

Michael Strong

List of Publications by Year in descending order

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719
citations

623734

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docs citations

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#	ARTICLE	IF	CITATIONS
1	Genomic Analysis of a Hospital-Associated Outbreak of <i>Mycobacterium abscessus</i> : Implications on Transmission. <i>Journal of Clinical Microbiology</i> , 2022, 60, JCM0154721.	3.9	10
2	Longitudinal analysis of SARS-CoV-2 spike and RNA-dependent RNA polymerase protein sequences reveals the emergence and geographic distribution of diverse mutations. <i>Infection, Genetics and Evolution</i> , 2022, 97, 105153.	2.3	16
3	Investigating Nontuberculous <i>Mycobacteria</i> Transmission at the Colorado Adult Cystic Fibrosis Program. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2022, 205, 1064-1074.	5.6	18
4	Soil Properties and Moisture Synergistically Influence Nontuberculous <i>Mycobacterial</i> Prevalence in Natural Environments of Hawai'i. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0001822.	3.1	7
5	Culturing <i>Mycobacteria</i> . <i>Methods in Molecular Biology</i> , 2021, 2314, 1-58.	0.9	10
6	Identification and Characterization of <i>Mycobacterial</i> Species Using Whole-Genome Sequences. <i>Methods in Molecular Biology</i> , 2021, 2314, 399-457.	0.9	0
7	Exposure Pathways of Nontuberculous <i>Mycobacteria</i> Through Soil, Streams, and Groundwater, Hawai'i, USA. <i>GeoHealth</i> , 2021, 5, e2020GH000350.	4.0	8
8	Population Genomics of <i>Mycobacterium abscessus</i> from U.S. Cystic Fibrosis Care Centers. <i>Annals of the American Thoracic Society</i> , 2021, 18, 1960-1969.	3.2	42
9	NASA GeneLab RNA-seq consensus pipeline: Standardized processing of short-read RNA-seq data. <i>IScience</i> , 2021, 24, 102361.	4.1	20
10	Genomic characterization of sporadic isolates of the dominant clone of <i>Mycobacterium abscessus</i> subspecies <i>massiliense</i> . <i>Scientific Reports</i> , 2021, 11, 15336.	3.3	11
11	Dissemination of <i>Mycobacterium abscessus</i> via global transmission networks. <i>Nature Microbiology</i> , 2021, 6, 1279-1288.	13.3	47
12	Intraspecies plasmid and genomic variation of <i>Mycobacterium kansasii</i> revealed by the complete genome sequences of two clinical isolates. <i>Microbial Genomics</i> , 2021, 7, .	2.0	7
13	Lower Recovery of Nontuberculous <i>Mycobacteria</i> from Outdoor Hawai'i Environmental Water Biofilms Compared to Indoor Samples. <i>Microorganisms</i> , 2021, 9, 224.	3.6	17
14	Defining events: 2020 in hindsight. <i>Science</i> , 2021, 371, 22-24.	12.6	0
15	Population Genomics and Inference of <i>Mycobacterium avium</i> Complex Clusters in Cystic Fibrosis Care Centers, United States. <i>Emerging Infectious Diseases</i> , 2021, 27, 2836-2846.	4.3	19
16	Healthcare-associated links in transmission of nontuberculous <i>mycobacteria</i> among people with cystic fibrosis (HALT NTM) study: Rationale and study design. <i>PLoS ONE</i> , 2021, 16, e0261628.	2.5	10
17	Assessment of Soil Features on the Growth of Environmental Nontuberculous <i>Mycobacterial</i> Isolates from Hawai'i. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	18
18	Seeking career clarity. <i>Science</i> , 2020, 368, 26-28.	12.6	0

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19	A scalable, efficient, and safe method to prepare high quality DNA from mycobacteria and other challenging cells. <i>Journal of Clinical Tuberculosis and Other Mycobacterial Diseases</i> , 2020, 19, 100150.	1.3	29
20	Nontuberculous Mycobacterial Disease and Molybdenum in Colorado Watersheds. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 3854.	2.6	18
21	News from a postpandemic world. <i>Science</i> , 2020, 369, 26-29.	12.6	5
22	A Geospatial Epidemiologic Analysis of Nontuberculous Mycobacterial Infection: An Ecological Study in Colorado. <i>Annals of the American Thoracic Society</i> , 2017, 14, 1523-1532.	3.2	36
23	<i>Mycobacterium chimaera</i> Outbreak Response: Experience From Four United States Healthcare Systems. <i>Open Forum Infectious Diseases</i> , 2016, 3, .	0.9	6
24	Sputum is a surrogate for bronchoalveolar lavage for monitoring <i>Mycobacterium tuberculosis</i> transcriptional profiles in TB patients. <i>Tuberculosis</i> , 2016, 100, 89-94.	1.9	27
25	Longitudinal whole genome analysis of pre and post drug treatment <i>Mycobacterium tuberculosis</i> isolates reveals progressive steps to drug resistance. <i>Tuberculosis</i> , 2016, 98, 50-55.	1.9	18
26	Environmental Nontuberculous Mycobacteria in the Hawaiian Islands. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005068.	3.0	65
27	MycoBASE: expanding the functional annotation coverage of mycobacterial genomes. <i>BMC Genomics</i> , 2015, 16, 1102.	2.8	10
28	High-level Relatedness among <i>Mycobacterium abscessus</i> subsp. <i>massiliense</i> Strains from Widely Separated Outbreaks. <i>Emerging Infectious Diseases</i> , 2014, 20, 364-371.	4.3	108
29	Genome Sequencing of <i>Mycobacterium abscessus</i> Isolates from Patients in the United States and Comparisons to Globally Diverse Clinical Strains. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3573-3582.	3.9	64
30	A minimum variance method for genome-wide data-driven normalization of quantitative real-time polymerase chain reaction expression data. <i>Analytical Biochemistry</i> , 2014, 458, 11-13.	2.4	5
31	Phylogenomics of Brazilian epidemic isolates of <i>Mycobacterium abscessus</i> subsp. <i>bolletii</i> reveals relationships of global outbreak strains. <i>Infection, Genetics and Evolution</i> , 2013, 20, 292-297.	2.3	44