

# Sebastien Gagneux

## List of Publications by Year in descending order

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Version: 2024-02-01

204  
papers

20,102  
citations

11608

70  
h-index

12910

131  
g-index

229  
all docs

229  
docs citations

229  
times ranked

11549  
citing authors

#	ARTICLE	IF	CITATIONS
1	Out-of-Africa migration and Neolithic coexpansion of <i>Mycobacterium tuberculosis</i> with modern humans. <i>Nature Genetics</i> , 2013, 45, 1176-1182.	9.4	900
2	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, 2869-2873.	3.3	897
3	Human T cell epitopes of <i>Mycobacterium tuberculosis</i> are evolutionarily hyperconserved. <i>Nature Genetics</i> , 2010, 42, 498-503.	9.4	642
4	Global phylogeography of <i>Mycobacterium tuberculosis</i> and implications for tuberculosis product development. <i>Lancet Infectious Diseases</i> , The, 2007, 7, 328-337.	4.6	634
5	The Competitive Cost of Antibiotic Resistance in <i>Mycobacterium tuberculosis</i> . <i>Science</i> , 2006, 312, 1944-1946.	6.0	559
6	High Functional Diversity in <i>Mycobacterium tuberculosis</i> Driven by Genetic Drift and Human Demography. <i>PLoS Biology</i> , 2008, 6, e311.	2.6	507
7	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. <i>Nature</i> , 2014, 514, 494-497.	13.7	506
8	Whole-genome sequencing of rifampicin-resistant <i>Mycobacterium tuberculosis</i> strains identifies compensatory mutations in RNA polymerase genes. <i>Nature Genetics</i> , 2012, 44, 106-110.	9.4	475
9	Evolutionary history and global spread of the <i>Mycobacterium tuberculosis</i> Beijing lineage. <i>Nature Genetics</i> , 2015, 47, 242-249.	9.4	466
10	Ecology and evolution of <i>Mycobacterium tuberculosis</i> . <i>Nature Reviews Microbiology</i> , 2018, 16, 202-213.	13.6	414
11	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.	2.1	410
12	<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, 784-790.	9.4	405
13	Consequences of genomic diversity in <i>Mycobacterium tuberculosis</i> . <i>Seminars in Immunology</i> , 2014, 26, 431-444.	2.7	404
14	Genomic analysis identifies targets of convergent positive selection in drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2013, 45, 1183-1189.	9.4	393
15	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.	1.1	377
16	<i>Mycobacterium tuberculosis</i> lineage 4 comprises globally distributed and geographically restricted sublineages. <i>Nature Genetics</i> , 2016, 48, 1535-1543.	9.4	326
17	Host-pathogen coevolution in human tuberculosis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 850-859.	1.8	324
18	Antimicrobial resistance in <i>Mycobacterium tuberculosis</i> : mechanistic and evolutionary perspectives. <i>FEMS Microbiology Reviews</i> , 2017, 41, 354-373.	3.9	307

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19	Acquired Resistance to Bedaquiline and Delamanid in Therapy for Tuberculosis. <i>New England Journal of Medicine</i> , 2015, 373, 1986-1988.	13.9	291
20	A standardised method for interpreting the association between mutations and phenotypic drug resistance in <i>Mycobacterium tuberculosis</i> . <i>European Respiratory Journal</i> , 2017, 50, 1701354.	3.1	273
21	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, 1037-1043.	1.9	269
22	Human Macrophage Responses to Clinical Isolates from the <i>Mycobacterium tuberculosis</i> Complex Discriminate between Ancient and Modern Lineages. <i>PLoS Pathogens</i> , 2011, 7, e1001307.	2.1	258
23	Co-evolution of <i>Mycobacterium tuberculosis</i> and <i>Homo sapiens</i> . <i>Immunological Reviews</i> , 2015, 264, 6-24.	2.8	244
24	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
25	Genomic Deletions Classify the Beijing/W Strains as a Distinct Genetic Lineage of <i>Mycobacterium tuberculosis</i> . <i>Journal of Clinical Microbiology</i> , 2005, 43, 3185-3191.	1.8	232
26	<i>Mycobacterium africanum</i> – Review of an Important Cause of Human Tuberculosis in West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e744.	1.3	221
27	The W-Beijing Lineage of <i>Mycobacterium tuberculosis</i> Overproduces Triglycerides and Has the DosR Dormancy Regulon Constitutively Upregulated. <i>Journal of Bacteriology</i> , 2007, 189, 2583-2589.	1.0	215
28	<i>Mycobacterial</i> Lineages Causing Pulmonary and Extrapulmonary Tuberculosis, Ethiopia. <i>Emerging Infectious Diseases</i> , 2013, 19, 460-463.	2.0	215
29	Impact of Bacterial Genetics on the Transmission of Isoniazid-Resistant <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2006, 2, e61.	2.1	196
30	Putative Compensatory Mutations in the <i>rpoC</i> Gene of Rifampin-Resistant <i>Mycobacterium tuberculosis</i> Are Associated with Ongoing Transmission. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 827-832.	1.4	184
31	Infectiousness, reproductive fitness and evolution of drug-resistant <i>Mycobacterium tuberculosis</i> . <i>International Journal of Tuberculosis and Lung Disease</i> , 2009, 13, 1456-66.	0.6	177
32	The heterogeneous evolution of multidrug-resistant <i>Mycobacterium tuberculosis</i> . <i>Trends in Genetics</i> , 2013, 29, 160-169.	2.9	165
33	A New Phylogenetic Framework for the Animal-Adapted <i>Mycobacterium tuberculosis</i> Complex. <i>Frontiers in Microbiology</i> , 2018, 9, 2820.	1.5	145
34	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
35	<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, 538-548.	5.1	142
36	KvarQ: targeted and direct variant calling from fastq reads of bacterial genomes. <i>BMC Genomics</i> , 2014, 15, 881.	1.2	141

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37	A sister lineage of the <i>Mycobacterium tuberculosis</i> complex discovered in the African Great Lakes region. <i>Nature Communications</i> , 2020, 11, 2917.	5.8	136
38	Does <i>M. tuberculosis</i> genomic diversity explain disease diversity?. <i>Drug Discovery Today Disease Mechanisms</i> , 2010, 7, e43-e59.	0.8	135
39	Relationship between <i>Mycobacterium tuberculosis</i> Genotype and the Clinical Phenotype of Pulmonary and Meningeal Tuberculosis. <i>Journal of Clinical Microbiology</i> , 2008, 46, 1363-1368.	1.8	134
40	Fit genotypes and escape variants of subgroup III <i>Neisseria meningitidis</i> during three pandemics of epidemic meningitis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 5234-5239.	3.3	132
41	The Past and Future of Tuberculosis Research. <i>PLoS Pathogens</i> , 2009, 5, e1000600.	2.1	130
42	Genomic Diversity among Drug Sensitive and Multidrug Resistant Isolates of <i>Mycobacterium tuberculosis</i> with Identical DNA Fingerprints. <i>PLoS ONE</i> , 2009, 4, e7407.	1.1	128
43	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.	0.6	123
44	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> , The, 2018, 18, 431-440.	4.6	121
45	Tremmer: a tool to reduce large phylogenetic datasets with minimal loss of diversity. <i>BMC Bioinformatics</i> , 2018, 19, 164.	1.2	121
46	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.	1.1	120
47	Reversion of antibiotic resistance in <i>Mycobacterium tuberculosis</i> by spiroisoxazoline SMART-420. <i>Science</i> , 2017, 355, 1206-1211.	6.0	119
48	Effect of Mutation and Genetic Background on Drug Resistance in <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 3047-3053.	1.4	115
49	The 2021 WHO catalogue of <i>Mycobacterium tuberculosis</i> complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273.	3.4	114
50	Towards host-directed therapies for tuberculosis. <i>Nature Reviews Drug Discovery</i> , 2015, 14, 511-512.	21.5	110
51	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, 2909-2919.	1.0	107
52	The molecular clock of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2019, 15, e1008067.	2.1	107
53	Epistasis between antibiotic resistance mutations drives the evolution of extensively drug-resistant tuberculosis. <i>Evolution, Medicine and Public Health</i> , 2013, 2013, 65-74.	1.1	103
54	Genomic Analysis Distinguishes <i>Mycobacterium africanum</i> . <i>Journal of Clinical Microbiology</i> , 2004, 42, 3594-3599.	1.8	102

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55	High-throughput metabolomic analysis predicts mode of action of uncharacterized antimicrobial compounds. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	102
56	Novel <i>Mycobacterium tuberculosis</i> Complex Isolate from a Wild Chimpanzee. <i>Emerging Infectious Diseases</i> , 2013, 19, 969-976.	2.0	100
57	Strain diversity, epistasis and the evolution of drug resistance in <i>Mycobacterium tuberculosis</i> . <i>Clinical Microbiology and Infection</i> , 2011, 17, 815-820.	2.8	98
58	The within-host population dynamics of <i>Mycobacterium tuberculosis</i> vary with treatment efficacy. <i>Genome Biology</i> , 2017, 18, 71.	3.8	95
59	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, 3260-3266.	1.8	94
60	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.	1.8	94
61	Compensatory evolution drives multidrug-resistant tuberculosis in Central Asia. <i>ELife</i> , 2018, 7, .	2.8	93
62	Beijing Sublineages of <i>Mycobacterium tuberculosis</i> Differ in Pathogenicity in the Guinea Pig. <i>Vaccine Journal</i> , 2012, 19, 1227-1237.	3.2	91
63	Transient Hyperglycemia in Patients With Tuberculosis in Tanzania: Implications for Diabetes Screening Algorithms. <i>Journal of Infectious Diseases</i> , 2016, 213, 1163-1172.	1.9	87
64	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.	1.8	85
65	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.	1.1	83
66	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
67	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, 1306-1316.	1.9	82
68	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.	3.9	81
69	PolyTB: A genomic variation map for <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2014, 94, 346-354.	0.8	79
70	HIV Infection Disrupts the Sympatric Host-Pathogen Relationship in Human Tuberculosis. <i>PLoS Genetics</i> , 2013, 9, e1003318.	1.5	78
71	TnSeq of <i>Mycobacterium tuberculosis</i> clinical isolates reveals strain-specific antibiotic liabilities. <i>PLoS Pathogens</i> , 2018, 14, e1006939.	2.1	78
72	<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, 1279-1286.	1.9	77

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73	Integrating standardized whole genome sequence analysis with a global Mycobacterium tuberculosis antibiotic resistance knowledgebase. <i>Scientific Reports</i> , 2018, 8, 15382.	1.6	75
74	Consensus numbering system for the rifampicin resistance-associated <i>rpoB</i> gene mutations in pathogenic mycobacteria. <i>Clinical Microbiology and Infection</i> , 2017, 23, 167-172.	2.8	72
75	Use of Whole Genome Sequencing to Determine the Microevolution of Mycobacterium tuberculosis during an Outbreak. <i>PLoS ONE</i> , 2013, 8, e58235.	1.1	72
76	A role for systems epidemiology in tuberculosis research. <i>Trends in Microbiology</i> , 2011, 19, 492-500.	3.5	71
77	Phylogenomics of Mycobacterium africanum reveals a new lineage and a complex evolutionary history. <i>Microbial Genomics</i> , 2021, 7, .	1.0	71
78	The Genome of Mycobacterium Africanum West African 2 Reveals a Lineage-Specific Locus and Genome Erosion Common to the M. tuberculosis Complex. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1552.	1.3	69
79	Mapping of Genotype-Phenotype Diversity among Clinical Isolates of Mycobacterium tuberculosis by Sequence-Based Transcriptional Profiling. <i>Genome Biology and Evolution</i> , 2013, 5, 1849-1862.	1.1	69
80	Old and new selective pressures on Mycobacterium tuberculosis. <i>Infection, Genetics and Evolution</i> , 2012, 12, 678-685.	1.0	66
81	Evolution of Drug Resistance in Tuberculosis: Recent Progress and Implications for Diagnosis and Therapy. <i>Drugs</i> , 2014, 74, 1063-1072.	4.9	64
82	DNA replication fidelity in Mycobacterium tuberculosis is mediated by an ancestral prokaryotic proofreader. <i>Nature Genetics</i> , 2015, 47, 677-681.	9.4	63
83	Mycobacterium africanum Is Associated with Patient Ethnicity in Ghana. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e3370.	1.3	61
84	Genomic determinants of speciation and spread of the <i>Mycobacterium tuberculosis</i> complex. <i>Science Advances</i> , 2019, 5, eaaw3307.	4.7	61
85	Whole-Genome Sequencing for Drug Resistance Profile Prediction in <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	59
86	Genotypic Diversity and Drug Susceptibility Patterns among M. tuberculosis Complex Isolates from South-Western Ghana. <i>PLoS ONE</i> , 2011, 6, e21906.	1.1	58
87	Impact of in vitro evolution on antigenic diversity of Mycobacterium bovis bacillus Calmette-Guerin (BCG). <i>Vaccine</i> , 2014, 32, 5998-6004.	1.7	57
88	Reference set of Mycobacterium tuberculosis clinical strains: A tool for research and product development. <i>PLoS ONE</i> , 2019, 14, e0214088.	1.1	56
89	Large Sequence Polymorphisms Classify <i>Mycobacterium tuberculosis</i> Strains with Ancestral Spoligotyping Patterns. <i>Journal of Clinical Microbiology</i> , 2007, 45, 3393-3395.	1.8	53
90	Use of Spoligotyping and Large Sequence Polymorphisms To Study the Population Structure of the <i>Mycobacterium tuberculosis</i> Complex in a Cohort Study of Consecutive Smear-Positive Tuberculosis Cases in The Gambia. <i>Journal of Clinical Microbiology</i> , 2009, 47, 994-1001.	1.8	53

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91	The Nature and Evolution of Genomic Diversity in the Mycobacterium tuberculosis Complex. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1019, 1-26.	0.8	52
92	<i>Mycobacterium tuberculosis</i> associated with severe tuberculosis evades cytosolic surveillance systems and modulates IL-1 $\beta$ production. <i>Nature Communications</i> , 2020, 11, 1949.	5.8	52
93	“Pseudo-Beijing” Evidence for Convergent Evolution in the Direct Repeat Region of <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2011, 6, e24737.	1.1	51
94	Transition bias influences the evolution of antibiotic resistance in <i>Mycobacterium tuberculosis</i> . <i>PLoS Biology</i> , 2019, 17, e3000265.	2.6	50
95	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.	1.1	49
96	Genomic interrogation of ancestral <i>Mycobacterium tuberculosis</i> from south India. <i>Infection, Genetics and Evolution</i> , 2008, 8, 474-483.	1.0	48
97	Lipidomics and genomics of <i>Mycobacterium tuberculosis</i> reveal lineage-specific trends in mycolic acid biosynthesis. <i>MicrobiologyOpen</i> , 2014, 3, 823-835.	1.2	48
98	Investigation of the high rates of extrapulmonary tuberculosis in Ethiopia reveals no single driving factor and minimal evidence for zoonotic transmission of <i>Mycobacterium bovis</i> infection. <i>BMC Infectious Diseases</i> , 2015, 15, 112.	1.3	46
99	Strain classification of <i>Mycobacterium tuberculosis</i> : congruence between large sequence polymorphisms and spoligotypes. <i>International Journal of Tuberculosis and Lung Disease</i> , 2011, 15, 131-3.	0.6	46
100	Drug susceptibility testing and mortality in patients treated for tuberculosis in high-burden countries: a multicentre cohort study. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 298-307.	4.6	45
101	Does Resistance to Pyrazinamide Accurately Indicate the Presence of <i>Mycobacterium bovis</i> ?. <i>Journal of Clinical Microbiology</i> , 2005, 43, 3530-3532.	1.8	44
102	Programmatically Selected Multidrug-Resistant Strains Drive the Emergence of Extensively Drug-Resistant Tuberculosis in South Africa. <i>PLoS ONE</i> , 2013, 8, e70919.	1.1	44
103	Single nucleotide polymorphisms in <i>Mycobacterium tuberculosis</i> and the need for a curated database. <i>Tuberculosis</i> , 2013, 93, 30-39.	0.8	43
104	Evidence for Diversifying Selection in a Set of <i>Mycobacterium tuberculosis</i> Genes in Response to Antibiotic- and Nonantibiotic-Related Pressure. <i>Molecular Biology and Evolution</i> , 2013, 30, 1326-1336.	3.5	43
105	Prisons as ecological drivers of fitness-compensated multidrug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Medicine</i> , 2021, 27, 1171-1177.	15.2	43
106	Spatio-Temporal Distribution of <i>Mycobacterium tuberculosis</i> Complex Strains in Ghana. <i>PLoS ONE</i> , 2016, 11, e0161892.	1.1	43
107	An African origin for <i>Mycobacterium bovis</i> . <i>Evolution, Medicine and Public Health</i> , 2020, 2020, 49-59.	1.1	42
108	<i>Mycobacterium tuberculosis</i> Transmission in a Country with Low Tuberculosis Incidence: Role of Immigration and HIV Infection. <i>Journal of Clinical Microbiology</i> , 2012, 50, 388-395.	1.8	41

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109	Influence of <i>M. tuberculosis</i> Lineage Variability within a Clinical Trial for Pulmonary Tuberculosis. <i>PLoS ONE</i> , 2010, 5, e10753.	1.1	40
110	Detection and characterization of drug-resistant conferring genes in <i>Mycobacterium tuberculosis</i> complex strains: A prospective study in two distant regions of Ghana. <i>Tuberculosis</i> , 2016, 99, 147-154.	0.8	40
111	Interaction between host genes and <i>Mycobacterium tuberculosis</i> lineage can affect tuberculosis severity: Evidence for coevolution?. <i>PLoS Genetics</i> , 2020, 16, e1008728.	1.5	40
112	Genetic Diversity in <i>Mycobacterium tuberculosis</i> . <i>Current Topics in Microbiology and Immunology</i> , 2013, 374, 1-25.	0.7	39
113	Long-term dominance of <i>Mycobacterium tuberculosis</i> Uganda family in peri-urban Kampala-Uganda is not associated with cavitory disease. <i>BMC Infectious Diseases</i> , 2013, 13, 484.	1.3	36
114	Prevalence and clinical relevance of helminth co-infections among tuberculosis patients in urban Tanzania. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005342.	1.3	36
115	Survival and sequelae of meningococcal meningitis in Ghana. <i>International Journal of Epidemiology</i> , 2001, 30, 1440-1446.	0.9	35
116	Emergence of W135 meningococcal meningitis in Ghana. <i>Tropical Medicine and International Health</i> , 2005, 10, 1229-1234.	1.0	35
117	Prevalence of Fluoroquinolone Resistance among Tuberculosis Patients in Shanghai, China. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 3170-3172.	1.4	35
118	Combination of Single Nucleotide Polymorphism and Variable-Number Tandem Repeats for Genotyping a Homogenous Population of <i>Mycobacterium tuberculosis</i> Beijing Strains in China. <i>Journal of Clinical Microbiology</i> , 2012, 50, 633-639.	1.8	35
119	Molecular epidemiology of <i>Mycobacterium africanum</i> in Ghana. <i>BMC Infectious Diseases</i> , 2016, 16, 385.	1.3	35
120	Within Host Evolution Selects for a Dominant Genotype of <i>Mycobacterium tuberculosis</i> while T Cells Increase Pathogen Genetic Diversity. <i>PLoS Pathogens</i> , 2016, 12, e1006111.	2.1	35
121	In Vivo Biosynthesis of Terpene Nucleosides Provides Unique Chemical Markers of <i>Mycobacterium tuberculosis</i> Infection. <i>Chemistry and Biology</i> , 2015, 22, 516-526.	6.2	34
122	Comparative genomics of <i>Mycobacterium africanum</i> Lineage 5 and Lineage 6 from Ghana suggests distinct ecological niches. <i>Scientific Reports</i> , 2018, 8, 11269.	1.6	34
123	Genome-wide mutational biases fuel transcriptional diversity in the <i>Mycobacterium tuberculosis</i> complex. <i>Nature Communications</i> , 2019, 10, 3994.	5.8	33
124	The Genetic Background Modulates the Evolution of Fluoroquinolone-Resistance in <i>Mycobacterium tuberculosis</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 195-207.	3.5	33
125	Clonal Groupings in Serogroup X <i>Neisseria meningitidis</i> . <i>Emerging Infectious Diseases</i> , 2002, 8, 462-466.	2.0	31
126	Interplay of strain and race/ethnicity in the innate immune response to <i>M. tuberculosis</i> . <i>PLoS ONE</i> , 2018, 13, e0195392.	1.1	31

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127	Independent Large Scale Duplications in Multiple <i>M. tuberculosis</i> Lineages Overlapping the Same Genomic Region. <i>PLoS ONE</i> , 2012, 7, e26038.	1.1	30
128	Tuberculosis transmission in public locations in Tanzania: A novel approach to studying airborne disease transmission. <i>Journal of Infection</i> , 2017, 75, 191-197.	1.7	30
129	Reduced transmission of <i>Mycobacterium africanum</i> compared to <i>Mycobacterium tuberculosis</i> in urban West Africa. <i>International Journal of Infectious Diseases</i> , 2018, 73, 30-42.	1.5	30
130	Leprosy in wild chimpanzees. <i>Nature</i> , 2021, 598, 652-656.	13.7	30
131	Multiple Introductions of <i>Mycobacterium tuberculosis</i> Lineage “Beijing Into Africa Over Centuries. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	1.1	29
132	Dispersal of <i>Mycobacterium tuberculosis</i> Driven by Historical European Trade in the South Pacific. <i>Frontiers in Microbiology</i> , 2019, 10, 2778.	1.5	28
133	The Influence of HIV on the Evolution of <i>Mycobacterium tuberculosis</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, 1654-1668.	3.5	27
134	Genomic analyses of <i>Mycobacterium tuberculosis</i> from human lung resections reveal a high frequency of polyclonal infections. <i>Nature Communications</i> , 2021, 12, 2716.	5.8	25
135	Evaluation of GenoType <sup>®</sup> MTBDR <sup>+</sup> for the rapid detection of drug-resistant tuberculosis in Ghana. <i>International Journal of Tuberculosis and Lung Disease</i> , 2015, 19, 954-959.	0.6	24
136	The Troika Host-Pathogen-Extrinsic Factors in Tuberculosis: Modulating Inflammation and Clinical Outcomes. <i>Frontiers in Immunology</i> , 2018, 8, 1948.	2.2	24
137	Model-based integration of genomics and metabolomics reveals SNP functionality in <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8494-8502.	3.3	24
138	The within-host evolution of antimicrobial resistance in <i>Mycobacterium tuberculosis</i> . <i>FEMS Microbiology Reviews</i> , 2021, 45, .	3.9	23
139	Local adaptation in populations of <i>Mycobacterium tuberculosis</i> endemic to the Indian Ocean Rim. <i>F1000Research</i> , 2021, 10, 60.	0.8	21
140	First Insights into the Phylogenetic Diversity of <i>Mycobacterium tuberculosis</i> in Nepal. <i>PLoS ONE</i> , 2012, 7, e52297.	1.1	21
141	Revised Interpretation of the Hain Lifescience GenoType MTBC To Differentiate <i>Mycobacterium canettii</i> and Members of the <i>Mycobacterium tuberculosis</i> Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	1.4	20
142	Molecular epidemiology and whole genome sequencing analysis of clinical <i>Mycobacterium bovis</i> from Ghana. <i>PLoS ONE</i> , 2019, 14, e0209395.	1.1	20
143	Diversity of <i>Mycobacterium tuberculosis</i> and drug resistance in different provinces of Papua New Guinea. <i>BMC Microbiology</i> , 2014, 14, 307.	1.3	19
144	Evaluation of spoligotyping, SNPs and customised MIRU-VNTR combination for genotyping <i>Mycobacterium tuberculosis</i> clinical isolates in Madagascar. <i>PLoS ONE</i> , 2017, 12, e0186088.	1.1	19

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145	Tuberculosis outbreak investigation using phylodynamic analysis. <i>Epidemics</i> , 2018, 25, 47-53.	1.5	19
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148	Molecular characterization of bovine tuberculosis strains in two slaughterhouses in Morocco. <i>BMC Veterinary Research</i> , 2017, 13, 272.	0.7	17
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