

Sebastien Gagneux

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211
papers

14,821
citations

64
h-index

119
g-index

229
ext. papers

18,166
ext. citations

9.7
avg, IF

6.7
L-index

#	Paper	IF	Citations
211	Variable host-pathogen compatibility in <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 2869-73	11.5	761
210	Out-of-Africa migration and Neolithic coexpansion of <i>Mycobacterium tuberculosis</i> with modern humans. <i>Nature Genetics</i> , 2013 , 45, 1176-82	36.3	676
209	Global phylogeography of <i>Mycobacterium tuberculosis</i> and implications for tuberculosis product development. <i>Lancet Infectious Diseases</i> , 2007 , 7, 328-37	25.5	544
208	Human T cell epitopes of <i>Mycobacterium tuberculosis</i> are evolutionarily hyperconserved. <i>Nature Genetics</i> , 2010 , 42, 498-503	36.3	509
207	The competitive cost of antibiotic resistance in <i>Mycobacterium tuberculosis</i> . <i>Science</i> , 2006 , 312, 1944-6	33.3	468
206	High functional diversity in <i>Mycobacterium tuberculosis</i> driven by genetic drift and human demography. <i>PLoS Biology</i> , 2008 , 6, e311	9.7	421
205	Whole-genome sequencing of rifampicin-resistant <i>Mycobacterium tuberculosis</i> strains identifies compensatory mutations in RNA polymerase genes. <i>Nature Genetics</i> , 2011 , 44, 106-10	36.3	376
204	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. <i>Nature</i> , 2014 , 514, 494-7	50.4	358
203	The influence of host and bacterial genotype on the development of disseminated disease with <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2008 , 4, e1000034	7.6	345
202	Evolutionary history and global spread of the <i>Mycobacterium tuberculosis</i> Beijing lineage. <i>Nature Genetics</i> , 2015 , 47, 242-9	36.3	344
201	Genotyping of genetically monomorphic bacteria: DNA sequencing in <i>Mycobacterium tuberculosis</i> highlights the limitations of current methodologies. <i>PLoS ONE</i> , 2009 , 4, e7815	3.7	317
200	<i>Mycobacterium tuberculosis</i> mutation rate estimates from different lineages predict substantial differences in the emergence of drug-resistant tuberculosis. <i>Nature Genetics</i> , 2013 , 45, 784-90	36.3	297
199	Genomic analysis identifies targets of convergent positive selection in drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2013 , 45, 1183-9	36.3	295
198	Host-pathogen coevolution in human tuberculosis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012 , 367, 850-9	5.8	255
197	Consequences of genomic diversity in <i>Mycobacterium tuberculosis</i> . <i>Seminars in Immunology</i> , 2014 , 26, 431-44	10.7	243
196	Acquired Resistance to Bedaquiline and Delamanid in Therapy for Tuberculosis. <i>New England Journal of Medicine</i> , 2015 , 373, 1986-8	59.2	229
195	Progression to active tuberculosis, but not transmission, varies by <i>Mycobacterium tuberculosis</i> lineage in The Gambia. <i>Journal of Infectious Diseases</i> , 2008 , 198, 1037-43	7	226

194	Ecology and evolution of Mycobacterium tuberculosis. <i>Nature Reviews Microbiology</i> , 2018 , 16, 202-213	22.2	225
193	Genomic deletions classify the Beijing/W strains as a distinct genetic lineage of Mycobacterium tuberculosis. <i>Journal of Clinical Microbiology</i> , 2005 , 43, 3185-91	9.7	209
192	Mycobacterium tuberculosis lineage 4 comprises globally distributed and geographically restricted sublineages. <i>Nature Genetics</i> , 2016 , 48, 1535-1543	36.3	208
191	A standardised method for interpreting the association between mutations and phenotypic drug resistance in. <i>European Respiratory Journal</i> , 2017 , 50,	13.6	198
190	Human macrophage responses to clinical isolates from the Mycobacterium tuberculosis complex discriminate between ancient and modern lineages. <i>PLoS Pathogens</i> , 2011 , 7, e1001307	7.6	193
189	The W-Beijing lineage of Mycobacterium tuberculosis overproduces triglycerides and has the DosR dormancy regulon constitutively upregulated. <i>Journal of Bacteriology</i> , 2007 , 189, 2583-9	3.5	191
188	Impact of bacterial genetics on the transmission of isoniazid-resistant Mycobacterium tuberculosis. <i>PLoS Pathogens</i> , 2006 , 2, e61	7.6	168
187	Co-evolution of Mycobacterium tuberculosis and Homo sapiens. <i>Immunological Reviews</i> , 2015 , 264, 6-24	11.3	166
186	Mycobacterium africanum--review of an important cause of human tuberculosis in West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2010 , 4, e744	4.8	165
185	Mycobacterial lineages causing pulmonary and extrapulmonary tuberculosis, Ethiopia. <i>Emerging Infectious Diseases</i> , 2013 , 19, 460-3	10.2	155
184	Antimicrobial resistance in Mycobacterium tuberculosis: mechanistic and evolutionary perspectives. <i>FEMS Microbiology Reviews</i> , 2017 , 41, 354-373	15.1	153
183	Putative compensatory mutations in the rpoC gene of rifampin-resistant Mycobacterium tuberculosis are associated with ongoing transmission. <i>Antimicrobial Agents and Chemotherapy</i> , 2013 , 57, 827-32	5.9	151
182	Infectiousness, reproductive fitness and evolution of drug-resistant Mycobacterium tuberculosis. <i>International Journal of Tuberculosis and Lung Disease</i> , 2009 , 13, 1456-66	2.1	147
181	The heterogeneous evolution of multidrug-resistant Mycobacterium tuberculosis. <i>Trends in Genetics</i> , 2013 , 29, 160-9	8.5	136
180	Genomic diversity among drug sensitive and multidrug resistant isolates of Mycobacterium tuberculosis with identical DNA fingerprints. <i>PLoS ONE</i> , 2009 , 4, e7407	3.7	124
179	Relationship between Mycobacterium tuberculosis genotype and the clinical phenotype of pulmonary and meningeal tuberculosis. <i>Journal of Clinical Microbiology</i> , 2008 , 46, 1363-8	9.7	120
178	Fit genotypes and escape variants of subgroup III Neisseria meningitidis during three pandemics of epidemic meningitis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 5234-9	11.5	118
177	Does M. tuberculosis genomic diversity explain disease diversity?. <i>Drug Discovery Today Disease Mechanisms</i> , 2010 , 7, e43-e59		117

176	The past and future of tuberculosis research. <i>PLoS Pathogens</i> , 2009 , 5, e1000600	7.6	112
175	Whole genome sequencing of <i>Mycobacterium tuberculosis</i> : current standards and open issues. <i>Nature Reviews Microbiology</i> , 2019 , 17, 533-545	22.2	109
174	Clinical implications of molecular drug resistance testing for <i>Mycobacterium tuberculosis</i> : a TBNET/RESIST-TB consensus statement. <i>International Journal of Tuberculosis and Lung Disease</i> , 2016 , 20, 24-42	2.1	101
173	Two new rapid SNP-typing methods for classifying <i>Mycobacterium tuberculosis</i> complex into the main phylogenetic lineages. <i>PLoS ONE</i> , 2012 , 7, e41253	3.7	100
172	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, 8136-41	11.5	97
171	<i>M. tuberculosis</i> T Cell Epitope Analysis Reveals Paucity of Antigenic Variation and Identifies Rare Variable TB Antigens. <i>Cell Host and Microbe</i> , 2015 , 18, 538-48	23.4	95
170	Genomic analysis distinguishes <i>Mycobacterium africanum</i> . <i>Journal of Clinical Microbiology</i> , 2004 , 42, 3594-9	4.9	90
169	KvarQ: targeted and direct variant calling from fastq reads of bacterial genomes. <i>BMC Genomics</i> , 2014 , 15, 881	4.5	89
168	Differential virulence and disease progression following <i>Mycobacterium tuberculosis</i> complex infection of the common marmoset (<i>Callithrix jacchus</i>). <i>Infection and Immunity</i> , 2013 , 81, 2909-19	3.7	83
167	A cluster of multidrug-resistant <i>Mycobacterium tuberculosis</i> among patients arriving in Europe from the Horn of Africa: a molecular epidemiological study. <i>Lancet Infectious Diseases</i> , 2018 , 18, 431-440	25.5	81
166	Reversion of antibiotic resistance in by spiroisoxazoline SMART-420. <i>Science</i> , 2017 , 355, 1206-1211	33.3	80
165	Towards host-directed therapies for tuberculosis. <i>Nature Reviews Drug Discovery</i> , 2015 , 14, 511-2	64.1	80
164	Effect of mutation and genetic background on drug resistance in <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2012 , 56, 3047-53	5.9	80
163	Novel <i>Mycobacterium tuberculosis</i> complex isolate from a wild chimpanzee. <i>Emerging Infectious Diseases</i> , 2013 , 19, 969-76	10.2	78
162	A19 The impact of HIV-1 on the evolution of <i>Mycobacterium tuberculosis</i> . <i>Virus Evolution</i> , 2018 , 4,	3.7	78
161	A New Phylogenetic Framework for the Animal-Adapted Complex. <i>Frontiers in Microbiology</i> , 2018 , 9, 2820	5.7	77
160	Beijing sublineages of <i>Mycobacterium tuberculosis</i> differ in pathogenicity in the guinea pig. <i>Vaccine Journal</i> , 2012 , 19, 1227-37		76
159	Strain diversity, epistasis and the evolution of drug resistance in <i>Mycobacterium tuberculosis</i> . <i>Clinical Microbiology and Infection</i> , 2011 , 17, 815-20	9.5	75

158	Tracking a tuberculosis outbreak over 21 years: strain-specific single-nucleotide polymorphism typing combined with targeted whole-genome sequencing. <i>Journal of Infectious Diseases</i> , 2015 , 211, 1306-16	7	72
157	Epistasis between antibiotic resistance mutations drives the evolution of extensively drug-resistant tuberculosis. <i>Evolution, Medicine and Public Health</i> , 2013 , 2013, 65-74	3	71
156	<i>Mycobacterium africanum</i> elicits an attenuated T cell response to early secreted antigenic target, 6 kDa, in patients with tuberculosis and their household contacts. <i>Journal of Infectious Diseases</i> , 2006 , 193, 1279-86	7	70
155	Clonal waves of <i>Neisseria</i> colonisation and disease in the African meningitis belt: eight-year longitudinal study in northern Ghana. <i>PLoS Medicine</i> , 2007 , 4, e101	11.6	70
154	Standard Genotyping Overestimates Transmission of <i>Mycobacterium tuberculosis</i> among Immigrants in a Low-Incidence Country. <i>Journal of Clinical Microbiology</i> , 2016 , 54, 1862-1870	9.7	70
153	Sequence diversity in the <i>pe_pgrs</i> genes of <i>Mycobacterium tuberculosis</i> is independent of human T cell recognition. <i>MBio</i> , 2014 , 5, e00960-13	7.8	69
152	A sister lineage of the <i>Mycobacterium tuberculosis</i> complex discovered in the African Great Lakes region. <i>Nature Communications</i> , 2020 , 11, 2917	17.4	68
151	High-throughput metabolomic analysis predicts mode of action of uncharacterized antimicrobial compounds. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	68
150	Population Genomics of <i>Mycobacterium tuberculosis</i> in Ethiopia Contradicts the Virgin Soil Hypothesis for Human Tuberculosis in Sub-Saharan Africa. <i>Current Biology</i> , 2015 , 25, 3260-6	6.3	66
149	PolyTB: a genomic variation map for <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2014 , 94, 346-54	2.6	64
148	Comparative analysis of <i>Mycobacterium tuberculosis</i> <i>pe</i> and <i>ppe</i> genes reveals high sequence variation and an apparent absence of selective constraints. <i>PLoS ONE</i> , 2012 , 7, e30593	3.7	64
147	HIV infection disrupts the sympatric host-pathogen relationship in human tuberculosis. <i>PLoS Genetics</i> , 2013 , 9, e1003318	6	61
146	The within-host population dynamics of <i>Mycobacterium tuberculosis</i> vary with treatment efficacy. <i>Genome Biology</i> , 2017 , 18, 71	18.3	60
145	Use of whole genome sequencing to determine the microevolution of <i>Mycobacterium tuberculosis</i> during an outbreak. <i>PLoS ONE</i> , 2013 , 8, e58235	3.7	60
144	Compensatory evolution drives multidrug-resistant tuberculosis in Central Asia. <i>ELife</i> , 2018 , 7,	8.9	60
143	Transient Hyperglycemia in Patients With Tuberculosis in Tanzania: Implications for Diabetes Screening Algorithms. <i>Journal of Infectious Diseases</i> , 2016 , 213, 1163-72	7	58
142	The genome of <i>Mycobacterium africanum</i> West African 2 reveals a lineage-specific locus and genome erosion common to the <i>M. tuberculosis</i> complex. <i>PLoS Neglected Tropical Diseases</i> , 2012 , 6, e1552	4.8	58
141	The molecular clock of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2019 , 15, e1008067	7.6	57

140	A role for systems epidemiology in tuberculosis research. <i>Trends in Microbiology</i> , 2011 , 19, 492-500	12.4	57
139	Evolution of drug resistance in tuberculosis: recent progress and implications for diagnosis and therapy. <i>Drugs</i> , 2014 , 74, 1063-72	12.1	55
138	Mapping of genotype-phenotype diversity among clinical isolates of mycobacterium tuberculosis by sequence-based transcriptional profiling. <i>Genome Biology and Evolution</i> , 2013 , 5, 1849-62	3.9	55
137	Large sequence polymorphisms classify Mycobacterium tuberculosis strains with ancestral spoligotyping patterns. <i>Journal of Clinical Microbiology</i> , 2007 , 45, 3393-5	9.7	52
136	Old and new selective pressures on Mycobacterium tuberculosis. <i>Infection, Genetics and Evolution</i> , 2012 , 12, 678-85	4.5	50
135	Use of spoligotyping and large sequence polymorphisms to study the population structure of the Mycobacterium tuberculosis complex in a cohort study of consecutive smear-positive tuberculosis cases in The Gambia. <i>Journal of Clinical Microbiology</i> , 2009 , 47, 994-1001	9.7	49
134	Consensus numbering system for the rifampicin resistance-associated rpoB gene mutations in pathogenic mycobacteria. <i>Clinical Microbiology and Infection</i> , 2017 , 23, 167-172	9.5	48
133	"Pseudo-Beijing": evidence for convergent evolution in the direct repeat region of Mycobacterium tuberculosis. <i>PLoS ONE</i> , 2011 , 6, e24737	3.7	48
132	TnSeq of Mycobacterium tuberculosis clinical isolates reveals strain-specific antibiotic liabilities. <i>PLoS Pathogens</i> , 2018 , 14, e1006939	7.6	47
131	China's tuberculosis epidemic stems from historical expansion of four strains of Mycobacterium tuberculosis. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1982-1992	12.3	47
130	Mycobacterium africanum is associated with patient ethnicity in Ghana. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e3370	4.8	46
129	DNA replication fidelity in Mycobacterium tuberculosis is mediated by an ancestral prokaryotic proofreader. <i>Nature Genetics</i> , 2015 , 47, 677-81	36.3	45
128	Treemmer: a tool to reduce large phylogenetic datasets with minimal loss of diversity. <i>BMC Bioinformatics</i> , 2018 , 19, 164	3.6	45
127	Impact of in vitro evolution on antigenic diversity of Mycobacterium bovis bacillus Calmette-Guerin (BCG). <i>Vaccine</i> , 2014 , 32, 5998-6004	4.1	45
126	Genomic interrogation of ancestral Mycobacterium tuberculosis from south India. <i>Infection, Genetics and Evolution</i> , 2008 , 8, 474-83	4.5	45
125	Genotypic diversity and drug susceptibility patterns among M. tuberculosis complex isolates from South-Western Ghana. <i>PLoS ONE</i> , 2011 , 6, e21906	3.7	45
124	Strain classification of Mycobacterium tuberculosis: congruence between large sequence polymorphisms and spoligotypes. <i>International Journal of Tuberculosis and Lung Disease</i> , 2011 , 15, 131-3 ^{2.1}		44
123	Single nucleotide polymorphisms in Mycobacterium tuberculosis and the need for a curated database. <i>Tuberculosis</i> , 2013 , 93, 30-9	2.6	39

122	Programmatically selected multidrug-resistant strains drive the emergence of extensively drug-resistant tuberculosis in South Africa. <i>PLoS ONE</i> , 2013 , 8, e70919	3.7	39
121	Genomic determinants of speciation and spread of the complex. <i>Science Advances</i> , 2019 , 5, eaaw3307	14.3	37
120	Mycobacterium tuberculosis transmission in a country with low tuberculosis incidence: role of immigration and HIV infection. <i>Journal of Clinical Microbiology</i> , 2012 , 50, 388-95	9.7	37
119	Does resistance to pyrazinamide accurately indicate the presence of Mycobacterium bovis?. <i>Journal of Clinical Microbiology</i> , 2005 , 43, 3530-2	9.7	37
118	Genetic diversity in Mycobacterium tuberculosis. <i>Current Topics in Microbiology and Immunology</i> , 2013 , 374, 1-25	3.3	36
117	Influence of M. tuberculosis lineage variability within a clinical trial for pulmonary tuberculosis. <i>PLoS ONE</i> , 2010 , 5, e10753	3.7	36
116	Investigation of the high rates of extrapulmonary tuberculosis in Ethiopia reveals no single driving factor and minimal evidence for zoonotic transmission of Mycobacterium bovis infection. <i>BMC Infectious Diseases</i> , 2015 , 15, 112	4	35
115	Integrating standardized whole genome sequence analysis with a global Mycobacterium tuberculosis antibiotic resistance knowledgebase. <i>Scientific Reports</i> , 2018 , 8, 15382	4.9	35
114	Anemia in tuberculosis cases and household controls from Tanzania: Contribution of disease, coinfections, and the role of hepcidin. <i>PLoS ONE</i> , 2018 , 13, e0195985	3.7	34
113	Evidence for diversifying selection in a set of Mycobacterium tuberculosis genes in response to antibiotic- and nonantibiotic-related pressure. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1326-36	8.3	34
112	Lipidomics and genomics of Mycobacterium tuberculosis reveal lineage-specific trends in mycolic acid biosynthesis. <i>MicrobiologyOpen</i> , 2014 , 3, 823-35	3.4	33
111	Prevalence of fluoroquinolone resistance among tuberculosis patients in Shanghai, China. <i>Antimicrobial Agents and Chemotherapy</i> , 2009 , 53, 3170-2	5.9	33
110	Emergence of W135 meningococcal meningitis in Ghana. <i>Tropical Medicine and International Health</i> , 2005 , 10, 1229-34	2.3	33
109	Long-term dominance of Mycobacterium tuberculosis Uganda family in peri-urban Kampala-Uganda is not associated with cavitory disease. <i>BMC Infectious Diseases</i> , 2013 , 13, 484	4	32
108	Survival and sequelae of meningococcal meningitis in Ghana. <i>International Journal of Epidemiology</i> , 2001 , 30, 1440-6	7.8	30
107	Drug susceptibility testing and mortality in patients treated for tuberculosis in high-burden countries: a multicentre cohort study. <i>Lancet Infectious Diseases</i> , 2019 , 19, 298-307	25.5	29
106	The Nature and Evolution of Genomic Diversity in the Mycobacterium tuberculosis Complex. <i>Advances in Experimental Medicine and Biology</i> , 2017 , 1019, 1-26	3.6	29
105	Spatio-Temporal Distribution of Mycobacterium tuberculosis Complex Strains in Ghana. <i>PLoS ONE</i> , 2016 , 11, e0161892	3.7	29

104	Phylogenomics of reveals a new lineage and a complex evolutionary history. <i>Microbial Genomics</i> , 2021 , 7,	4.4	29
103	Whole-Genome Sequencing for Drug Resistance Profile Prediction in. <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 63,	5.9	28
102	Prevalence and clinical relevance of helminth co-infections among tuberculosis patients in urban Tanzania. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005342	4.8	28
101	Clonal groupings in serogroup X Neisseria meningitidis. <i>Emerging Infectious Diseases</i> , 2002 , 8, 462-6	10.2	28
100	Transition bias influences the evolution of antibiotic resistance in Mycobacterium tuberculosis. <i>PLoS Biology</i> , 2019 , 17, e3000265	9.7	27
99	Combination of single nucleotide polymorphism and variable-number tandem repeats for genotyping a homogenous population of Mycobacterium tuberculosis Beijing strains in China. <i>Journal of Clinical Microbiology</i> , 2012 , 50, 633-9	9.7	27
98	Independent large scale duplications in multiple M. tuberculosis lineages overlapping the same genomic region. <i>PLoS ONE</i> , 2012 , 7, e26038	3.7	26
97	Within Host Evolution Selects for a Dominant Genotype of Mycobacterium tuberculosis while T Cells Increase Pathogen Genetic Diversity. <i>PLoS Pathogens</i> , 2016 , 12, e1006111	7.6	26
96	Reference set of Mycobacterium tuberculosis clinical strains: A tool for research and product development. <i>PLoS ONE</i> , 2019 , 14, e0214088	3.7	24
95	In vivo biosynthesis of terpene nucleosides provides unique chemical markers of Mycobacterium tuberculosis infection. <i>Chemistry and Biology</i> , 2015 , 22, 516-526		24
94	Mycobacterium tuberculosis associated with severe tuberculosis evades cytosolic surveillance systems and modulates IL-1 β production. <i>Nature Communications</i> , 2020 , 11, 1949	17.4	24
93	Comparative genomics of Mycobacterium africanum Lineage 5 and Lineage 6 from Ghana suggests distinct ecological niches. <i>Scientific Reports</i> , 2018 , 8, 11269	4.9	24
92	Detection and characterization of drug-resistant conferring genes in Mycobacterium tuberculosis complex strains: A prospective study in two distant regions of Ghana. <i>Tuberculosis</i> , 2016 , 99, 147-154	2.6	24
91	Molecular epidemiology of Mycobacterium africanum in Ghana. <i>BMC Infectious Diseases</i> , 2016 , 16, 385	4	23
90	Reduced transmission of Mycobacterium africanum compared to Mycobacterium tuberculosis in urban West Africa. <i>International Journal of Infectious Diseases</i> , 2018 , 73, 30-42	10.5	20
89	Interplay of strain and race/ethnicity in the innate immune response to M. tuberculosis. <i>PLoS ONE</i> , 2018 , 13, e0195392	3.7	19
88	Multiple Introductions of Mycobacterium tuberculosis Lineage 2 Beijing Into Africa Over Centuries. <i>Frontiers in Ecology and Evolution</i> , 2019 , 7,	3.7	19
87	Evaluation of GenoType MTBDRplus for the rapid detection of drug-resistant tuberculosis in Ghana. <i>International Journal of Tuberculosis and Lung Disease</i> , 2015 , 19, 954-959	2.1	18

86	An African origin for. <i>Evolution, Medicine and Public Health</i> , 2020 , 2020, 49-59	3	18
85	First insights into the phylogenetic diversity of Mycobacterium tuberculosis in Nepal. <i>PLoS ONE</i> , 2012 , 7, e52297	3.7	18
84	The Influence of HIV on the Evolution of Mycobacterium tuberculosis. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1654-1668	8.3	17
83	Evaluation of spoligotyping, SNPs and customised MIRU-VNTR combination for genotyping Mycobacterium tuberculosis clinical isolates in Madagascar. <i>PLoS ONE</i> , 2017 , 12, e0186088	3.7	16
82	The Host-Pathogen-Extrinsic Factors in Tuberculosis: Modulating Inflammation and Clinical Outcomes. <i>Frontiers in Immunology</i> , 2017 , 8, 1948	8.4	16
81	Evaluation of customised lineage-specific sets of MIRU-VNTR loci for genotyping Mycobacterium tuberculosis complex isolates in Ghana. <i>PLoS ONE</i> , 2014 , 9, e92675	3.7	16
80	Dispersal of Driven by Historical European Trade in the South Pacific. <i>Frontiers in Microbiology</i> , 2019 , 10, 2778	5.7	16
79	The Genetic Background Modulates the Evolution of Fluoroquinolone-Resistance in Mycobacterium tuberculosis. <i>Molecular Biology and Evolution</i> , 2020 , 37, 195-207	8.3	16
78	Genome-wide mutational biases fuel transcriptional diversity in the Mycobacterium tuberculosis complex. <i>Nature Communications</i> , 2019 , 10, 3994	17.4	15
77	Model-based integration of genomics and metabolomics reveals SNP functionality in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 8494-8502	11.5	14
76	Interaction between host genes and Mycobacterium tuberculosis lineage can affect tuberculosis severity: Evidence for coevolution?. <i>PLoS Genetics</i> , 2020 , 16, e1008728	6	14
75	Tuberculosis transmission in public locations in Tanzania: A novel approach to studying airborne disease transmission. <i>Journal of Infection</i> , 2017 , 75, 191-197	18.9	14
74	Diversity of Mycobacterium tuberculosis and drug resistance in different provinces of Papua New Guinea. <i>BMC Microbiology</i> , 2014 , 14, 307	4.5	14
73	Genetic diversity of Mycobacterium tuberculosis in Madang, Papua New Guinea. <i>International Journal of Tuberculosis and Lung Disease</i> , 2012 , 16, 1100-7	2.1	14
72	Tuberculosis outbreak investigation using phylodynamic analysis. <i>Epidemics</i> , 2018 , 25, 47-53	5.1	13
71	Significant under expression of the DosR regulon in M. tuberculosis complex lineage 6 in sputum. <i>Tuberculosis</i> , 2017 , 104, 58-64	2.6	12
70	Revised Interpretation of the Hain Lifescience GenoType MTBC To Differentiate and Members of the Mycobacterium tuberculosis Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 63,	5.9	12
69	Molecular characterization of bovine tuberculosis strains in two slaughterhouses in Morocco. <i>BMC Veterinary Research</i> , 2017 , 13, 272	2.7	11

68	Molecular epidemiology and whole genome sequencing analysis of clinical <i>Mycobacterium bovis</i> from Ghana. <i>PLoS ONE</i> , 2019 , 14, e0209395	3.7	10
67	Preservation of sputum samples with cetylpyridinium chloride (CPC) for tuberculosis cultures and Xpert MTB/RIF in a low-income country. <i>BMC Infectious Diseases</i> , 2017 , 17, 542	4	10
66	Distinct clinical characteristics and helminth co-infections in adult tuberculosis patients from urban compared to rural Tanzania. <i>Infectious Diseases of Poverty</i> , 2018 , 7, 24	10.4	10
65	Genetic diversity within <i>Mycobacterium tuberculosis</i> complex impacts on the accuracy of genotypic pyrazinamide drug-susceptibility assay. <i>Tuberculosis</i> , 2014 , 94, 451-3	2.6	10
64	Tuberculosis in HIV-negative and HIV-infected patients in a low-incidence country: clinical characteristics and treatment outcomes. <i>PLoS ONE</i> , 2012 , 7, e34186	3.7	10
63	<i>Mycobacterium tuberculosis</i> lineage 1 genetic diversity in Pará-Brazil, suggests common ancestry with east-African isolates potentially linked to historical slave trade. <i>Infection, Genetics and Evolution</i> , 2019 , 73, 337-341	4.5	9
62	Prisons as ecological drivers of fitness-compensated multidrug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Medicine</i> , 2021 , 27, 1171-1177	50.5	9
61	Classifying recurrent <i>Mycobacterium tuberculosis</i> cases in Georgia using MIRU-VNTR typing. <i>PLoS ONE</i> , 2019 , 14, e0223610	3.7	8
60	Low sensitivity of the MPT64 identification test to detect lineage 5 of the <i>Mycobacterium tuberculosis</i> complex. <i>Journal of Medical Microbiology</i> , 2018 , 67, 1718-1727	3.2	8
59	Local adaptation in populations of <i>Mycobacterium tuberculosis</i> endemic to the Indian Ocean Rim. <i>F1000Research</i> , 2021 , 10, 60	3.6	8
58	Home-Based and Facility-Based Directly Observed Therapy of Tuberculosis Treatment under Programmatic Conditions in Urban Tanzania. <i>PLoS ONE</i> , 2016 , 11, e0161171	3.7	8
57	Association between tuberculosis, diabetes and 25 hydroxyvitamin D in Tanzania: a longitudinal case control study. <i>BMC Infectious Diseases</i> , 2016 , 16, 626	4	7
56	Tuberculosis in Swiss captive Asian elephants: microevolution of <i>Mycobacterium tuberculosis</i> characterized by multilocus variable-number tandem-repeat analysis and whole-genome sequencing. <i>Scientific Reports</i> , 2017 , 7, 14647	4.9	7
55	Leprosy in wild chimpanzees. <i>Nature</i> , 2021 , 598, 652-656	50.4	7
54	Leprosy in wild chimpanzees		7
53	Local adaptation in populations of endemic to the Indian Ocean Rim. <i>F1000Research</i> , 2021 , 10, 60	3.6	7
52	Pathways and associated costs of care in patients with confirmed and presumptive tuberculosis in Tanzania: A cross-sectional study. <i>BMJ Open</i> , 2019 , 9, e025079	3	6
51	TB-diabetes co-morbidity in Ghana: The importance of <i>Mycobacterium africanum</i> infection. <i>PLoS ONE</i> , 2019 , 14, e0211822	3.7	6

50	Impact of diagnostic test Xpert MTB/RIF [®] on health outcomes for tuberculosis. <i>The Cochrane Library</i> , 2018 ,	5.2	6
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