

# Josephine M Bryant

## List of Publications by Year in descending order

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Version: 2024-02-01

25  
papers

3,643  
citations

394421

19  
h-index

580821

25  
g-index

26  
all docs

26  
docs citations

26  
times ranked

4586  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Whole-genome sequencing to identify transmission of <i>Mycobacterium abscessus</i> between patients with cystic fibrosis: a retrospective cohort study. <i>Lancet, The</i> , 2013, 381, 1551-1560.                      | 13.7 | 596       |
| 2  | Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. <i>Nature</i> , 2014, 514, 494-497.   | 27.8 | 506       |
| 3  | Emergence and spread of a human-transmissible multidrug-resistant nontuberculous mycobacterium. <i>Science</i> , 2016, 354, 751-757.  | 12.6 | 462       |
| 4  | Evolution and transmission of drug-resistant tuberculosis in a Russian population. <i>Nature Genetics</i> , 2014, 46, 279-286.  | 21.4 | 451       |
| 5  | Rapid Whole-Genome Sequencing of <i>Mycobacterium tuberculosis</i> Isolates Directly from Clinical Samples. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2230-2237.  | 3.9  | 242       |
| 6  | Whole-Genome Sequencing for Rapid Susceptibility Testing of <i>M. tuberculosis</i> . <i>New England Journal of Medicine</i> , 2013, 369, 290-292.   | 27.0 | 195       |
| 7  | Whole-genome sequencing to establish relapse or re-infection with <i>Mycobacterium tuberculosis</i> : a retrospective observational study. <i>Lancet Respiratory Medicine</i> , the, 2013, 1, 786-792.                  | 10.7 | 184       |
| 8  | Inferring patient to patient transmission of <i>Mycobacterium tuberculosis</i> from whole genome sequencing data. <i>BMC Infectious Diseases</i> , 2013, 13, 110.   | 2.9  | 180       |
| 9  | Direct Whole-Genome Sequencing of Sputum Accurately Identifies Drug-Resistant <i>Mycobacterium tuberculosis</i> Faster than MGIT Culture Sequencing. <i>Journal of Clinical Microbiology</i> , 2018, 56, .              | 3.9  | 131       |
| 10 | Comparison of Next-Generation Sequencing Technologies for Comprehensive Assessment of Full-Length Hepatitis C Viral Genomes. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2470-2484.                             | 3.9  | 112       |
| 11 | Stepwise pathogenic evolution of <i>Mycobacterium abscessus</i> . <i>Science</i> , 2021, 372, .   | 12.6 | 91        |
| 12 | Developing insights into the mechanisms of evolution of bacterial pathogens from whole-genome sequences. <i>Future Microbiology</i> , 2012, 7, 1283-1296.   | 2.0  | 81        |
| 13 | Rapid Whole-Genome Sequencing for Investigation of a Suspected Tuberculosis Outbreak. <i>Journal of Clinical Microbiology</i> , 2013, 51, 611-614.  | 3.9  | 80        |
| 14 | Phylogenomic exploration of the relationships between strains of <i>Mycobacterium avium</i> subspecies paratuberculosis. <i>BMC Genomics</i> , 2016, 17, 79.  | 2.8  | 71        |
| 15 | The Genome of <i>Mycobacterium Africanum</i> West African 2 Reveals a Lineage-Specific Locus and Genome Erosion Common to the <i>M. tuberculosis</i> Complex. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1552. | 3.0  | 69        |
| 16 | Dissemination of <i>Mycobacterium abscessus</i> via global transmission networks. <i>Nature Microbiology</i> , 2021, 6, 1279-1288.  | 13.3 | 47        |
| 17 | Atypical AT Skew in Firmicute Genomes Results from Selection and Not from Mutation. <i>PLoS Genetics</i> , 2011, 7, e1002283.   | 3.5  | 36        |
| 18 | <i>Mycobacterium abscessus</i> Complex Identification with Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2355-2358.                 | 3.9  | 30        |

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|----|---|------|-----------|
| 19 | Genomic epidemiology of a national outbreak of post-surgical <i>Mycobacterium abscessus</i> wound infections in Brazil. <i>Microbial Genomics</i> , 2017, 3, e000111.   | 2.0  | 22        |
| 20 | Novel Single Nucleotide Polymorphism-Based Assay for Genotyping <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> . <i>Journal of Clinical Microbiology</i> , 2016, 54, 556-564.  | 3.9  | 18        |
| 21 | Consequences of <i>whiB7</i> ( <i>Rv3197A</i> ) Mutations in Beijing Genotype Isolates of the <i>Mycobacterium tuberculosis</i> Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3461-3461.  | 3.2  | 17        |
| 22 | Transmission of <i>M. abscessus</i> in patients with cystic fibrosis – Authors' reply. <i>Lancet, The</i> , 2013, 382, 504.   | 13.7 | 10        |
| 23 | Comment on: Characterization of the <i>embB</i> gene in <i>Mycobacterium tuberculosis</i> isolates from Barcelona and rapid detection of main mutations related to ethambutol resistance using a low-density DNA array. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2298-2299. | 3.0  | 8         |
| 24 | Personalizing therapy for multidrug resistant TB: the potential of Rapid Whole Genome Sequencing. <i>Expert Review of Anti-Infective Therapy</i> , 2016, 14, 1-3.   | 4.4  | 3         |
| 25 | Culture-free club. <i>Nature Reviews Microbiology</i> , 2013, 11, 434-434.  | 28.6 | 1         |