobacter spp. clinical isolates from the UK. Journal of Antimicrobial Chemotherapy, 2009, 63, 659-667.	3.0	390
5	Complete Nucleotide Sequences of Plasmids pEK204, pEK499, and pEK516, Encoding CTX-M Enzymes in Three Major Escherichia coli Lineages from the United Kingdom, All Belonging to the International O25:H4-ST131 Clone. Antimicrobial Agents and Chemotherapy, 2009, 53, 4472-4482.	3.2	256
6	Detection of the plasmid-mediatedmcr-1gene conferring colistin resistance in human and food isolates ofSalmonella entericaandEscherichia coliin England and Wales. Journal of Antimicrobial Chemotherapy, 2016, 71, 2300-2305.	3.0	247
7	Plasmid Classification in an Era of Whole-Genome Sequencing: Application in Studies of Antibiotic Resistance Epidemiology. Frontiers in Microbiology, 2017, 8, 182.	3.5	191
8	The diversity of Klebsiella pneumoniae surface polysaccharides. Microbial Genomics, 2016, 2, e000073.	2.0	185
9	Rapid Bacterial Whole-Genome Sequencing to Enhance Diagnostic and Public Health Microbiology. JAMA Internal Medicine, 2013, 173, 1397.	5.1	181
10	Emergence of methicillin resistance predates the clinical use of antibiotics. Nature, 2022, 602, 135-141.	27.8	138
11	Discordant bioinformatic predictions of antimicrobial resistance from whole-genome sequencing data of bacterial isolates: an inter-laboratory study. Microbial Genomics, 2020, 6, .	2.0	69
12	Molecular epidemiology of Klebsiella pneumoniae invasive infections over a decade at Kilifi County Hospital in Kenya. International Journal of Medical Microbiology, 2017, 307, 422-429.	3.6	61
13	Emergence and clonal spread of colistin resistance due to multiple mutational mechanisms in carbapenemase-producing Klebsiella pneumoniae in London. Scientific Reports, 2017, 7, 12711.	3.3	55
14	Association of Novel Nonsynonymous Single Nucleotide Polymorphisms in ampD with Cephalosporin Resistance and Phylogenetic Variations in ampC , ampR , ompF , and ompC in Enterobacter cloacae Isolates That Are Highly Resistant to Carbapenems. Antimicrobial Agents and Chemotherapy, 2016, 60, 2383-2390.	3.2	47
15	Emergent and evolving antimicrobial resistance cassettes in community-associated fusidic acid and meticillin-resistant Staphylococcus aureus. International Journal of Antimicrobial Agents, 2015, 45, 477-484.	2.5	39
16	Multicentre evaluation of a real-time PCR assay to detect genes encoding clinically relevant carbapenemases in cultured bacteria. International Journal of Antimicrobial Agents, 2016, 47, 151-154.	2.5	39
17	Whatâ€™s in a Name? Species-Wide Whole-Genome Sequencing Resolves Invasive and Noninvasive Lineages of Salmonella enterica Serotype Paratyphi B. MBio, 2016, 7, .	4.1	29
18	Global Scale Dissemination of ST93: A Divergent Staphylococcus aureus Epidemic Lineage That Has Recently Emerged From Remote Northern Australia. Frontiers in Microbiology, 2018, 9, 1453.	3.5	29

#	Article	IF	Citations
19	A Multispecies Cluster of GES-5 Carbapenemaseâ€“Producing Enterobacterales Linked by a Geographically Disseminated Plasmid. Clinical Infectious Diseases, 2020, 71, 2553-2560.	5.8	29
20	Activity of Î²-lactam/taniborbactam (VNRX-5133) combinations against carbapenem-resistant Gram-negative bacteria. Journal of Antimicrobial Chemotherapy, 2021, 76, 160-170.	3.0	29
21	Contrasting patterns of longitudinal population dynamics and antimicrobial resistance mechanisms in two priority bacterial pathogens over 7Âyears in a single center. Genome Biology, 2019, 20, 184.	8.8	22
22	The differential importance of mutations within AmpD in cephalosporin resistance of Enterobacter aerogenes and Enterobacter cloacae. International Journal of Antimicrobial Agents, 2016, 48, 555-558.	2.5	15
23	Prevalence of carbapenem resistance and carbapenemase production among Enterobacteriaceae isolated from urine in the UK: results of the UK infection-Carbapenem Resistance Evaluation Surveillance Trial (iCREST-UK). Journal of Antimicrobial Chemotherapy, 2018, 73, 698-702.	3.0	15
24	Characterization of Carbapenemase-Producing Enterobacteriaceae from Patients in Amman, Jordan. Microbial Drug Resistance, 2018, 24, 1121-1127.	2.0	13
25	Detection of the transferable tigecycline resistance gene tet(X4) in Escherichia coli from pigs in the United Kingdom. Journal of Antimicrobial Chemotherapy, 2022, 77, 846-848.	3.0	11
26	Diversity of carbapenemase-producing Enterobacterales in England as revealed by whole-genome sequencing of isolates referred to a national reference laboratory over a 30-month period. Journal of Medical Microbiology, 2022, 71, .	1.8	10
27	Alterations in chromosomal genes nfsA, nfsB, and ribE are associated with nitrofurantoin resistance in Escherichia coli from the United Kingdom. Microbial Genomics, 2021, 7, .	2.0	9
28	NDM-1 carbapenemase resistance gene vehicles emergent on distinct plasmid backbones from the IncL/M family. Journal of Antimicrobial Chemotherapy, 2022, 77, 620-624.	3.0	6
29	Bacterial genotypic and patient risk factors for adverse outcomes in Escherichia coli bloodstream infections: a prospective molecular epidemiological study. Journal of Antimicrobial Chemotherapy, 2022, 77, 1753-1761.	3.0	5
30	Sampling and diversity of Escherichia coli from the enteric microbiota in patients with Escherichia coli bacteraemia. BMC Research Notes, 2019, 12, 335.	1.4	4
31	A survey of metallo-Â-lactamase sequence accuracy before the data deluge. Journal of Antimicrobial Chemotherapy, 2014, 69, 3431-3435.	3.0	1
32	Nitrofurantoin-resistant Escherichia coli in the UK: genetic determinants, diversity, and undetected occurrences. Access Microbiology, 2022, 4, .	0.5	0