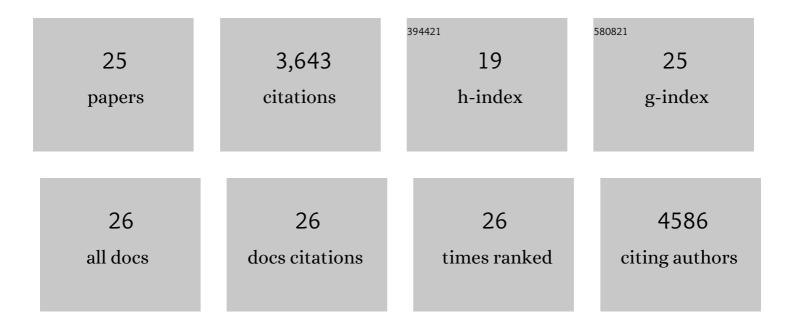
Josephine M Bryant

List of Publications by Year in descending order

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

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