

CITATION REPORT

List of articles citing

Relapse Versus Reinfection of Recurrent Tuberculosis Patients in a National Tuberculosis Specialized Hospital in Beijing, China

DOI: 10.3389/fmicb.2018.01858
Frontiers in Microbiology, 2018, 9, 1858.

Source: <https://exaly.com/paper-pdf/70975987/citation-report.pdf>

Version: 2024-04-28

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
35	Recurrence Is a Noticeable Cause of Rifampicin-Resistant in the Elderly Population in Jiangxi, China. <i>Frontiers in Public Health</i> , 2019 , 7, 182	6	2
34	Rate and risk factors of recurrent tuberculosis in Yemen: a 5-year prospective study. <i>Infectious Diseases</i> , 2020 , 52, 161-169	3.1	7
33	Tuberculosis relapse is more common than reinfection in Beijing, China. <i>Infectious Diseases</i> , 2020 , 52, 858-865	3.1	7
32	Screening and identification of plasma lncRNAs uc.48+ and NR_105053 as potential novel biomarkers for cured pulmonary tuberculosis. <i>International Journal of Infectious Diseases</i> , 2020 , 92, 141-150	10.5	6
31	Proteomic analysis of infected primary human leucocytes revealed PSTK as potential treatment-monitoring marker for active and latent tuberculosis. <i>PLoS ONE</i> , 2020 , 15, e0231834	3.7	2
30	Assessment of Strategies and Epidemiological Characteristics of Tuberculosis in Henan Province, China: Observational Study. <i>JMIR Public Health and Surveillance</i> , 2021 , 7, e24830	11.4	2
29	SplitStrains, a tool to identify and separate mixed Mycobacterium tuberculosis infections from WGS data.		
28	Epidemiology of Recurrent Pulmonary Tuberculosis in Henan Province, China: Observational study (Preprint).		
27	Relapse or Re-Infection, the Situation of Recurrent Tuberculosis in Eastern China. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021 , 11, 638990	5.9	3
26	Genomic epidemiological analysis identifies high relapse among individuals with recurring tuberculosis and provides evidence of recent household-related transmission of tuberculosis in Ghana. <i>International Journal of Infectious Diseases</i> , 2021 , 106, 13-22	10.5	1
25	SplitStrains, a tool to identify and separate mixed infections from WGS data. <i>Microbial Genomics</i> , 2021 , 7,	4.4	1
24	Acetylase Status Among Newly Diagnosed and Recurrent Tuberculosis Patients from Kupang, Eastern Part of Indonesia. <i>Pharmacogenomics and Personalized Medicine</i> , 2021 , 14, 737-744	2.1	
23	The Relevance of Genomic Epidemiology for Control of Tuberculosis in West Africa. <i>Frontiers in Public Health</i> , 2021 , 9, 706651	6	0
22	A Prospective Cohort Study on the Prevalent and Recurrent Tuberculosis Isolates Using the MIRU-VNTR Typing. <i>Frontiers in Medicine</i> , 2021 , 8, 685368	4.9	1
21	Tuberculosis recurrence over a 7-year follow-up period in successfully treated patients in a routine program setting in China: a prospective longitudinal study. <i>International Journal of Infectious Diseases</i> , 2021 , 110, 403-409	10.5	2
20	Initiation of Post-Primary Tuberculosis of the Lungs: Exploring the Secret Role of Bone Marrow Derived Stem Cells. <i>Frontiers in Immunology</i> , 2020 , 11, 594572	8.4	3
19	What Can Go Wrong When Applying Immune Modulation Therapies to Target Persistent Bacterial Infections. <i>Journal of Cellular Immunology</i> , 2020 , 2, 1-5	1.9	

18 H. Mucosal-Associated Invariant and V β V α T Cells. **2021**, 233-245

17 Analysis of Serial Multidrug-Resistant Tuberculosis Strains Causing Treatment Failure and Within-Host Evolution by Whole-Genome Sequencing. *MSphere*, **2020**, 5, 1

16 Assessment of Strategies and Epidemiological Characteristics of Tuberculosis in Henan Province, China: Observational Study (Preprint).

15 Investigation on the cause of recurrent tuberculosis in a rural area in China using whole-genome sequencing: A retrospective cohort study.. *Tuberculosis*, **2022**, 133, 102174 2.6 2

14 Risk factors for types of recurrent tuberculosis (reactivation versus reinfection): A global systematic review and meta-analysis.. *International Journal of Infectious Diseases*, **2021**, 10.5 2

13 Distinguishing Relapse From Reinfection With Whole-Genome Sequencing in Recurrent Pulmonary Tuberculosis: A Retrospective Cohort Study in Beijing, China.. *Frontiers in Microbiology*, **2021**, 12, 754352^{5.7} 0

12 Heightened microbial translocation is a prognostic biomarker of recurrent tuberculosis.. *Clinical Infectious Diseases*, **2022**, 11.6 0

11 Tuberculosis reinfection and relapse in eastern China: A prospective study using whole-genome sequencing. *Clinical Microbiology and Infection*, **2022**, 9.5 0

10 Incidence of pulmonary tuberculosis under the regular COVID-19 epidemic prevention and control in China. **2022**, 22, 0

9 Epidemiology of recurrent pulmonary tuberculosis by bacteriological features of 100 million residents in China. **2022**, 22, 1

8 Long-term results of 10 years of observation of cured cases of pulmonary tuberculosis. **2022**, 6, 007-011 0

7 Recent Transmission and Prevalent Characterization of the Beijing Family Mycobacterium tuberculosis in Jiangxi, China. **2022**, 71, 371-380 0

6 Microbial Persistence, Replacement and Local Antimicrobial Therapy in Recurrent Bone and Joint Infection. **2023**, 12, 708 0

5 A tuberculosis epidemic model as a proxy for the assessment of the novel M72/AS01E vaccine. **2023**, 120, 107162 0

4 Endogenous relapse and exogenous reinfection in recurrent pulmonary tuberculosis: A retrospective study revealed by whole genome sequencing. 14, 0

3 Machine Learning Prediction Model of Tuberculosis Incidence Based on Meteorological Factors and Air Pollutants. **2023**, 20, 3910 0

2 Advantages of analysing both pairwise SNV-distance and differing SNVs between Mycobacterium tuberculosis isolates for recurrent tuberculosis cause determination. **2023**, 9, 0

1 Multiomics Integration of Tuberculosis Pathogenesis. **2023**, 937-967 0

