Zhenhua Yang

List of Publications by Year in descending order

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Ζηένημα Υγνς

#	Article	IF	CITATIONS
1	Identification of Risk Factors for Extrapulmonary Tuberculosis. Clinical Infectious Diseases, 2004, 38, 199-205.	5.8	304
2	Simultaneous detection of isoniazid, rifampin, and ethambutol resistance of Mycobacterium tuberculosis by a single multiplex allele-specific polymerase chain reaction (PCR) assay. Diagnostic Microbiology and Infectious Disease, 2005, 53, 201-208.	1.8	51
3	Clinical Relevance ofMycobacterium tuberculosis plcDGene Mutations. American Journal of Respiratory and Critical Care Medicine, 2005, 171, 1436-1442.	5.6	43
4	Insight to the Epidemiology and Risk Factors of Extrapulmonary Tuberculosis in Tianjin, China during 2006-2011. PLoS ONE, 2014, 9, e112213.	2.5	31
5	Epitope promiscuity and population coverage of Mycobacterium tuberculosis protein antigens in current subunit vaccines under development. Infection, Genetics and Evolution, 2020, 80, 104186.	2.3	23
6	Epidemiology and Clinical Characteristics of Pediatric Drug-Resistant Tuberculosis in Chongqing, China. PLoS ONE, 2016, 11, e0151303.	2.5	17
7	How dormant is Mycobacterium tuberculosis during latency? A study integrating genomics and molecular epidemiology. Infection, Genetics and Evolution, 2011, 11, 1164-1167.	2.3	13
8	The Road to Tuberculosis (Mycobacterium tuberculosis) Elimination in Arkansas; a Re-Examination of Risk Groups. PLoS ONE, 2014, 9, e90664.	2.5	13
9	Effectiveness of contact investigations for tuberculosis control in Arkansas. Journal of Theoretical Biology, 2015, 380, 238-246.	1.7	12
10	Drug-Resistant tuberculosis in Ethiopia: Characteristics of cases in a referral hospital and the implications. International Journal of Mycobacteriology, 2018, 7, 167.	0.6	8
11	Molecular epidemiology of tuberculosis. Frontiers in Bioscience - Landmark, 2003, 8, d440-450.	3.0	7
12	Conservation in gene encoding Mycobacterium tuberculosis antigen Rv2660 and a high predicted population coverage of H56 multistage vaccine in South Africa. Infection, Genetics and Evolution, 2017, 55, 244-250.	2.3	6
13	Characteristics Indicative of Tuberculosis/HIV Coinfection in a High-Burden Setting: Lessons from 13,802 Incident Tuberculosis Cases in Harare, Zimbabwe. American Journal of Tropical Medicine and Hygiene, 2020, 103, 214-220.	1.4	6
14	Trends of sputum-smear positive tuberculosis in Zimbabwe: 2008–2011. BMC Research Notes, 2015, 8, 575.	1.4	4
15	Contextualizing tuberculosis risk in time and space: comparing time-restricted genotypic case clusters and geospatial clusters to evaluate the relative contribution of recent transmission to incidence of TB using nine years of case data from Michigan, USA. Annals of Epidemiology, 2019, 40, 21-27.e3.	1.9	4
16	Predicted Structural Variability of Mycobacterium tuberculosis PPE18 Protein With Immunological Implications Among Clinical Strains. Frontiers in Microbiology, 2020, 11, 595312.	3.5	4
17	Characterizing Pediatric Tuberculosis with and without Human Immunodeficiency Virus Coinfection in Harare, Zimbabwe. American Journal of Tropical Medicine and Hygiene, 2018, 99, 601-607.	1.4	3
18	Comparison of ambient air survival of Mycobacterium tuberculosis clinical strains associated with different epidemiological phenotypes. International Journal of Mycobacteriology, 2014, 3, 211-213.	0.6	2

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19	Factors associated with unfavorable treatment outcomes among pediatric tuberculosis cases in Harare, Zimbabwe during 2013–2017. International Journal of Infectious Diseases, 2020, 101, 403-408.	3.3	2
20	Identification of Mycobacterium tuberculosis Antigens with Vaccine Potential Using a Machine Learning-Based Reverse Vaccinology Approach. Vaccines, 2021, 9, 1098.	4.4	2
21	Whole-Genome Sequences of Mycobacterium tuberculosis TB282 and TB284, a Widespread and a Unique Strain, Respectively, Identified in a Previous Study of Tuberculosis Transmission in Central Los Angeles, California, USA. Genome Announcements, 2017, 5, .	0.8	0