

Josephine M Bryant

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2466091/publications.pdf>

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	Stepwise pathogenic evolution of <i>Mycobacterium abscessus</i> . <i>Science</i> , 2021, 372, .	12.6	91
2	Dissemination of <i>Mycobacterium abscessus</i> via global transmission networks. <i>Nature Microbiology</i> , 2021, 6, 1279-1288.	13.3	47
3	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
4	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
5	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
6	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
7	Emergence and spread of a human-transmissible multidrug-resistant nontuberculous mycobacterium. <i>Science</i> , 2016, 354, 751-757.	12.6	462
8	Phylogenomic exploration of the relationships between strains of <i>Mycobacterium avium</i> subspecies paratuberculosis. <i>BMC Genomics</i> , 2016, 17, 79.	2.8	71
9	Novel Single Nucleotide Polymorphism-Based Assay for Genotyping <i>Mycobacterium avium</i> subsp. paratuberculosis. <i>Journal of Clinical Microbiology</i> , 2016, 54, 556-564.	3.9	18
10	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
11	<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
12	Comment on: Characterization of the embB 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
13	Evolution and transmission of drug-resistant tuberculosis in a Russian population. <i>Nature Genetics</i> , 2014, 46, 279-286.	21.4	451
14	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. <i>Nature</i> , 2014, 514, 494-497.	27.8	506
15	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
16	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
17	Whole-genome sequencing to establish relapse or re-infection with <i>Mycobacterium tuberculosis</i> : a retrospective observational study. <i>Lancet Respiratory Medicine, the</i> , 2013, 1, 786-792.	10.7	184
18	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

#	ARTICLE	IF	CITATIONS
19	Culture-free club. Nature Reviews Microbiology, 2013, 11, 434-434.	28.6	1
20	Rapid Whole-Genome Sequencing for Investigation of a Suspected Tuberculosis Outbreak. Journal of Clinical Microbiology, 2013, 51, 611-614.	3.9	80
21	Transmission of <i>M. abscessus</i> in patients with cystic fibrosis – Authors' reply. Lancet, The, 2013, 382, 504.	13.7	10
22	Consequences of <i>whiB7</i> (<i>Rv3197A</i>) Mutations in Beijing Genotype Isolates of the <i>Mycobacterium tuberculosis</i> Complex. Antimicrobial Agents and Chemotherapy, 2013, 57, 3461-3461.	3.2	17
23	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. PLoS Neglected Tropical Diseases, 2012, 6, e1552.	3.0	69
24	Developing insights into the mechanisms of evolution of bacterial pathogens from whole-genome sequences. Future Microbiology, 2012, 7, 1283-1296.	2.0	81
25	Atypical AT Skew in Firmicute Genomes Results from Selection and Not from Mutation. PLoS Genetics, 2011, 7, e1002283.	3.5	36