

Sebastien Gagneux

List of Publications by Year in Descending Order

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

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	Using population-specific add-on polymorphisms to improve genotype imputation in underrepresented populations.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009628	5	0
210	Whole genome sequencing has the potential to improve treatment for rifampicin-resistant tuberculosis in high burden settings: a retrospective cohort study.. <i>Journal of Clinical Microbiology</i> , 2022 , jcm0236221	9.7	1
209	Developing customized stepwise MIRU-VNTR typing for tuberculosis surveillance in Georgia.. <i>PLoS ONE</i> , 2022 , 17, e0264472	3.7	
208	Mycobacterium leprae Infection in a Wild Nine-Banded Armadillo, Nuevo Leñ, Mexico.. <i>Emerging Infectious Diseases</i> , 2022 , 28, 747-749	10.2	0
207	The 2021 WHO catalogue of complex mutations associated with drug resistance: A genotypic analysis.. <i>Lancet Microbe</i> , The , 2022 , 3, e265-e273	22.2	3
206	CD38 Expression by Antigen-Specific CD4 T Cells Is Significantly Restored 5 Months After Treatment Initiation Independently of Sputum Bacterial Load at the Time of Tuberculosis Diagnosis.. <i>Frontiers in Medicine</i> , 2022 , 9, 821776	4.9	0
205	The within-host evolution of antimicrobial resistance in Mycobacterium tuberculosis. <i>FEMS Microbiology Reviews</i> , 2021 , 45,	15.1	4
204	Evaluation of drug susceptibility profile of Mycobacterium tuberculosis Lineage 1 from Brazil based on whole genome sequencing and phenotypic methods. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2021 , 115, e200520	2.6	1
203	Leprosy in wild chimpanzees. <i>Nature</i> , 2021 , 598, 652-656	50.4	7
202	Local adaptation in populations of Mycobacterium tuberculosis endemic to the Indian Ocean Rim. <i>F1000Research</i> , 2021 , 10, 60	3.6	8
201	High burden of tuberculosis infection and disease among people receiving medication-assisted treatment for substance use disorder in Tanzania. <i>PLoS ONE</i> , 2021 , 16, e0250038	3.7	2
200	Mortality from drug-resistant tuberculosis in high-burden countries comparing routine drug susceptibility testing with whole-genome sequencing: a multicentre cohort study.. <i>Lancet Microbe</i> , The , 2021 , 2, e320-e330	22.2	5
199	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
198	Prisons as ecological drivers of fitness-compensated multidrug-resistant Mycobacterium tuberculosis. <i>Nature Medicine</i> , 2021 , 27, 1171-1177	50.5	9
197	Genomic analyses of Mycobacterium tuberculosis from human lung resections reveal a high frequency of polyclonal infections. <i>Nature Communications</i> , 2021 , 12, 2716	17.4	3
196	Melting the : Nondetection of Kanamycin Resistance Markers by Routine Diagnostic Tests and Identification of New Promoter Variants. <i>Antimicrobial Agents and Chemotherapy</i> , 2021 , 65, e0250220	5.9	
195	Case-control diagnostic accuracy study of a non-sputum CD38-based TAM-TB test from a single milliliter of blood. <i>Scientific Reports</i> , 2021 , 11, 13190	4.9	4

194	Is the new WHO definition of extensively drug-resistant tuberculosis easy to apply in practice?. <i>European Respiratory Journal</i> , 2021 , 58,	13.6	2
193	complex lineage 5 exhibits high levels of within-lineage genomic diversity and differing gene content compared to the type strain H37Rv. <i>Microbial Genomics</i> , 2021 , 7,	4.4	3
192	Multiple Merger Genealogies in Outbreaks of Mycobacterium tuberculosis. <i>Molecular Biology and Evolution</i> , 2021 , 38, 290-306	8.3	2
191	Local adaptation in populations of endemic to the Indian Ocean Rim. <i>F1000Research</i> , 2021 , 10, 60	3.6	7
190	Phylogenomics of reveals a new lineage and a complex evolutionary history. <i>Microbial Genomics</i> , 2021 , 7,	4.4	29
189	Genotypic and phenotypic diversity of Mycobacterium tuberculosis complex genotypes prevalent in West Africa. <i>PLoS ONE</i> , 2021 , 16, e0255433	3.7	1
188	Rifampicin-Monoresistant Tuberculosis Is Not the Same as Multidrug-Resistant Tuberculosis: a Descriptive Study from Khayelitsha, South Africa. <i>Antimicrobial Agents and Chemotherapy</i> , 2021 , 65, e0036421	5.9	1
187	The Sputum Microbiome in Pulmonary Tuberculosis and Its Association With Disease Manifestations: A Cross-Sectional Study. <i>Frontiers in Microbiology</i> , 2021 , 12, 633396	5.7	3
186	Expression Dysregulation as a Mediator of Fitness Costs in Antibiotic Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2021 , 65, e0050421	5.9	1
185	Potential contribution of HIV during first-line tuberculosis treatment to subsequent rifampicin-monoresistant tuberculosis and acquired tuberculosis drug resistance in South Africa: a retrospective molecular epidemiology study. <i>Lancet Microbe</i> , 2021 , 2, e584-e593	22.2	3
184	Quantifying transmission fitness costs of multi-drug resistant tuberculosis. <i>Epidemics</i> , 2021 , 36, 100471	5.1	1
183	A sister lineage of the Mycobacterium tuberculosis complex discovered in the African Great Lakes region. <i>Nature Communications</i> , 2020 , 11, 2917	17.4	68
182	Whole Genome Sequencing and Spatial Analysis Identifies Recent Tuberculosis Transmission Hotspots in Ghana. <i>Frontiers in Medicine</i> , 2020 , 7, 161	4.9	3
181	An African origin for. <i>Evolution, Medicine and Public Health</i> , 2020 , 2020, 49-59	3	18
180	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
179	Interaction between host genes and Mycobacterium tuberculosis lineage can affect tuberculosis severity: Evidence for coevolution?. <i>PLoS Genetics</i> , 2020 , 16, e1008728	6	14
178	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
177	HIV Coinfection Is Associated with Low-Fitness Variants in Rifampicin-Resistant Mycobacterium tuberculosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2020 , 64,	5.9	1

176	Natural Polymorphisms in Mycobacterium tuberculosis Conferring Resistance to Delamanid in Drug-Naive Patients. <i>Antimicrobial Agents and Chemotherapy</i> , 2020 , 64,	5.9	6
175	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
174	Genome-wide mutational biases fuel transcriptional diversity in the Mycobacterium tuberculosis complex. <i>Nature Communications</i> , 2019 , 10, 3994	17.4	15
173	The molecular clock of Mycobacterium tuberculosis. <i>PLoS Pathogens</i> , 2019 , 15, e1008067	7.6	57
172	Genetic variability and consequence of Mycobacterium tuberculosis lineage 3 in Kampala-Uganda. <i>PLoS ONE</i> , 2019 , 14, e0221644	3.7	4
171	Whole-Genome Sequencing for Drug Resistance Profile Prediction in. <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 63,	5.9	28
170	Whole genome sequencing of Mycobacterium tuberculosis: current standards and open issues. <i>Nature Reviews Microbiology</i> , 2019 , 17, 533-545	22.2	109
169	Mycobacterium tuberculosis 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
168	Genomic determinants of speciation and spread of the complex. <i>Science Advances</i> , 2019 , 5, eaaw3307	14.3	37
167	Transition bias influences the evolution of antibiotic resistance in Mycobacterium tuberculosis. <i>PLoS Biology</i> , 2019 , 17, e3000265	9.7	27
166	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
165	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
164	Reference set of Mycobacterium tuberculosis clinical strains: A tool for research and product development. <i>PLoS ONE</i> , 2019 , 14, e0214088	3.7	24
163	Molecular epidemiology and whole genome sequencing analysis of clinical Mycobacterium bovis from Ghana. <i>PLoS ONE</i> , 2019 , 14, e0209395	3.7	10
162	Insights into the genetic diversity of Mycobacterium tuberculosis in Tanzania. <i>PLoS ONE</i> , 2019 , 14, e0206374	3.7	4
161	Drug susceptibility testing and mortality in patients treated for tuberculosis in high-burden countries: a multicentre cohort study. <i>Lancet Infectious Diseases, The</i> , 2019 , 19, 298-307	25.5	29
160	TB-diabetes co-morbidity in Ghana: The importance of Mycobacterium africanum infection. <i>PLoS ONE</i> , 2019 , 14, e0211822	3.7	6
159	Multiple Introductions of Mycobacterium tuberculosis Lineage 2Beijing Into Africa Over Centuries. <i>Frontiers in Ecology and Evolution</i> , 2019 , 7,	3.7	19

158	Classifying recurrent Mycobacterium tuberculosis cases in Georgia using MIRU-VNTR typing. <i>PLoS ONE</i> , 2019 , 14, e0223610	3.7	8
157	Dispersal of Driven by Historical European Trade in the South Pacific. <i>Frontiers in Microbiology</i> , 2019 , 10, 2778	5.7	16
156	Prevalence and clinical significance of respiratory viruses and bacteria detected in tuberculosis patients compared to household contact controls in Tanzania: a cohort study. <i>Clinical Microbiology and Infection</i> , 2019 , 25, 107.e1-107.e7	9.5	5
155	High-throughput metabolomic analysis predicts mode of action of uncharacterized antimicrobial compounds. <i>Science Translational Medicine</i> , 2018 , 10,	17.5	68
154	Impact of diagnostic test Xpert MTB/RIF [®] on health outcomes for tuberculosis. <i>The Cochrane Library</i> , 2018 ,	5.2	6
153	Hyperglycaemia is inversely correlated with live <i>M. bovis</i> BCG-specific CD4 T cell responses in Tanzanian adults with latent or active tuberculosis. <i>Immunity, Inflammation and Disease</i> , 2018 , 6, 345-353 ^{2,4}	3.4	4
152	Ecology and evolution of Mycobacterium tuberculosis. <i>Nature Reviews Microbiology</i> , 2018 , 16, 202-213	22.2	225
151	A cluster of multidrug-resistant Mycobacterium tuberculosis 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
150	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
149	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
148	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
147	Interplay of strain and race/ethnicity in the innate immune response to <i>M. tuberculosis</i> . <i>PLoS ONE</i> , 2018 , 13, e0195392	3.7	19
146	Treemmer: a tool to reduce large phylogenetic datasets with minimal loss of diversity. <i>BMC Bioinformatics</i> , 2018 , 19, 164	3.6	45
145	Tuberculosis outbreak investigation using phylodynamic analysis. <i>Epidemics</i> , 2018 , 25, 47-53	5.1	13
144	TnSeq of Mycobacterium tuberculosis clinical isolates reveals strain-specific antibiotic liabilities. <i>PLoS Pathogens</i> , 2018 , 14, e1006939	7.6	47
143	Compensatory evolution drives multidrug-resistant tuberculosis in Central Asia. <i>ELife</i> , 2018 , 7,	8.9	60
142	Low sensitivity of the MPT64 identification test to detect lineage 5 of the Mycobacterium tuberculosis complex. <i>Journal of Medical Microbiology</i> , 2018 , 67, 1718-1727	3.2	8
141	Discovery and Characterization of sp. nov., a Nontuberculous Mycobacterium Isolated From Human Lungs. <i>Frontiers in Microbiology</i> , 2018 , 9, 3184	5.7	3

140	A New Phylogenetic Framework for the Animal-Adapted Complex. <i>Frontiers in Microbiology</i> , 2018 , 9, 2820	5.7	77
139	Analysis of potential household transmission events of tuberculosis in the city of Belem, Brazil. <i>Tuberculosis</i> , 2018 , 113, 125-129	2.6	6
138	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
137	Integrating standardized whole genome sequence analysis with a global Mycobacterium tuberculosis antibiotic resistance knowledgebase. <i>Scientific Reports</i> , 2018 , 8, 15382	4.9	35
136	A19 The impact of HIV-1 on the evolution of Mycobacterium tuberculosis. <i>Virus Evolution</i> , 2018 , 4,	3.7	78
135	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
134	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
133	The within-host population dynamics of Mycobacterium tuberculosis vary with treatment efficacy. <i>Genome Biology</i> , 2017 , 18, 71	18.3	60
132	Antimicrobial resistance in Mycobacterium tuberculosis: mechanistic and evolutionary perspectives. <i>FEMS Microbiology Reviews</i> , 2017 , 41, 354-373	15.1	153
131	The Influence of HIV on the Evolution of Mycobacterium tuberculosis. <i>Molecular Biology and Evolution</i> , 2017 , 34, 1654-1668	8.3	17
130	Reversion of antibiotic resistance in by spiroisoxazoline SMART-420. <i>Science</i> , 2017 , 355, 1206-1211	33.3	80
129	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
128	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
127	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
126	The Host-Pathogen-Extrinsic Factors in Tuberculosis: Modulating Inflammation and Clinical Outcomes. <i>Frontiers in Immunology</i> , 2017 , 8, 1948	8.4	16
125	Tuberculosis in Swiss captive Asian elephants: microevolution of Mycobacterium tuberculosis characterized by multilocus variable-number tandem-repeat analysis and whole-genome sequencing. <i>Scientific Reports</i> , 2017 , 7, 14647	4.9	7
124	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
123	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

122	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
121	A standardised method for interpreting the association between mutations and phenotypic drug resistance in. <i>European Respiratory Journal</i> , 2017 , 50,	13.6	198
120	Molecular Evolution of Mycobacteria 2017 , 393-416		3
119	Molecular characterization of bovine tuberculosis strains in two slaughterhouses in Morocco. <i>BMC Veterinary Research</i> , 2017 , 13, 272	2.7	11
118	Mycobacterium tuberculosis lineage 4 comprises globally distributed and geographically restricted sublineages. <i>Nature Genetics</i> , 2016 , 48, 1535-1543	36.3	208
117	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
116	Clinical implications of molecular drug resistance testing for Mycobacterium tuberculosis: a TBNET/RESIST-TB consensus statement. <i>International Journal of Tuberculosis and Lung Disease</i> , 2016 , 20, 24-42	2.1	101
115	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
114	Spatio-Temporal Distribution of Mycobacterium tuberculosis Complex Strains in Ghana. <i>PLoS ONE</i> , 2016 , 11, e0161892	3.7	29
113	Molecular epidemiology of Mycobacterium africanum in Ghana. <i>BMC Infectious Diseases</i> , 2016 , 16, 385	4	23
112	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
111	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
110	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
109	The First population structure and comparative genomics analysis of Mycobacterium africanum strains from Ghana reveals higher diversity of Lineage 5. <i>International Journal of Mycobacteriology</i> , 2016 , 5 Suppl 1, S80-S81	0.9	4
108	Standard Genotyping Overestimates Transmission of Mycobacterium tuberculosis among Immigrants in a Low-Incidence Country. <i>Journal of Clinical Microbiology</i> , 2016 , 54, 1862-1870	9.7	70
107	Evolutionary history and global spread of the Mycobacterium tuberculosis Beijing lineage. <i>Nature Genetics</i> , 2015 , 47, 242-9	36.3	344
106	Co-evolution of Mycobacterium tuberculosis and Homo sapiens. <i>Immunological Reviews</i> , 2015 , 264, 6-24	11.3	166
105	Southern East Asian origin and coexpansion of Mycobacterium tuberculosis 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

104	Towards host-directed therapies for tuberculosis. <i>Nature Reviews Drug Discovery</i> , 2015 , 14, 511-2	64.1	80
103	<i>Mycobacterium africanum</i> is associated with patient ethnicity in Ghana. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e3370	4.8	46
102	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		24
101	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	4	35
100	DNA replication fidelity in <i>Mycobacterium tuberculosis</i> is mediated by an ancestral prokaryotic proofreader. <i>Nature Genetics</i> , 2015 , 47, 677-81	36.3	45
99	<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
98	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
97	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
96	A single-nucleotide-polymorphism real-time PCR assay for genotyping of <i>Mycobacterium tuberculosis</i> complex in peri-urban Kampala. <i>BMC Infectious Diseases</i> , 2015 , 15, 396	4	3
95	Distribution and transmission of <i>Mycobacterium tuberculosis</i> complex lineages among children in peri-urban Kampala, Uganda. <i>BMC Pediatrics</i> , 2015 , 15, 140	2.6	4
94	Acquired Resistance to Bedaquiline and Delamanid in Therapy for Tuberculosis. <i>New England Journal of Medicine</i> , 2015 , 373, 1986-8	59.2	229
93	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
92	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. <i>Nature</i> , 2014 , 514, 494-7	50.4	358
91	Evolution of drug resistance in tuberculosis: recent progress and implications for diagnosis and therapy. <i>Drugs</i> , 2014 , 74, 1063-72	12.1	55
90	Impact of in vitro evolution on antigenic diversity of <i>Mycobacterium bovis</i> bacillus Calmette-Guerin (BCG). <i>Vaccine</i> , 2014 , 32, 5998-6004	4.1	45
89	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
88	PolyTB: a genomic variation map for <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2014 , 94, 346-54	2.6	64
87	Consequences of genomic diversity in <i>Mycobacterium tuberculosis</i> . <i>Seminars in Immunology</i> , 2014 , 26, 431-44	10.7	243

86	Diversity of Mycobacterium tuberculosis and drug resistance in different provinces of Papua New Guinea. <i>BMC Microbiology</i> , 2014 , 14, 307	4.5	14
85	Lipidomics and genomics of Mycobacterium tuberculosis reveal lineage-specific trends in mycolic acid biosynthesis. <i>MicrobiologyOpen</i> , 2014 , 3, 823-35	3.4	33
84	Sequence diversity in the pe_pgrs genes of Mycobacterium tuberculosis is independent of human T cell recognition. <i>MBio</i> , 2014 , 5, e00960-13	7.8	69
83	KvarQ: targeted and direct variant calling from fastq reads of bacterial genomes. <i>BMC Genomics</i> , 2014 , 15, 881	4.5	89
82	Comment on: characterization of the embB gene in Mycobacterium tuberculosis isolates from Barcelona and rapid detection of main mutations related to ethambutol resistance using a low-density DNA array. <i>Journal of Antimicrobial Chemotherapy</i> , 2014 , 69, 2298-9	5.1	6
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	Genomic analysis identifies targets of convergent positive selection in drug-resistant Mycobacterium tuberculosis. <i>Nature Genetics</i> , 2013 , 45, 1183-9	36.3	295
79	Out-of-Africa migration and Neolithic coexpansion of Mycobacterium tuberculosis with modern humans. <i>Nature Genetics</i> , 2013 , 45, 1176-82	36.3	676
78	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
77	The heterogeneous evolution of multidrug-resistant Mycobacterium tuberculosis. <i>Trends in Genetics</i> , 2013 , 29, 160-9	8.5	136
76	Single nucleotide polymorphisms in Mycobacterium tuberculosis and the need for a curated database. <i>Tuberculosis</i> , 2013 , 93, 30-9	2.6	39
75	Mycobacterium tuberculosis 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
74	Genetic diversity in Mycobacterium tuberculosis. <i>Current Topics in Microbiology and Immunology</i> , 2013 , 374, 1-25	3.3	36
73	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
72	Mycobacterial lineages causing pulmonary and extrapulmonary tuberculosis, Ethiopia. <i>Emerging Infectious Diseases</i> , 2013 , 19, 460-3	10.2	155
71	Novel Mycobacterium tuberculosis complex isolate from a wild chimpanzee. <i>Emerging Infectious Diseases</i> , 2013 , 19, 969-76	10.2	78
70	HIV infection disrupts the sympatric host-pathogen relationship in human tuberculosis. <i>PLoS Genetics</i> , 2013 , 9, e1003318	6	61
69	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

68	Differential virulence and disease progression following Mycobacterium tuberculosis complex infection of the common marmoset (<i>Callithrix jacchus</i>). <i>Infection and Immunity</i> , 2013 , 81, 2909-19	3.7	83
67	Putative compensatory mutations in the <i>rpoC</i> gene of rifampin-resistant Mycobacterium tuberculosis are associated with ongoing transmission. <i>Antimicrobial Agents and Chemotherapy</i> , 2013 , 57, 827-32	5.9	151
66	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
65	Advances in tuberculosis. <i>African Journal of Microbiology Research</i> , 2013 , 7, 73-81	0.5	
64	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
63	Use of whole genome sequencing to determine the microevolution of Mycobacterium tuberculosis during an outbreak. <i>PLoS ONE</i> , 2013 , 8, e58235	3.7	60
62	Old and new selective pressures on Mycobacterium tuberculosis. <i>Infection, Genetics and Evolution</i> , 2012 , 12, 678-85	4.5	50
61	Independent large scale duplications in multiple M. tuberculosis lineages overlapping the same genomic region. <i>PLoS ONE</i> , 2012 , 7, e26038	3.7	26
60	Comparative analysis of Mycobacterium tuberculosis <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
59	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
58	Effect of mutation and genetic background on drug resistance in Mycobacterium tuberculosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2012 , 56, 3047-53	5.9	80
57	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, e15528	4.8	58
56	Two new rapid SNP-typing methods for classifying Mycobacterium tuberculosis complex into the main phylogenetic lineages. <i>PLoS ONE</i> , 2012 , 7, e41253	3.7	100
55	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
54	Host-pathogen coevolution in human tuberculosis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012 , 367, 850-9	5.8	255
53	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
52	Beijing sublineages of Mycobacterium tuberculosis differ in pathogenicity in the guinea pig. <i>Vaccine Journal</i> , 2012 , 19, 1227-37		76
51	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

50	First insights into the phylogenetic diversity of Mycobacterium tuberculosis in Nepal. <i>PLoS ONE</i> , 2012 , 7, e52297	3.7	18
49	Whole-genome sequencing of rifampicin-resistant Mycobacterium tuberculosis strains identifies compensatory mutations in RNA polymerase genes. <i>Nature Genetics</i> , 2011 , 44, 106-10	36.3	376
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12	Local adaptation in populations of <i>Mycobacterium tuberculosis</i> endemic to the Indian Ocean Rim		1
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10	Multiple Introductions of the <i>Mycobacterium tuberculosis</i> Lineage 2 Beijing into Africa over centuries		2
9	Interaction between host genes and <i>M. tuberculosis</i> lineage can affect tuberculosis severity: evidence for coevolution		1
8	Multiple merger genealogies in outbreaks of <i>Mycobacterium tuberculosis</i>		2
7	A sister lineage of the <i>Mycobacterium tuberculosis</i> complex discovered in the African Great Lakes region		3
6	Phylogenomics of <i>Mycobacterium africanum</i> reveals a new lineage and a complex evolutionary history		4
5	Leprosy in wild chimpanzees		7
4	Genomic determinants of speciation and spread of the <i>Mycobacterium tuberculosis</i> complex		1
3	Reference Set of <i>Mycobacterium tuberculosis</i> Clinical Strains: A tool for research and product development		2
2	Model-based integration of genomics and metabolomics reveals SNP functionality in <i>Mycobacterium tuberculosis</i>		2
1	A new nomenclature for the livestock-associated <i>Mycobacterium tuberculosis</i> complex based on phylogenomics. <i>Open Research Europe</i> , 1, 100		0