

# Elizabeth M Batty

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1705471/publications.pdf>

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  | Diverse Sources of <i>C. difficile</i> Infection Identified on Whole-Genome Sequencing. <i>New England Journal of Medicine</i> , 2013, 369, 1195-1205.   | 27.0 | 595       |
| 2  | Predicting antimicrobial susceptibilities for <i>Escherichia coli</i> and <i>Klebsiella pneumoniae</i> isolates using whole genomic sequence data. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 2234-2244.   | 3.0  | 314       |
| 3  | Evolutionary History of the Global Emergence of the <i>Escherichia coli</i> Epidemic Clone ST131. <i>MBio</i> , 2016, 7, e02162.   | 4.1  | 289       |
| 4  | MinION Analysis and Reference Consortium: Phase 1 data release and analysis. <i>F1000Research</i> , 2015, 4, 1075.   | 1.6  | 270       |
| 5  | Evolutionary dynamics of <i>Staphylococcus aureus</i> during progression from carriage to disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4550-4555.  | 7.1  | 244       |
| 6  | A pilot study of rapid benchtop sequencing of <i>Staphylococcus aureus</i> and <i>Clostridium difficile</i> for outbreak detection and surveillance. <i>BMJ Open</i> , 2012, 2, e001124.   | 1.9  | 228       |
| 7  | Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <i>Genome Biology</i> , 2012, 13, R118.  | 9.6  | 199       |
| 8  | Within-Host Evolution of <i>Staphylococcus aureus</i> during Asymptomatic Carriage. <i>PLoS ONE</i> , 2013, 8, e61319.   | 2.5  | 194       |
| 9  | Genome Sequencing of an Extended Series of NDM-Producing <i>Klebsiella pneumoniae</i> Isolates from Neonatal Infections in a Nepali Hospital Characterizes the Extent of Community- versus Hospital-Associated Transmission in an Endemic Setting. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 7347-7357. | 3.2  | 142       |
| 10 | Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2014, 5, 3956.  | 12.8 | 128       |
| 11 | Recombinational Switching of the <i>Clostridium difficile</i> S-Layer and a Novel Glycosylation Gene Cluster Revealed by Large-Scale Whole-Genome Sequencing. <i>Journal of Infectious Diseases</i> , 2013, 207, 675-686.  | 4.0  | 93        |
| 12 | A Modified RNA-Seq Approach for Whole Genome Sequencing of RNA Viruses from Faecal and Blood Samples. <i>PLoS ONE</i> , 2013, 8, e66129.   | 2.5  | 62        |
| 13 | The role of tandem duplicator phenotype in tumour evolution in high-grade serous ovarian cancer. <i>Journal of Pathology</i> , 2012, 226, 703-712.   | 4.5  | 56        |
| 14 | Long-read whole genome sequencing and comparative analysis of six strains of the human pathogen <i>Orientia tsutsugamushi</i> . <i>PLoS Neglected Tropical Diseases</i> , 2018, 12, e0006566.  | 3.0  | 50        |
| 15 | Large duplications at reciprocal translocation breakpoints that might be the counterpart of large deletions and could arise from stalled replication bubbles. <i>Genome Research</i> , 2011, 21, 525-534.  | 5.5  | 32        |
| 16 | Structural analysis of the genome of breast cancer cell line ZR-75-30 identifies twelve expressed fusion genes. <i>BMC Genomics</i> , 2012, 13, 719.   | 2.8  | 32        |
| 17 | Healthcare-associated outbreak of methicillin-resistant <i>Staphylococcus aureus</i> bacteraemia: role of a cryptic variant of an epidemic clone. <i>Journal of Hospital Infection</i> , 2014, 86, 83-89.  | 2.9  | 31        |
| 18 | Insights into Platypus Population Structure and History from Whole-Genome Sequencing. <i>Molecular Biology and Evolution</i> , 2018, 35, 1238-1252.  | 8.9  | 27        |

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|----|--|-----|-----------|
| 19 | Genomic surveillance of SARS-CoV-2 in Thailand reveals mixed imported populations, a local lineage expansion and a virus with truncated ORF7a. <i>Virus Research</i> , 2021, 292, 198233.                      | 2.2 | 27        |
| 20 | Oxford Nanopore MinION Sequencing Enables Rapid Whole Genome Assembly of <i>Rickettsia typhi</i> in a Resource-Limited Setting. <i>American Journal of Tropical Medicine and Hygiene</i> , 2020, 102, 408-414. | 1.4 | 22        |
| 21 | 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. <i>Wellcome Open Research</i> , 2021, 6, 64.             | 1.8 | 11        |
| 22 | The spread of chloramphenicol-resistant <i>Neisseria meningitidis</i> in Southeast Asia. <i>International Journal of Infectious Diseases</i> , 2020, 95, 198-203.  | 3.3 | 6         |
| 23 | Targeted capture and sequencing of <i>Orientia tsutsugamushi</i> genomes from chiggers and humans. <i>Infection, Genetics and Evolution</i> , 2021, 91, 104818.  | 2.3 | 6         |
| 24 | Comparative analysis of targeted next-generation sequencing for <i>Plasmodium falciparum</i> drug resistance markers. <i>Scientific Reports</i> , 2022, 12, 5563.  | 3.3 | 3         |
| 25 | Harnessing genomics in the battle against antimicrobial resistance and neglected tropical diseases. <i>EBioMedicine</i> , 2021, 63, 103178.  | 6.1 | 0         |