

# Elizabeth M Batty

## List of Publications by Year in descending order

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Version: 2024-02-01

25  
papers

3,072  
citations

394421

19  
h-index

610901

24  
g-index

29  
all docs

29  
docs citations

29  
times ranked

4724  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative analysis of targeted next-generation sequencing for Plasmodium falciparum drug resistance markers. Scientific Reports, 2022, 12, 5563.	3.3	3
2	Harnessing genomics in the battle against antimicrobial resistance and neglected tropical diseases. EBioMedicine, 2021, 63, 103178.	6.1	0
3	Genomic surveillance of SARS-CoV-2 in Thailand reveals mixed imported populations, a local lineage expansion and a virus with truncated ORF7a. Virus Research, 2021, 292, 198233.	2.2	27
4	Defining the burden of febrile illness in rural South and Southeast Asia: an open letter to announce the launch of the Rural Febrile Illness project. Wellcome Open Research, 2021, 6, 64.	1.8	11
5	Targeted capture and sequencing of Orientia tsutsugamushi genomes from chiggers and humans. Infection, Genetics and Evolution, 2021, 91, 104818.	2.3	6
6	The spread of chloramphenicol-resistant Neisseria meningitidis in Southeast Asia. International Journal of Infectious Diseases, 2020, 95, 198-203.	3.3	6
7	Oxford Nanopore MinION Sequencing Enables Rapid Whole Genome Assembly of Rickettsia typhi in a Resource-Limited Setting. American Journal of Tropical Medicine and Hygiene, 2020, 102, 408-414.	1.4	22
8	Insights into Platypus Population Structure and History from Whole-Genome Sequencing. Molecular Biology and Evolution, 2018, 35, 1238-1252.	8.9	27
9	Long-read whole genome sequencing and comparative analysis of six strains of the human pathogen Orientia tsutsugamushi. PLoS Neglected Tropical Diseases, 2018, 12, e0006566.	3.0	50
10	Evolutionary History of the Global Emergence of the Escherichia coli Epidemic Clone ST131. MBio, 2016, 7, e02162.	4.1	289
11	MinION Analysis and Reference Consortium: Phase 1 data release and analysis. F1000Research, 2015, 4, 1075.	1.6	270
12	Mobile elements drive recombination hotspots in the core genome of Staphylococcus aureus. Nature Communications, 2014, 5, 3956.	12.8	128
13	Genome Sequencing of an Extended Series of NDM-Producing Klebsiella pneumoniae Isolates from Neonatal Infections in a Nepali Hospital Characterizes the Extent of Community- versus Hospital-Associated Transmission in an Endemic Setting. Antimicrobial Agents and Chemotherapy, 2014, 58, 7347-7357.	3.2	142
14	Healthcare-associated outbreak of methicillin-resistant Staphylococcus aureus bacteraemia: role of a cryptic variant of an epidemic clone. Journal of Hospital Infection, 2014, 86, 83-89.	2.9	31
15	Recombinational Switching of the Clostridium difficile S-Layer and a Novel Glycosylation Gene Cluster Revealed by Large-Scale Whole-Genome Sequencing. Journal of Infectious Diseases, 2013, 207, 675-686.	4.0	93
16	Diverse Sources of C. difficile Infection Identified on Whole-Genome Sequencing. New England Journal of Medicine, 2013, 369, 1195-1205.	27.0	595
17	Predicting antimicrobial susceptibilities for Escherichia coli and Klebsiella pneumoniae isolates using whole genomic sequence data. Journal of Antimicrobial Chemotherapy, 2013, 68, 2234-2244.	3.0	314
18	Within-Host Evolution of Staphylococcus aureus during Asymptomatic Carriage. PLoS ONE, 2013, 8, e61319.	2.5	194

#	ARTICLE	IF	CITATIONS
19	A Modified RNA-Seq Approach for Whole Genome Sequencing of RNA Viruses from Faecal and Blood Samples. PLoS ONE, 2013, 8, e66129.	2.5	62
20	Evolutionary dynamics of <i>Staphylococcus aureus</i> during progression from carriage to disease. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4550-4555.	7.1	244
21	Structural analysis of the genome of breast cancer cell line ZR-75-30 identifies twelve expressed fusion genes. BMC Genomics, 2012, 13, 719.	2.8	32
22	A pilot study of rapid benchtop sequencing of <i>Staphylococcus aureus</i> and <i>Clostridium difficile</i> for outbreak detection and surveillance. BMJ Open, 2012, 2, e001124.	1.9	228
23	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. Genome Biology, 2012, 13, R118.	9.6	199
24	The role of tandem duplicator phenotype in tumour evolution in high-grade serous ovarian cancer. Journal of Pathology, 2012, 226, 703-712.	4.5	56
25	Large duplications at reciprocal translocation breakpoints that might be the counterpart of large deletions and could arise from stalled replication bubbles. Genome Research, 2011, 21, 525-534.	5.5	32