

# Qingyun Liu

## List of Publications by Year in descending order

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Version: 2024-02-01

41  
papers

2,407  
citations

394286

19  
h-index

315616

38  
g-index

48  
all docs

48  
docs citations

48  
times ranked

2629  
citing authors

#	ARTICLE	IF	CITATIONS
1	SAM-TB: a whole genome sequencing data analysis website for detection of <i>Mycobacterium tuberculosis</i> drug resistance and transmission. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	26
2	Modern Beijing sublineage of <i>Mycobacterium tuberculosis</i> shift macrophage into a hyperinflammatory status. <i>Emerging Microbes and Infections</i> , 2022, 11, 715-724.	3.0	6
3	The microbial metabolite trimethylamine N-oxide promotes antitumor immunity in triple-negative breast cancer. <i>Cell Metabolism</i> , 2022, 34, 581-594.e8.	7.2	105
4	Using an Unsupervised Clustering Model to Detect the Early Spread of SARS-CoV-2 Worldwide. <i>Genes</i> , 2022, 13, 648.	1.0	1
5	Multiplexed Strain Phenotyping Defines Consequences of Genetic Diversity in <i>Mycobacterium tuberculosis</i> for Infection and Vaccination Outcomes. <i>MSystems</i> , 2022, 7, e0011022.	1.7	3
6	Comprehensive genomic analysis of <i>Mycobacterium tuberculosis</i> reveals limited impact of high-fitness genotypes on MDR-TB transmission. <i>Journal of Infection</i> , 2022, 85, 49-56.	1.7	7
7	A tRNA-Acetylating Toxin and Detoxifying Enzyme in <i>Mycobacterium tuberculosis</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
8	Lesion Heterogeneity and Long-Term Heteroresistance in Multidrug-Resistant Tuberculosis. <i>Journal of Infectious Diseases</i> , 2021, 224, 889-893.	1.9	10
9	A population-based genomic epidemiological study of the source of tuberculosis infections in an emerging city: Shenzhen, China. <i>The Lancet Regional Health - Western Pacific</i> , 2021, 8, 100106.	1.3	8
10	Local adaptation of <i>Mycobacterium tuberculosis</i> on the Tibetan Plateau. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	21
11	<i>Mycobacterial</i> fatty acid catabolism is repressed by FdmR to sustain lipogenesis and virulence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	20
12	Population genomics provides insights into the evolution and adaptation to humans of the waterborne pathogen <i>Mycobacterium kansasii</i> . <i>Nature Communications</i> , 2021, 12, 2491.	5.8	20
13	Deep whole-genome sequencing reveals no evidence for heteroresistance influencing treatment outcomes among drug-susceptible tuberculosis patients. <i>Tuberculosis</i> , 2021, 130, 102120.	0.8	6
14	Citywide Transmission of Multidrug-resistant Tuberculosis Under China's Rapid Urbanization: A Retrospective Population-based Genomic Spatial Epidemiological Study. <i>Clinical Infectious Diseases</i> , 2020, 71, 142-151.	2.9	46
15	<i>Staphylococcus epidermidis</i> Contributes to Healthy Maturation of the Nasal Microbiome by Stimulating Antimicrobial Peptide Production. <i>Cell Host and Microbe</i> , 2020, 27, 68-78.e5.	5.1	99
16	<i>Mycobacterium tuberculosis</i> strains of the modern Beijing sublineage excessively accumulate triacylglycerols in vitro. <i>Tuberculosis</i> , 2020, 120, 101892.	0.8	10
17	<i>Mycobacterium tuberculosis</i> clinical isolates carry mutational signatures of host immune environments. <i>Science Advances</i> , 2020, 6, eaba4901.	4.7	33
18	Genomic variant-identification methods may alter <i>Mycobacterium tuberculosis</i> transmission inferences. <i>Microbial Genomics</i> , 2020, 6, .	1.0	24

#	ARTICLE	IF	CITATIONS
19	Mutations in dnaA and a cryptic interaction site increase drug resistance in Mycobacterium tuberculosis. PLoS Pathogens, 2020, 16, e1009063.	2.1	23
20	Title is missing!. , 2020, 16, e1009063.		0
21	Title is missing!. , 2020, 16, e1009063.		0
22	Title is missing!. , 2020, 16, e1009063.		0
23	Title is missing!. , 2020, 16, e1009063.		0
24	Whole genome sequencing of Mycobacterium tuberculosis: current standards and open issues. Nature Reviews Microbiology, 2019, 17, 533-545.	13.6	237
25	Characterization of linezolid-resistance-associated mutations in Mycobacterium tuberculosis through WGS. Journal of Antimicrobial Chemotherapy, 2019, 74, 1795-1798.	1.3	23
26	Internal migration and transmission dynamics of tuberculosis in Shanghai, China: an epidemiological, spatial, genomic analysis. Lancet Infectious Diseases, The, 2018, 18, 788-795.	4.6	85
27	Assessment of tuberculosis contact investigation in Shanghai, China: An 8-year cohort study. Tuberculosis, 2018, 108, 10-15.	0.8	10
28	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. New England Journal of Medicine, 2018, 379, 1403-1415.	13.9	405
29	China's tuberculosis epidemic stems from historical expansion of four strains of Mycobacterium tuberculosis. Nature Ecology and Evolution, 2018, 2, 1982-1992.	3.4	83
30	Phylogenetic analysis and virulence determinant of the host-adapted <i>Staphylococcus aureus</i> lineage ST188 in China. Emerging Microbes and Infections, 2018, 7, 1-11.	3.0	37
31	Have compensatory mutations facilitated the current epidemic of multidrug-resistant tuberculosis?. Emerging Microbes and Infections, 2018, 7, 1-8.	3.0	22
32	Transmission of multidrug-resistant Mycobacterium tuberculosis in Shanghai, China: a retrospective observational study using whole-genome sequencing and epidemiological investigation. Lancet Infectious Diseases, The, 2017, 17, 275-284.	4.6	205
33	The within-host population dynamics of Mycobacterium tuberculosis vary with treatment efficacy. Genome Biology, 2017, 18, 71.	3.8	95
34	Transmission is a Noticeable Cause of Resistance Among Treated Tuberculosis Patients in Shanghai, China. Scientific Reports, 2017, 7, 7691.	1.6	16
35	Deep Whole-Genome Sequencing to Detect Mixed Infection of Mycobacterium tuberculosis. PLoS ONE, 2016, 11, e0159029.	1.1	35
36	Mycobacterium tuberculosis lineage 4 comprises globally distributed and geographically restricted sublineages. Nature Genetics, 2016, 48, 1535-1543.	9.4	326

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37	Genetic features of <i>Mycobacterium tuberculosis</i> modern Beijing sublineage. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-8.	3.0	35
38	Within patient microevolution of <i>Mycobacterium tuberculosis</i> correlates with heterogeneous responses to treatment. <i>Scientific Reports</i> , 2015, 5, 17507.	1.6	80
39	Southern East Asian origin and coexpansion of <i>Mycobacterium tuberculosis</i> Beijing family with Han Chinese. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8136-8141.	3.3	142
40	Association of <i>gyrA/B</i> mutations and resistance levels to fluoroquinolones in clinical isolates of <i>Mycobacterium tuberculosis</i> . <i>Emerging Microbes and Infections</i> , 2014, 3, 1-5.	3.0	65
41	Triplex real-time PCR melting curve analysis for detecting <i>Mycobacterium tuberculosis</i> mutations associated with resistance to second-line drugs in a single reaction. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 1097-1103.	1.3	21