

# Nalin Rastogi

## List of Publications by Year in descending order

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325  
papers

13,920  
citations

36303

51  
h-index

30922

102  
g-index

349  
all docs

349  
docs citations

349  
times ranked

6709  
citing authors

#	ARTICLE	IF	CITATIONS
1	SITVITBovis™ a publicly available database and mapping tool to get an improved overview of animal and human cases caused by <i>Mycobacterium bovis</i> . Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	3
2	First approach to the population structure of Mycobacterium tuberculosis complex in the indigenous population in Puerto Nariño-Amazonas, Colombia. PLoS ONE, 2021, 16, e0245084.	2.5	5
3	Practical approach to detection and surveillance of emerging highly resistant Mycobacterium tuberculosis Beijing 1071-32-cluster. Scientific Reports, 2021, 11, 21392.	3.3	5
4	Title is missing!. , 2021, 16, e0245084.		0
5	Title is missing!. , 2021, 16, e0245084.		0
6	Title is missing!. , 2021, 16, e0245084.		0
7	Title is missing!. , 2021, 16, e0245084.		0
8	Genetic diversity of Mycobacterium tuberculosis clinical isolates from HIV-TB patients from two public hospitals at Bogotá, Colombia. Infection, Genetics and Evolution, 2020, 77, 104059.	2.3	0
9	Peculiar features of the Mycobacterium tuberculosis population structure in Albania. Infection, Genetics and Evolution, 2020, 78, 104136.	2.3	4
10	Detection of Beijing strains of MDR M. tuberculosis and their association with drug resistance mutations in katG, rpoB, and embB genes. BMC Infectious Diseases, 2020, 20, 752.	2.9	9
11	Local adaptive evolution of two distinct clades of Beijing and T families of Mycobacterium tuberculosis in Chongqing: a Bayesian population structure and phylogenetic study. Infectious Diseases of Poverty, 2020, 9, 59.	3.7	1
12	Population structure of multidrug-resistant Mycobacterium tuberculosis clinical isolates in Colombia. Tuberculosis, 2020, 125, 102011.	1.9	4
13	Novel methods included in SpolLineages tool for fast and precise prediction of Mycobacterium tuberculosis complex spoligotype families. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	7
14	Two tales: Worldwide distribution of Central Asian (CAS) versus ancestral East-African Indian (EAI) lineages of Mycobacterium tuberculosis underlines a remarkable cleavage for phylogeographical, epidemiological and demographical characteristics. PLoS ONE, 2019, 14, e0219706.	2.5	25
15	Insights on the Mycobacterium tuberculosis population structure associated with migrants from Portuguese-speaking countries over a three-year period in Greater Lisbon, Portugal: Implications at the public health level. Infection, Genetics and Evolution, 2019, 71, 159-165.	2.3	4
16	Macro-geographical specificities of the prevailing tuberculosis epidemic as seen through SITVIT2, an updated version of the Mycobacterium tuberculosis genotyping database. Infection, Genetics and Evolution, 2019, 72, 31-43.	2.3	100
17	Clonal expansion across the seas as seen through CPLP-TB database: A joint effort in cataloguing Mycobacterium tuberculosis genetic diversity in Portuguese-speaking countries. Infection, Genetics and Evolution, 2019, 72, 44-58.	2.3	18
18	Mycobacterial biomaterials and resources for researchers. Pathogens and Disease, 2018, 76, .	2.0	14

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19	Genotypic diversity of <i>Mycobacterium tuberculosis</i> in Buenos Aires, Argentina. <i>Infection, Genetics and Evolution</i> , 2018, 62, 1-7.	2.3	8
20	Molecular epidemiology of <i>Mycobacterium tuberculosis</i> strains from prison populations in Santa Catarina, Southern Brazil. <i>Infection, Genetics and Evolution</i> , 2018, 58, 34-39.	2.3	6
21	Interaction between <i>rpsL</i> and <i>gyrA</i> mutations affects the fitness and dual resistance of <i>Mycobacterium tuberculosis</i> clinical isolates against streptomycin and fluoroquinolones. <i>Infection and Drug Resistance</i> , 2018, Volume 11, 431-440.	2.7	16
22	Geospatial distribution of <i>Mycobacterium tuberculosis</i> genotypes in Africa. <i>PLoS ONE</i> , 2018, 13, e0200632.	2.5	54
23	Phylogenomic analysis of the species of the <i>Mycobacterium tuberculosis</i> complex demonstrates that <i>Mycobacterium africanum</i> , <i>Mycobacterium bovis</i> , <i>Mycobacterium caprae</i> , <i>Mycobacterium microti</i> and <i>Mycobacterium pinnipedii</i> are later heterotypic synonyms of <i>Mycobacterium tuberculosis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 324-332.	1.7	130
24	Comparative study of genotypes of <i>Mycobacterium tuberculosis</i> from a Northern Indian setting with strains reported from other parts of India and neighboring countries. <i>Tuberculosis</i> , 2017, 105, 60-72.	1.9	12
25	SpolSimilaritySearch – A web tool to compare and search similarities between spoligotypes of <i>Mycobacterium tuberculosis</i> complex. <i>Tuberculosis</i> , 2017, 105, 49-52.	1.9	20
26	Genetic diversity of <i>Mycobacterium tuberculosis</i> from Pará, Brazil, reveals a higher frequency of ancestral strains than previously reported in South America. <i>Infection, Genetics and Evolution</i> , 2017, 56, 62-72.	2.3	9
27	New <i>Mycobacterium tuberculosis</i> Beijing clonal complexes in China revealed by phylogenetic and Bayesian population structure analyses of 24-loci MIRU-VNTRs. <i>Scientific Reports</i> , 2017, 7, 6065.	3.3	4
28	<i>Mycobacterium tuberculosis</i> genotypes and predominant clones among the multidrug-resistant isolates in Spain 1998–2005. <i>Infection, Genetics and Evolution</i> , 2017, 55, 117-126.	2.3	3
29	Molecular epidemiology of <i>Mycobacterium tuberculosis</i> in Baja California, Mexico: A result of human migration?. <i>Infection, Genetics and Evolution</i> , 2017, 55, 378-383.	2.3	12
30	Bayesian population structure analysis reveals presence of phylogeographically specific sublineages within previously ill-defined T group of <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2017, 12, e0171584.	2.5	5
31	Predictive factors for a one-year improvement in nontuberculous mycobacterial pulmonary disease: An 11-year retrospective and multicenter study. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005841.	3.0	9
32	New <i>Mycobacterium tuberculosis</i> LAM sublineage with geographical specificity for the Old World revealed by phylogenetical and Bayesian analyses. <i>Tuberculosis</i> , 2016, 101, 62-66.	1.9	0
33	A snapshot of the predominant single nucleotide polymorphism cluster groups of <i>Mycobacterium tuberculosis</i> clinical isolates in Delhi, India. <i>Tuberculosis</i> , 2016, 100, 72-81.	1.9	5
34	Genetic diversity of <i>Mycobacterium tuberculosis</i> complex strains isolated from patients with pulmonary tuberculosis in Anambra State, Nigeria. <i>International Journal of Mycobacteriology</i> , 2016, 5, 74-79.	0.6	12
35	Methodological and Clinical Aspects of the Molecular Epidemiology of <i>Mycobacterium tuberculosis</i> and Other Mycobacteria. <i>Clinical Microbiology Reviews</i> , 2016, 29, 239-290.	13.6	131
36	First insight into the molecular epidemiology of <i>Mycobacterium tuberculosis</i> in Santa Catarina, southern Brazil. <i>Tuberculosis</i> , 2016, 97, 57-64.	1.9	12

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37	Characterization of mutations in streptomycin-resistant <i>Mycobacterium tuberculosis</i> isolates in Sichuan, China and the association between Beijing-lineage and dual-mutation in <i>gidB</i> . <i>Tuberculosis</i> , 2016, 96, 102-106.	1.9	40
38	Combined Genotypic, Phylogenetic, and Epidemiologic Analyses of <i>Mycobacterium tuberculosis</i> Genetic Diversity in the Rhône Alpes Region, France. <i>PLoS ONE</i> , 2016, 11, e0153580.	2.5	19
39	Mapping of <i>Mycobacterium tuberculosis</i> Complex Genetic Diversity Profiles in Tanzania and Other African Countries. <i>PLoS ONE</i> , 2016, 11, e0154571.	2.5	41
40	Analysis of <i>Mycobacterium tuberculosis</i> Genotypic Lineage Distribution in Chile and Neighboring Countries. <i>PLoS ONE</i> , 2016, 11, e0160434.	2.5	12
41	Predominance of Uganda genotype of <i>Mycobacterium tuberculosis</i> isolated from Ugandan patients with tuberculous lymphadenitis. <i>BMC Research Notes</i> , 2015, 8, 398.	1.4	4
42	<i>Mycobacterium tuberculosis</i> causing tuberculous lymphadenitis in Maputo, Mozambique. <i>BMC Microbiology</i> , 2015, 15, 268.	3.3	10
43	Heterogeneity among <i>Mycobacterium ulcerans</i> from French Guiana Revealed by Multilocus Variable Number Tandem Repeat Analysis (MLVA). <i>PLoS ONE</i> , 2015, 10, e0118597.	2.5	8
44	The Association between <i>Mycobacterium Tuberculosis</i> Genotype and Drug Resistance in Peru. <i>PLoS ONE</i> , 2015, 10, e0126271.	2.5	24
45	Genetic Structuration, Demography and Evolutionary History of <i>Mycobacterium tuberculosis</i> LAM9 Sublineage in the Americas as Two Distinct Subpopulations Revealed by Bayesian Analyses. <i>PLoS ONE</i> , 2015, 10, e0140911.	2.5	13
46	Evolutionary history and global spread of the <i>Mycobacterium tuberculosis</i> Beijing lineage. <i>Nature Genetics</i> , 2015, 47, 242-249.	21.4	466
47	<i>Mycobacterium tuberculosis</i> polyclonal infections and microevolution identified by MIRU-VNTRs in an epidemiological study. <i>International Journal of Mycobacteriology</i> , 2015, 4, 222-227.	0.6	20
48	Prevalence of Latin-American-Mediterranean genetic family in population structure of <i>Mycobacterium tuberculosis</i> in Bulgaria. <i>International Journal of Mycobacteriology</i> , 2015, 4, 191-195.	0.6	2
49	Mixed Infections and Rifampin Heteroresistance among <i>Mycobacterium tuberculosis</i> Clinical Isolates. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2138-2147.	3.9	37
50	Tuberculosis – A global emergency: Tools and methods to monitor, understand, and control the epidemic with specific example of the Beijing lineage. <i>Tuberculosis</i> , 2015, 95, S177-S189.	1.9	47
51	Genetic diversity and drug susceptibility profile of <i>Mycobacterium tuberculosis</i> isolated from different regions of India. <i>Journal of Infection</i> , 2015, 71, 207-219.	3.3	38
52	Spacer-Based Macroarrays for CRISPR Genotyping. <i>Methods in Molecular Biology</i> , 2015, 1311, 111-131.	0.9	17
53	Multidrug-Resistant <i>Mycobacterium tuberculosis</i> of the Latin American Mediterranean Lineage, Wrongly Identified as <i>Mycobacterium pinnipedii</i> (Spoligotype International Type 863 [SIT863]), Causing Active Tuberculosis in South Brazil. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3805-3811.	3.9	13
54	Human multidrug-resistant <i>Mycobacterium bovis</i> infection in Mexico. <i>Tuberculosis</i> , 2015, 95, 802-809.	1.9	17

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55	Finer characterization of <i>Mycobacterium tuberculosis</i> using spoligotyping and 15-loci MIRU-VNTRs reveals phylogeographical specificities of isolates circulating in Guyana and Suriname. <i>Infection, Genetics and Evolution</i> , 2015, 30, 114-119.	2.3	8
56	A First Insight on the Population Structure of <i>Mycobacterium tuberculosis</i> Complex as Studied by Spoligotyping and MIRU-VNTRs in Santiago, Chile. <i>PLoS ONE</i> , 2015, 10, e0118007.	2.5	28
57	Characterization of the Genetic Diversity of Extensively-Drug Resistant <i>Mycobacterium tuberculosis</i> Clinical Isolates from Pulmonary Tuberculosis Patients in Peru. <i>PLoS ONE</i> , 2014, 9, e112789.	2.5	20
58	Study of <i>Mycobacterium tuberculosis</i> Complex Genotypic Diversity in Malaysia Reveals a Predominance of Ancestral East-African-Indian Lineage with a Malaysia-Specific Signature. <i>PLoS ONE</i> , 2014, 9, e114832.	2.5	21
59	Current Methods in the Molecular Typing of <i>Mycobacterium tuberculosis</i> and Other Mycobacteria. <i>BioMed Research International</i> , 2014, 2014, 1-21.	1.9	108
60	Recent Developments in Mycobacteriology: A Clinical and Diagnostic Perspective. <i>BioMed Research International</i> , 2014, 2014, 1-2.	1.9	0
61	Genotypic characterization and historical perspective of <i>Mycobacterium tuberculosis</i> among older and younger Finns, 2008–2011. <i>Clinical Microbiology and Infection</i> , 2014, 20, 1134-1139.	6.0	7
62	Strain Diversity of <i>Mycobacterium tuberculosis</i> Isolates from Pulmonary Tuberculosis Patients in Afar Pastoral Region of Ethiopia. <i>BioMed Research International</i> , 2014, 2014, 1-12.	1.9	40
63	Suitability of IS6110-RFLP and MIRU-VNTR for Differentiating Spoligotyped Drug-Resistant <i>Mycobacterium tuberculosis</i> Clinical Isolates from Sichuan in China. <i>BioMed Research International</i> , 2014, 2014, 1-11.	1.9	16
64	A First Assessment of <i>Mycobacterium tuberculosis</i> Genetic Diversity and Drug-Resistance Patterns in Twelve Caribbean Territories. <i>BioMed Research International</i> , 2014, 2014, 1-11.	1.9	11
65	A Systematic Follow-Up of <i>Mycobacterium tuberculosis</i> Drug-Resistance and Associated Genotypic Lineages in the French Departments of the Americas over a Seventeen-Year Period. <i>BioMed Research International</i> , 2014, 2014, 1-14.	1.9	10
66	Molecular Epidemiology and Genotyping of <i>Mycobacterium tuberculosis</i> Isolated in Baghdad. <i>BioMed Research International</i> , 2014, 2014, 1-15.	1.9	12
67	Phylogenetic associations with drug-resistant <i>Mycobacterium tuberculosis</i> isolates in a paediatric population. <i>International Journal of Tuberculosis and Lung Disease</i> , 2014, 18, 1172-1179.	1.2	6
68	Population Structure among <i>Mycobacterium tuberculosis</i> Isolates from Pulmonary Tuberculosis Patients in Colombia. <i>PLoS ONE</i> , 2014, 9, e93848.	2.5	46
69	Predicting <i>Mycobacterium tuberculosis</i> Complex Clades Using Knowledge-Based Bayesian Networks. <i>BioMed Research International</i> , 2014, 2014, 1-11.	1.9	8
70	Treatment outcomes of multidrug-resistant tuberculosis patients in Gauteng, South Africa. <i>Infection</i> , 2014, 42, 405-413.	4.7	30
71	Multilocus sequence typing scheme for the <i>Mycobacterium abscessus</i> complex. <i>Research in Microbiology</i> , 2014, 165, 82-90.	2.1	49
72	Proposal of a Consensus Set of Hypervariable Mycobacterial Interspersed Repetitive-Unit Variable-Number Tandem-Repeat Loci for Subtyping of <i>Mycobacterium tuberculosis</i> Beijing Isolates. <i>Journal of Clinical Microbiology</i> , 2014, 52, 164-172.	3.9	81

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73	Snapshot of the genetic diversity of Mycobacterium tuberculosis isolates in Iraq. International Journal of Mycobacteriology, 2014, 3, 184-196.	0.6	15
74	Real-Time PCR Assay for Rapid Detection of Epidemiologically and Clinically Significant Mycobacterium tuberculosis Beijing Genotype Isolates. Journal of Clinical Microbiology, 2014, 52, 1691-1693.	3.9	28
75	Four year longitudinal study of Mycobacterium tuberculosis complex isolates in a region of North-Eastern Italy. Infection, Genetics and Evolution, 2014, 26, 58-64.	2.3	15
76	Contribution of spoligotyping and MIRU-VNTRs to characterize prevalent Mycobacterium tuberculosis genotypes infecting tuberculosis patients in Morocco. Infection, Genetics and Evolution, 2014, 21, 463-471.	2.3	19
77	Second worldwide proficiency study on variable number of tandem repeats typing of <I>Mycobacterium tuberculosis</I> complex. International Journal of Tuberculosis and Lung Disease, 2014, 18, 594-600.	1.2	23
78	Strain Classification of Mycobacterium tuberculosis Isolates in Brazil Based on Genotypes Obtained by Spoligotyping, Mycobacterial Interspersed Repetitive Unit Typing and the Presence of Large Sequence and Single Nucleotide Polymorphism. PLoS ONE, 2014, 9, e107747.	2.5	30
79	A study of Mycobacterium tuberculosis genotypic diversity & drug resistance mutations in Varanasi, north India. Indian Journal of Medical Research, 2014, 139, 892-902.	1.0	15
80	Evolutionary robust SNPs reveal the misclassification of Mycobacterium tuberculosis Beijing family strains into sublineages. Infection, Genetics and Evolution, 2013, 16, 174-177.	2.3	29
81	Molecular snapshot of Mycobacterium tuberculosis population structure and drug-resistance in Kyrgyzstan. Tuberculosis, 2013, 93, 501-507.	1.9	12
82	Efficient discrimination by MIRU-VNTRs of Mycobacterium tuberculosis clinical isolates belonging to the predominant SIT11/EAI3-IND ancestral genotypic lineage in Kerala, India. International Journal of Mycobacteriology, 2013, 2, 244-247.	0.6	3
83	Predominance of Beijing genotype in extensively drug resistant Mycobacterium tuberculosis isolates from a tertiary care hospital in New Delhi, India. International Journal of Mycobacteriology, 2013, 2, 109-113.	0.6	9
84	Utility and diagnostic performance of Mycobacterium tuberculosis complex by two immunochromatographic assays as compared with the molecular Genotype assay in Nigeria. International Journal of Mycobacteriology, 2013, 2, 34-37.	0.6	2
85	Use of genotyping based clustering to quantify recent tuberculosis transmission in Guadeloupe during a seven years period: analysis of risk factors and access to health care. BMC Infectious Diseases, 2013, 13, 364.	2.9	9
86	Population structure and circulating genotypes of drug-sensitive and drug-resistant Mycobacterium tuberculosis clinical isolates in São Paulo state, Brazil. Infection, Genetics and Evolution, 2013, 14, 39-45.	2.3	10
87	Mycobacterium tuberculosis population structure shift in a 5-year molecular epidemiology surveillance follow-up study in a low endemic agro-industrial setting in São Paulo, Brazil. International Journal of Mycobacteriology, 2013, 2, 156-165.	0.6	4
88	Multidrug resistance and demography of newly diagnosed tuberculosis patients in Cross River State, Nigeria. International Journal of Mycobacteriology, 2013, 2, 89-93.	0.6	6
89	Genetic diversity among multidrug-resistant Mycobacterium tuberculosis strains in Mexico. Infection, Genetics and Evolution, 2013, 14, 434-443.	2.3	30
90	Molecular epidemiology of Mycobacterium tuberculosis isolates from Kerala, India using IS6110-RFLP, spoligotyping and MIRU-VNTRs. Infection, Genetics and Evolution, 2013, 16, 157-164.	2.3	25

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91	The geographic diversity of nontuberculous mycobacteria isolated from pulmonary samples: an NTM-NET collaborative study. <i>European Respiratory Journal</i> , 2013, 42, 1604-1613.	6.7	683
92	Epidemic Spread of Multidrug-Resistant Tuberculosis in Johannesburg, South Africa. <i>Journal of Clinical Microbiology</i> , 2013, 51, 1818-1825.	3.9	70
93	Nontuberculous Mycobacteria in Guadeloupe, Martinique, and French Guiana from 1994 to 2012. <i>Tuberculosis Research and Treatment</i> , 2013, 2013, 1-8.	0.6	7
94	Molecular Epidemiology of Tuberculosis in Finland, 2008-2011. <i>PLoS ONE</i> , 2013, 8, e85027.	2.5	23
95	Genetic Diversity of Mycobacterium tuberculosis in Peru and Exploration of Phylogenetic Associations with Drug Resistance. <i>PLoS ONE</i> , 2013, 8, e65873.	2.5	38
96	Mycobacterium tuberculosis Beijing Genotype Is Associated with HIV Infection in Mozambique. <i>PLoS ONE</i> , 2013, 8, e71999.	2.5	21
97	Characterization of Extensively Drug-Resistant Tuberculosis Cases from Valle del Cauca, Colombia. <i>Journal of Clinical Microbiology</i> , 2012, 50, 4185-4187.	3.9	18
98	Inferred Spoligoforest Topology Unravels Spatially Bimodal Distribution of Mutations in the DR Region. <i>IEEE Transactions on Nanobioscience</i> , 2012, 11, 191-202.	3.3	2
99	Genetic characterization of Mycobacterium tuberculosis in the West Bank, Palestinian Territories. <i>BMC Research Notes</i> , 2012, 5, 270.	1.4	9
100	High initial multidrug-resistant tuberculosis rate in Buenaventura, Colombia: a public-private initiative: Table 1. <i>European Respiratory Journal</i> , 2012, 40, 1569-1572.	6.7	9
101	The Genotypic Population Structure of Mycobacterium tuberculosis Complex from Moroccan Patients Reveals a Predominance of Euro-American Lineages. <i>PLoS ONE</i> , 2012, 7, e47113.	2.5	22
102	High-resolution MIRU-VNTRs typing reveals the unique nature of Mycobacterium tuberculosis Beijing genotype in Okinawa, Japan. <i>Infection, Genetics and Evolution</i> , 2012, 12, 637-641.	2.3	10
103	A first insight on the population structure of Mycobacterium tuberculosis complex as studied by spoligotyping and MIRU-VNTRs in Bogotá, Colombia. <i>Infection, Genetics and Evolution</i> , 2012, 12, 657-663.	2.3	42
104	Molecular epidemiology and genetic diversity of Mycobacterium tuberculosis complex in the Cross River State, Nigeria. <i>Infection, Genetics and Evolution</i> , 2012, 12, 671-677.	2.3	43
105	Spoligotypes of Mycobacterium tuberculosis complex isolates from patients residents of 11 states of Brazil. <i>Infection, Genetics and Evolution</i> , 2012, 12, 649-656.	2.3	49
106	Mycobacterium tuberculosis spoligotypes that may derive from mixed strain infections are revealed by a novel computational approach. <i>Infection, Genetics and Evolution</i> , 2012, 12, 798-806.	2.3	30
107	The population structure of drug-resistant Mycobacterium tuberculosis clinical isolates from Sichuan in China. <i>Infection, Genetics and Evolution</i> , 2012, 12, 718-724.	2.3	19
108	SITVITWEB – A publicly available international multimer database for studying Mycobacterium tuberculosis genetic diversity and molecular epidemiology. <i>Infection, Genetics and Evolution</i> , 2012, 12, 755-766.	2.3	380



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109	TB-Lineage: An online tool for classification and analysis of strains of Mycobacterium tuberculosis complex. <i>Infection, Genetics and Evolution</i> , 2012, 12, 789-797.	2.3	87
110	Special Issue on Molecular evolution, epidemiology and pathogenesis of Mycobacterium tuberculosis and other mycobacteria. <i>Infection, Genetics and Evolution</i> , 2012, 12, 601.	2.3	0
111	Distribution of Spoligotyping Defined Genotypic Lineages among Drug-Resistant Mycobacterium tuberculosis Complex Clinical Isolates in Ankara, Turkey. <i>PLoS ONE</i> , 2012, 7, e30331.	2.5	33
112	MLVA Based Classification of Mycobacterium tuberculosis Complex Lineages for a Robust Phylogeographic Snapshot of Its Worldwide Molecular Diversity. <i>PLoS ONE</i> , 2012, 7, e41991.	2.5	24
113	Mycobacterium tuberculosis Strains Potentially Involved in the TB Epidemic in Sweden a Century Ago. <i>PLoS ONE</i> , 2012, 7, e46848.	2.5	11
114	Multidrug-resistant tuberculosis in Port-au-Prince, Haiti. <i>Revista Panamericana De Salud Publica/Pan American Journal of Public Health</i> , 2012, 31, 221-224.	1.1	16
115	Innovations in the molecular epidemiology of tuberculosis. <i>Enfermedades Infecciosas Y Microbiología Clínica</i> , 2011, 29, 8-13.	0.5	48
116	Spoligotyping of clinical Mycobacterium tuberculosis isolates from the state of Minas Gerais, Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2011, 106, 267-273.	1.6	13
117	Mycobacterium tuberculosis Complex Genotype Diversity and Drug Resistance Profiles in a Pediatric Population in Mexico. <i>Tuberculosis Research and Treatment</i> , 2011, 2011, 1-9.	0.6	13
118	The Guinea-Bissau Family of Mycobacterium tuberculosis Complex Revisited. <i>PLoS ONE</i> , 2011, 6, e18601.	2.5	47
119	Comparison of spoligotyping, mycobacterial interspersed repetitive units typing and IS6110-RFLP in a study of genotypic diversity of Mycobacterium tuberculosis in Delhi, North India. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2011, 106, 524-535.	1.6	43
120	Impact of immigration on tuberculosis epidemiology in a low-incidence country. <i>Clinical Microbiology and Infection</i> , 2011, 17, 881-887.	6.0	41
121	The use of microbead-based spoligotyping for Mycobacterium tuberculosis complex to evaluate the quality of the conventional method: Providing guidelines for Quality Assurance when working on membranes. <i>BMC Infectious Diseases</i> , 2011, 11, 110.	2.9	27
122	Highlighting the genetic and epidemiologic disparities of Mycobacterium tuberculosis epidemic in 12 Caribbean territories in a first global study. <i>BMC Proceedings</i> , 2011, 5, .	1.6	1
123	Automated Extraction and Amplification for Direct Detection of Mycobacterium tuberculosis Complex in Various Clinical Samples. <i>Journal of Clinical Microbiology</i> , 2011, 49, 1700-1701.	3.9	2
124	Impact of Immigration on the Molecular Epidemiology of Tuberculosis in Rhode Island. <i>Journal of Clinical Microbiology</i> , 2011, 49, 834-844.	3.9	27
125	Finer Snapshot of Circulating Mycobacterium tuberculosis Genotypes in Guadeloupe, Martinique, and French Guiana. <i>Journal of Clinical Microbiology</i> , 2011, 49, 2685-2687.	3.9	6
126	Spoligotype Profile of Mycobacterium tuberculosis Complex Strains from HIV-Positive and -Negative Patients in Nigeria: a Comparative Analysis. <i>Journal of Clinical Microbiology</i> , 2011, 49, 220-226.	3.9	15



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127	Molecular diversity of <i>Mycobacterium tuberculosis</i> isolates from patients with pulmonary tuberculosis in Mozambique. <i>BMC Microbiology</i> , 2010, 10, 195.	3.3	42
128	Molecular diversity of <i>Mycobacterium tuberculosis</i> isolates from patients with tuberculosis in Honduras. <i>BMC Microbiology</i> , 2010, 10, 208.	3.3	25
129	First case of multidrug-resistant tuberculosis caused by a rare "Beijing-like" genotype of <i>Mycobacterium tuberculosis</i> in Bogotá, Colombia. <i>Infection, Genetics and Evolution</i> , 2010, 10, 678-681.	2.3	16
130	Bulgarian specificity and controversial phylogeography of <i>Mycobacterium tuberculosis</i> spoligotype ST125_BGR. <i>FEMS Immunology and Medical Microbiology</i> , 2010, 59, 90-99.	2.7	9
131	<i>Mycobacterium tuberculosis</i> Spoligotypes in Monterrey, Mexico. <i>Journal of Clinical Microbiology</i> , 2010, 48, 448-455.	3.9	32
132	Spoligotype-Based Comparative Population Structure Analysis of Multidrug-Resistant and Isoniazid-Monoresistant <i>Mycobacterium tuberculosis</i> Complex Clinical Isolates in Poland. <i>Journal of Clinical Microbiology</i> , 2010, 48, 3899-3909.	3.9	30
133	The emergence of Beijing genotype of <i>mycobacterium tuberculosis</i> in the Kingdom of Saudi Arabia. <i>Annals of Thoracic Medicine</i> , 2010, 5, 149.	1.8	12
134	Simple and rapid method for detection of nitrate reductase activity of <i>Mycobacterium tuberculosis</i> and <i>Mycobacterium canettii</i> grown in the Bactec MGIT960 system. <i>Journal of Microbiological Methods</i> , 2010, 81, 208-210.	1.6	5
135	Unexpectedly High Proportion of Ancestral Manu Genotype <i>Mycobacterium tuberculosis</i> Strains Cultured from Tuberculosis Patients in Egypt. <i>Journal of Clinical Microbiology</i> , 2009, 47, 2794-2801.	3.9	33
136	Multidrug-Resistant <i>Mycobacterium tuberculosis</i> Strain from Equatorial Guinea Detected in Spain. <i>Emerging Infectious Diseases</i> , 2009, 15, 1858b-1860.	4.3	11
137	First Insight into <i>Mycobacterium tuberculosis</i> Epidemiology and Genetic Diversity in Trinidad and Tobago. <i>Journal of Clinical Microbiology</i> , 2009, 47, 1911-1914.	3.9	14
138	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.	3.9	53
139	Unsuspected and extensive transmission of a drug-susceptible <i>Mycobacterium tuberculosis</i> strain. <i>BMC Pulmonary Medicine</i> , 2009, 9, 3.	2.0	15
140	At Baltic crossroads: a molecular snapshot of <i>Mycobacterium tuberculosis</i> population diversity in Kaliningrad, Russia. <i>FEMS Immunology and Medical Microbiology</i> , 2009, 55, 13-22.	2.7	30
141	Association of <i>Mycobacterium tuberculosis</i> complex isolates of BOVIS and Central Asian (CAS) genotypic lineages with extrapulmonary disease. <i>Clinical Microbiology and Infection</i> , 2009, 15, 538-543.	6.0	41
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272	Activity of subinhibitory concentrations of dapson alone and in combination with cell-wall inhibitors against <i>Mycobacterium avium</i> complex organisms. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 1993, 12, 954-958.	2.9	7
273	Mode of action of antituberculous drugs and mechanisms of drug resistance in <i>Mycobacterium tuberculosis</i> . <i>Research in Microbiology</i> , 1993, 144, 133-143.	2.1	40
274	Emergence of multiple-drug-resistant tuberculosis: fundamental and applied research aspects, global issues and current strategies. <i>Research in Microbiology</i> , 1993, 144, 103.	2.1	29
275	Effect of pH on radiometric MICs of clarithromycin against 18 species of mycobacteria. <i>Antimicrobial Agents and Chemotherapy</i> , 1992, 36, 2841-2842.	3.2	40
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277	Epidemiological and genetic markers, virulence factors and intracellular growth of <i>Mycobacterium avium</i> in AIDS. <i>Research in Microbiology</i> , 1992, 143, 423-430.	2.1	34
278	Comparative ability of human monocytes and macrophages to control the intracellular growth of <i>Mycobacterium avium</i> and <i>Mycobacterium tuberculosis</i> : effect of interferon-gamma and indomethacin. <i>FEMS Microbiology Letters</i> , 1992, 89, 329-334.	1.8	15
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287	A rapid microbead method for breaking pathogenic mycobacteria: Application in SDS-PAGE and western blot analysis. <i>Current Microbiology</i> , 1992, 24, 311-317.	2.2	3
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