

# Qingyun Liu

## List of Publications by Year in descending order

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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	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018, 379, 1403-1415.	13.9	405
2	<i>Mycobacterium tuberculosis</i> lineage 4 comprises globally distributed and geographically restricted sublineages. <i>Nature Genetics</i> , 2016, 48, 1535-1543.	9.4	326
3	Whole genome sequencing of <i>Mycobacterium tuberculosis</i> : current standards and open issues. <i>Nature Reviews Microbiology</i> , 2019, 17, 533-545.	13.6	237
4	Transmission of multidrug-resistant <i>Mycobacterium tuberculosis</i> in Shanghai, China: a retrospective observational study using whole-genome sequencing and epidemiological investigation. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 275-284.	4.6	205
5	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
6	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
7	<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
8	The within-host population dynamics of <i>Mycobacterium tuberculosis</i> vary with treatment efficacy. <i>Genome Biology</i> , 2017, 18, 71.	3.8	95
9	Internal migration and transmission dynamics of tuberculosis in Shanghai, China: an epidemiological, spatial, genomic analysis. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 788-795.	4.6	85
10	China's tuberculosis epidemic stems from historical expansion of four strains of <i>Mycobacterium tuberculosis</i> . <i>Nature Ecology and Evolution</i> , 2018, 2, 1982-1992.	3.4	83
11	Within patient microevolution of <i>Mycobacterium tuberculosis</i> correlates with heterogeneous responses to treatment. <i>Scientific Reports</i> , 2015, 5, 17507.	1.6	80
12	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
13	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
14	Phylogenetic analysis and virulence determinant of the host-adapted <i>Staphylococcus aureus</i> lineage ST188 in China. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-11.	3.0	37
15	Deep Whole-Genome Sequencing to Detect Mixed Infection of <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2016, 11, e0159029.	1.1	35
16	Genetic features of <i>Mycobacterium tuberculosis</i> modern Beijing sublineage. <i>Emerging Microbes and Infections</i> , 2016, 5, 1-8.	3.0	35
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	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

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19	Genomic variant-identification methods may alter Mycobacterium tuberculosis transmission inferences. <i>Microbial Genomics</i> , 2020, 6, .	1.0	24
20	Characterization of linezolid-resistance-associated mutations in Mycobacterium tuberculosis through WGS. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 1795-1798.	1.3	23
21	Mutations in dnaA and a cryptic interaction site increase drug resistance in Mycobacterium tuberculosis. <i>PLoS Pathogens</i> , 2020, 16, e1009063.	2.1	23
22	Have compensatory mutations facilitated the current epidemic of multidrug-resistant tuberculosis?. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-8.	3.0	22
23	Triplex real-time PCR melting curve analysis for detecting Mycobacterium tuberculosis 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
24	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
25	Mycobacterial 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
26	Population genomics provides insights into the evolution and adaptation to humans of the waterborne pathogen Mycobacterium kansasii. <i>Nature Communications</i> , 2021, 12, 2491.	5.8	20
27	Transmission is a Noticeable Cause of Resistance Among Treated Tuberculosis Patients in Shanghai, China. <i>Scientific Reports</i> , 2017, 7, 7691.	1.6	16
28	Assessment of tuberculosis contact investigation in Shanghai, China: An 8-year cohort study. <i>Tuberculosis</i> , 2018, 108, 10-15.	0.8	10
29	Mycobacterium tuberculosis strains of the modern Beijing sublineage excessively accumulate triacylglycerols in vitro. <i>Tuberculosis</i> , 2020, 120, 101892.	0.8	10
30	Lesion Heterogeneity and Long-Term Heteroresistance in Multidrug-Resistant Tuberculosis. <i>Journal of Infectious Diseases</i> , 2021, 224, 889-893.	1.9	10
31	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
32	Comprehensive genomic analysis of Mycobacterium tuberculosis reveals limited impact of high-fitness genotypes on MDR-TB transmission. <i>Journal of Infection</i> , 2022, 85, 49-56.	1.7	7
33	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
34	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
35	A tRNA-Acetylating Toxin and Detoxifying Enzyme in Mycobacterium tuberculosis. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
36	Multiplexed Strain Phenotyping Defines Consequences of Genetic Diversity in Mycobacterium tuberculosis for Infection and Vaccination Outcomes. <i>MSystems</i> , 2022, 7, e0011022.	1.7	3

#	ARTICLE	IF	CITATIONS
37	Using an Unsupervised Clustering Model to Detect the Early Spread of SARS-CoV-2 Worldwide. Genes, 2022, 13, 648.	1.0	1
38	Title is missing!. , 2020, 16, e1009063.		0
39	Title is missing!. , 2020, 16, e1009063.		0
40	Title is missing!. , 2020, 16, e1009063.		0
41	Title is missing!. , 2020, 16, e1009063.		0