List of Publications by Year in descending order

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TANIA STADIED

#	Article	IF	CITATIONS
1	BEAST 2.5: An advanced software platform for Bayesian evolutionary analysis. PLoS Computational Biology, 2019, 15, e1006650.	3.2	2,484
2	Amazonia Through Time: Andean Uplift, Climate Change, Landscape Evolution, and Biodiversity. Science, 2010, 330, 927-931.	12.6	1,826
3	Impacts of the Cretaceous Terrestrial Revolution and KPg Extinction on Mammal Diversification. Science, 2011, 334, 521-524.	12.6	1,264
4	The conditioned reconstructed process. Journal of Theoretical Biology, 2008, 253, 769-778.	1.7	845
5	The fossilized birth–death process for coherent calibration of divergence-time estimates. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2957-66.	7.1	612
6	Birth–death skyline plot reveals temporal changes of epidemic spread in HIV and hepatitis C virus (HCV). Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 228-233.	7.1	454
7	Macroevolutionary Dynamics and Historical Biogeography of Primate Diversification Inferred from a Species Supermatrix. PLoS ONE, 2012, 7, e49521.	2.5	447
8	Mammalian phylogeny reveals recent diversification rate shifts. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6187-6192.	7.1	387
9	Sampling-through-time in birth–death trees. Journal of Theoretical Biology, 2010, 267, 396-404.	1.7	379
10	Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. Nature, 2021, 595, 707-712.	27.8	363
11	Practical considerations for measuring the effective reproductive number, Rt. PLoS Computational Biology, 2020, 16, e1008409.	3.2	343
12	On incomplete sampling under birth–death models and connections to the sampling-based coalescent. Journal of Theoretical Biology, 2009, 261, 58-66.	1.7	330
13	Total-Evidence Dating under the Fossilized Birth–Death Process. Systematic Biology, 2016, 65, 228-249.	5.6	304
14	Diversity-dependence brings molecular phylogenies closer to agreement with the fossil record. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 1300-1309.	2.6	281
15	Bayesian Inference of Sampled Ancestor Trees for Epidemiology and Fossil Calibration. PLoS Computational Biology, 2014, 10, e1003919.	3.2	276
16	Bayesian Total-Evidence Dating Reveals the Recent Crown Radiation of Penguins. Systematic Biology, 2017, 66, syw060.	5.6	255
17	Simulating Trees with a Fixed Number of Extant Species. Systematic Biology, 2011, 60, 676-684.	5.6	241
18	Estimating the Basic Reproductive Number from Viral Sequence Data. Molecular Biology and Evolution, 2012, 29, 347-357.	8.9	206

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19	CoV-Spectrum: analysis of globally shared SARS-CoV-2 data to identify and characterize new variants. Bioinformatics, 2022, 38, 1735-1737.	4.1	191
20	Geographical and temporal distribution of SARS-CoV-2 clades in the WHO European Region, January to June 2020. Eurosurveillance, 2020, 25, .	7.0	186
21	The contrasting phylodynamics of human influenza B viruses. ELife, 2015, 4, e05055.	6.0	166
22	Bayesian Inference of Species Networks from Multilocus Sequence Data. Molecular Biology and Evolution, 2018, 35, 504-517.	8.9	158
23	Inferring Speciation and Extinction Rates under Different Sampling Schemes. Molecular Biology and Evolution, 2011, 28, 2577-2589.	8.9	144
24	Phylodynamics with Migration: A Computational Framework to Quantify Population Structure from Genomic Data. Molecular Biology and Evolution, 2016, 33, 2102-2116.	8.9	131
25	Uncovering epidemiological dynamics in heterogeneous host populations using phylogenetic methods. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120198.	4.0	117
26	Recovering speciation and extinction dynamics based on phylogenies. Journal of Evolutionary Biology, 2013, 26, 1203-1219.	1.7	116
27	Tracking the international spread of SARS-CoV-2 lineages B.1.1.7 and B.1.351/501Y-V2. Wellcome Open Research, 2021, 6, 121.	1.8	115
28	Phylogenetic Approach Reveals That Virus Genotype Largely Determines HIV Set-Point Viral Load. PLoS Pathogens, 2010, 6, e1001123.	4.7	108
29	Birth–death models and coalescent point processes: The shape and probability of reconstructed phylogenies. Theoretical Population Biology, 2013, 90, 113-128.	1.1	107
30	The relationship between transmission time and clustering methods in Mycobacterium tuberculosis epidemiology. EBioMedicine, 2018, 37, 410-416.	6.1	106
31	Simultaneous reconstruction of evolutionary history and epidemiological dynamics from viral sequences with the birth–death SIR model. Journal of the Royal Society Interface, 2014, 11, 20131106.	3.4	104
32	Epiphytic leafy liverworts diversified in angiosperm-dominated forests. Scientific Reports, 2014, 4, 5974.	3.3	104
33	How Can We Improve Accuracy of Macroevolutionary Rate Estimates?. Systematic Biology, 2013, 62, 321-329.	5.6	99
34	The Structured Coalescent and Its Approximations. Molecular Biology and Evolution, 2017, 34, 2970-2981.	8.9	98
35	Wastewater-Based Estimation of the Effective Reproductive Number of SARS-CoV-2. Environmental Health Perspectives, 2022, 130, .	6.0	92
36	Vaccination of dogs in an African city interrupts rabies transmission and reduces human exposure. Science Translational Medicine, 2017, 9, .	12.4	87

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37	Inferring Epidemic Contact Structure from Phylogenetic Trees. PLoS Computational Biology, 2012, 8, e1002413.	3.2	85
38	The fossilized birth-death model for the analysis of stratigraphic range data under different speciation modes. Journal of Theoretical Biology, 2018, 447, 41-55.	1.7	83
39	The origin and early spread of SARS-CoV-2 in Europe. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	83
40	Bayesian Evaluation of Temporal Signal in Measurably Evolving Populations. Molecular Biology and Evolution, 2020, 37, 3363-3379.	8.9	81
41	Dating Phylogenies with Sequentially Sampled Tips. Systematic Biology, 2013, 62, 674-688.	5.6	79
42	Taming the BEAST—A Community Teaching Material Resource for BEAST 2. Systematic Biology, 2018, 67, 170-174.	5.6	79
43	MASCOT: parameter and state inference under the marginal structured coalescent approximation. Bioinformatics, 2018, 34, 3843-3848.	4.1	78
44	Sampling Trees from Evolutionary Models. Systematic Biology, 2010, 59, 465-476.	5.6	75
45	Closing the gap between palaeontological and neontological speciation and extinction rate estimates. Nature Communications, 2018, 9, 5237.	12.8	72
46	Insights into the Early Epidemic Spread of Ebola in Sierra Leone Provided by Viral Sequence Data. PLOS Currents, 2014, 6, .	1.4	71
47	FOSSILS AND A LARGE MOLECULAR PHYLOGENY SHOW THAT THE EVOLUTION OF SPECIES RICHNESS, GENERIC DIVERSITY, AND TURNOVER RATES ARE DISCONNECTED. Evolution; International Journal of Organic Evolution, 2014, 68, 2821-2832.	2.3	70
48	Outbreak investigation for toxigenic Corynebacterium diphtheriae wound infections in refugees from Northeast Africa and Syria in Switzerland and Germany by whole genome sequencing. Clinical Microbiology and Infection, 2016, 22, 1003.e1-1003.e8.	6.0	70
49	Early detection and surveillance of SARS-CoV-2 genomic variants in wastewater using COJAC. Nature Microbiology, 2022, 7, 1151-1160.	13.3	69
50	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 12522-12523.	7.1	68
51	Branch Lengths on Birth–Death Trees and the Expected Loss of Phylogenetic Diversity. Systematic Biology, 2012, 61, 195-203.	5.6	67
52	Plasmid- and strain-specific factors drive variation in ESBL-plasmid spread in vitro and in vivo. ISME Journal, 2021, 15, 862-878.	9.8	66
53	Reproductive number of the COVID-19 epidemic in Switzerland with a focus on the Cantons of Basel-Stadt and Basel-Landschaft. Swiss Medical Weekly, 2020, 150, w20271.	1.6	64
54	Age-Dependent Speciation Can Explain the Shape of Empirical Phylogenies. Systematic Biology, 2015, 64, 432-440.	5.6	63

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55	A New Method for Handling Missing Species in Diversification Analysis Applicable to Randomly or Nonrandomly Sampled Phylogenies. Systematic Biology, 2012, 61, 785-792.	5.6	62
56	New Analytic Results for Speciation Times in Neutral Models. Bulletin of Mathematical Biology, 2008, 70, 1082-1097.	1.9	60
57	Inference of Epidemiological Dynamics Based on Simulated Phylogenies Using Birth-Death and Coalescent Models. PLoS Computational Biology, 2014, 10, e1003913.	3.2	58
58	Using an Epidemiological Model for Phylogenetic Inference Reveals Density Dependence in HIV Transmission. Molecular Biology and Evolution, 2014, 31, 6-17.	8.9	55
59	Inferring speciation and extinction processes from extant species data. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16145-16146.	7.1	54
60	Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison. Molecular Biology and Evolution, 2017, 34, 185-203.	8.9	53
61	Quantifying the fitness cost of HIV-1 drug resistance mutations through phylodynamics. PLoS Pathogens, 2018, 14, e1006895.	4.7	53
62	Detection and Genome Sequencing of SARS-CoV-2 in a Domestic Cat with Respiratory Signs in Switzerland. Viruses, 2021, 13, 496.	3.3	53
63	Distribution of branch lengths and phylogenetic diversity under homogeneous speciation models. Journal of Theoretical Biology, 2012, 297, 33-40.	1.7	52
64	Mathematical and Computational Evolutionary Biology (2013). Systematic Biology, 2015, 64, 1-2.	5.6	52
65	Phylodynamics of Enterovirus A71-Associated Hand, Foot, and Mouth Disease in Viet Nam. Journal of Virology, 2015, 89, 8871-8879.	3.4	51
66	Phylodynamics for cell biologists. Science, 2021, 371, .	12.6	51
67	Comparison of methods for phylogenetic B-cell lineage inference using time-resolved antibody repertoire simulations (AbSim). Bioinformatics, 2017, 33, 3938-3946.	4.1	50
68	lgnoring stratigraphic age uncertainty leads to erroneous estimates of species divergence times under the fossilized birth–death process. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20190685.	2.6	50
69	Stochastic properties of generalised Yule models, with biodiversity applications. Journal of Mathematical Biology, 2008, 57, 713-735.	1.9	47
70	The abrupt climate change at the Eocene–Oligocene boundary and the emergence of South-East Asia triggered the spread of sapindaceous lineages. Annals of Botany, 2013, 112, 151-160.	2.9	46
71	The probability distribution of ranked gene trees on a species tree. Mathematical Biosciences, 2012, 235, 45-55.	1.9	44
72	On Age and Species Richness of Higher Taxa. American Naturalist, 2014, 184, 447-455.	2.1	44

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73	A Multitype Birth–Death Model for Bayesian Inference of Lineage-Specific Birth and Death Rates. Systematic Biology, 2020, 69, 973-986.	5.6	44
74	Testing the spatial and temporal framework of speciation in an ancient lake species flock: the leech genus <i>Dina</i> (Hirudinea: Erpobdellidae) in Lake Ohrid. Biogeosciences, 2010, 7, 3387-3402.	3.3	40
75	Estimating Speciation and Extinction Rates for Phylogenies of Higher Taxa. Systematic Biology, 2013, 62, 220-230.	5.6	40
76	On the Need for Mechanistic Models in Computational Genomics and Metagenomics. Genome Biology and Evolution, 2013, 5, 2008-2018.	2.5	40
77	Estimating Epidemic Incidence and Prevalence from Genomic Data. Molecular Biology and Evolution, 2019, 36, 1804-1816.	8.9	39
78	Getting to the root of epidemic spread with phylodynamic analysis of genomic data. Trends in Microbiology, 2015, 23, 383-386.	7.7	36
79	Lineages-through-time plots of neutral models for speciation. Mathematical Biosciences, 2008, 216, 163-171.	1.9	35
80	Impact of the tree prior on estimating clock rates during epidemic outbreaks. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4200-4205.	7.1	35
81	Ignoring Fossil Age Uncertainty Leads to Inaccurate Topology and Divergence Time Estimates in Time Calibrated Tree Inference. Frontiers in Ecology and Evolution, 2020, 8, .	2.2	35
82	Bayesian inference of reassortment networks reveals fitness benefits of reassortment in human influenza viruses. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17104-17111.	7.1	35
83	Bayesian phylogenetic estimation of fossil ages. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20150129.	4.0	34
84	Quantitative and Qualitative Analysis of Humoral Immunity Reveals Continued and Personalized Evolution in Chronic Viral Infection. Cell Reports, 2020, 30, 997-1012.e6.	6.4	34
85	Quantification of the spread of SARS-CoV-2 variant B.1.1.7 in Switzerland. Epidemics, 2021, 37, 100480.	3.0	34
86	Transmission of ESBL-producing Enterobacteriaceae and their mobile genetic elements—identification of sources by whole genome sequencing: study protocol for an observational study in Switzerland. BMJ Open, 2018, 8, e021823.	1.9	32
87	Quantifying Age-dependent Extinction from Species Phylogenies. Systematic Biology, 2016, 65, 35-50.	5.6	31
88	The influence of phylodynamic model specifications on parameter estimates of the Zika virus epidemic. Virus Evolution, 2018, 4, vex044.	4.9	31
89	Automatic generation of evolutionary hypotheses using mixed Gaussian phylogenetic models. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16921-16926.	7.1	31
90	Fast likelihood calculation for multivariate Gaussian phylogenetic models with shifts. Theoretical Population Biology, 2020, 131, 66-78.	1.1	31

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91	A Method for Investigating Relative Timing Information on Phylogenetic Trees. Systematic Biology, 2009, 58, 167-183.	5.6	30
92	Inferring Epidemiological Dynamics with Bayesian Coalescent Inference: The Merits of Deterministic and Stochastic Models. Genetics, 2015, 199, 595-607.	2.9	30
93	Assessing the impact of incomplete species sampling on estimates of speciation and extinction rates. Paleobiology, 2020, 46, 137-157.	2.0	30
94	How well can the exponential-growth coalescent approximate constant-rate birth–death population dynamics?. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20150420.	2.6	29
95	Assessment of Overlap of Phylogenetic Transmission Clusters and Communities in Simple Sexual Contact Networks: Applications to HIV-1. PLoS ONE, 2016, 11, e0148459.	2.5	28
96	Tracing Antibody Repertoire Evolution by Systems Phylogeny. Frontiers in Immunology, 2018, 9, 2149.	4.8	26
97	Social Meets Molecular: Combining Phylogenetic and Latent Class Analyses to Understand HIV-1 Transmission in Switzerland. American Journal of Epidemiology, 2014, 179, 1514-1525.	3.4	25
98	Phylodynamic Model Adequacy Using Posterior Predictive Simulations. Systematic Biology, 2019, 68, 358-364.	5.6	25
99	Inferring Epidemiological Parameters on the Basis of Allele Frequencies. Genetics, 2011, 188, 663-672.	2.9	24
100	A transmissible cancer shifts from emergence to endemism in Tasmanian devils. Science, 2020, 370, .	12.6	24
101	Origins of Biodiversity—Response. Science, 2011, 331, 399-400.	12.6	23
102	Origin, imports and exports of HIV-1 subtype C in South Africa: A historical perspective. Infection, Genetics and Evolution, 2016, 46, 200-208.	2.3	23
103	Tracking external introductions of HIV using phylodynamics reveals a major source of infections in rural KwaZulu-Natal, South Africa. Virus Evolution, 2018, 4, vey037.	4.9	22
104	Detection of HIV transmission clusters from phylogenetic trees using a multi-state birth–death model. Journal of the Royal Society Interface, 2018, 15, 20180512.	3.4	22
105	Earlier Initiation of Antiretroviral Treatment Coincides With an Initial Control of the HIV-1 Sub-Subtype F1 Outbreak Among Men-Having-Sex-With-Men in Flanders, Belgium. Frontiers in Microbiology, 2019, 10, 613.	3.5	21
106	Inferring time-dependent migration and coalescence patterns from genetic sequence and predictor data in structured populations. Virus Evolution, 2019, 5, vez030.	4.9	20
107	<i>TreeSim<scp>GM</scp></i> : Simulating phylogenetic trees under general Bellman–Harris models with lineageâ€specific shifts of speciation and extinction in R. Methods in Ecology and Evolution, 2018, 9, 754-760.	5.2	19
108	Tuberculosis outbreak investigation using phylodynamic analysis. Epidemics, 2018, 25, 47-53.	3.0	19

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109	Does Gene Tree Discordance Explain the Mismatch between Macroevolutionary Models and Empirical Patterns of Tree Shape and Branching Times?. Systematic Biology, 2016, 65, 628-639.	5.6	18
110	A Practical Guide to Estimating the Heritability of Pathogen Traits. Molecular Biology and Evolution, 2018, 35, 756-772.	8.9	18
111	Coupling adaptive molecular evolution to phylodynamics using fitness-dependent birth-death models. ELife, 2019, 8, .	6.0	18
112	Exact vs. Approximate Computation: Reconciling Different Estimates of Mycobacterium tuberculosis Epidemiological Parameters. Genetics, 2014, 196, 1227-1230.	2.9	17
113	Characterising the epidemic spread of influenza A/H3N2 within a city through phylogenetics. PLoS Pathogens, 2020, 16, e1008984.	4.7	17
114	UNEXPECTEDLY MANY EXTINCT HOMININS. Evolution; International Journal of Organic Evolution, 2012, 66, 2969-2974.	2.3	16
115	Finding the best resolution for the Kingman–Tajima coalescent: theory and applications. Journal of Mathematical Biology, 2015, 70, 1207-1247.	1.9	16
116	Phylodynamics on local sexual contact networks. PLoS Computational Biology, 2017, 13, e1005448.	3.2	16
117	A Characterization of the Set of Species Trees that Produce Anomalous Ranked Gene Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1558-1568.	3.0	15
118	On the statistical analysis of single cell lineage trees. Journal of Theoretical Biology, 2018, 439, 160-165.	1.7	15
119	The probability distribution of the reconstructed phylogenetic tree with occurrence data. Journal of Theoretical Biology, 2020, 488, 110115.	1.7	13
120	Quantifying transmission fitness costs of multi-drug resistant tuberculosis. Epidemics, 2021, 36, 100471.	3.0	13
121	Exploring the power of Bayesian birthâ€death skyline models to detect mass extinction events from phylogenies with only extant taxa. Evolution; International Journal of Organic Evolution, 2019, 73, 1133-1150.	2.3	12
122	PIQMEE: Bayesian Phylodynamic Method for Analysis of Large Data Sets with Duplicate Sequences. Molecular Biology and Evolution, 2020, 37, 3061-3075.	8.9	12
123	The probability distribution of the ancestral population size conditioned on the reconstructed phylogenetic tree with occurrence data. Journal of Theoretical Biology, 2021, 509, 110400.	1.7	12
124	A polynomial time algorithm for calculating the probability of a ranked gene tree given a species tree. Algorithms for Molecular Biology, 2012, 7, 7.	1.2	11
125	Analyzing and reconstructing reticulation networks under timing constraints. Journal of Mathematical Biology, 2010, 61, 715-737.	1.9	10
126	Swapping Birth and Death: Symmetries and Transformations in Phylodynamic Models. Systematic Biology, 2019, 68, 852-858.	5.6	10

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127	The Occurrence Birth–Death Process for Combined-Evidence Analysis in Macroevolution and Epidemiology. Systematic Biology, 2022, 71, 1440-1452.	5.6	10
128	Evaluation of two workflows for whole genome sequencing-based typing of influenza A viruses. Journal of Virological Methods, 2019, 266, 30-33.	2.1	9
129	Novel Integrative Modeling of Molecules and Morphology across Evolutionary Timescales. Systematic Biology, 2021, 71, 208-220.	5.6	9
130	What can phylodynamics bring to animal health research?. Trends in Ecology and Evolution, 2021, 36, 837-847.	8.7	9
131	Joint Inference of Migration and Reassortment Patterns for Viruses with Segmented Genomes. Molecular Biology and Evolution, 2022, 39, .	8.9	9
132	Phylogenetic analysis accounting for age-dependent death and sampling with applications to epidemics. Journal of Theoretical Biology, 2014, 352, 60-70.	1.7	8
133	SARS-CoV-2 Vaccine Alpha and Delta Variant Breakthrough Infections Are Rare and Mild but Can Happen Relatively Early after Vaccination. Microorganisms, 2022, 10, 857.	3.6	8
134	Parallel likelihood calculation for phylogenetic comparative models: The <scp>SPLITT</scp> C++ library. Methods in Ecology and Evolution, 2019, 10, 493-506.	5.2	7
135	Identification of influenza urban transmission patterns by geographical, epidemiological and whole genome sequencing data: protocol for an observational study. BMJ Open, 2019, 9, e030913.	1.9	7
136	Estimating shifts in diversification rates based on higher-level phylogenies. Biology Letters, 2016, 12, 20160273.	2.3	6
137	Asymmetric division events promote variability in cell cycle duration in animal cells and Escherichia coli. Nature Communications, 2019, 10, 1901.	12.8	6
138	Inter- and intraspecies comparison of phylogenetic fingerprints and sequence diversity of immunoglobulin variable genes. Immunogenetics, 2020, 72, 279-294.	2.4	5
139	IgM Antibody Repertoire Fingerprints in Mice Are Personalized but Robust to Viral Infection Status. Frontiers in Cellular and Infection Microbiology, 2020, 10, 254.	3.9	5
140	DeepSARS: simultaneous diagnostic detection and genomic surveillance of SARS-CoV-2. BMC Genomics, 2022, 23, 289.	2.8	5
141	Estimating the Relative Order of Speciation or Coalescence Events on a Given Phylogeny. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	1.2	3
142	Identification of a Cluster of Extended-spectrum Beta-Lactamase–Producing Klebsiella pneumoniae Sequence Type 101 Isolated From Food and Humans. Clinical Infectious Diseases, 2020, 73, 332-335.	5.8	3
143	Advancing genomic epidemiology by addressing the bioinformatics bottleneck: Challenges, design principles, and a Swiss example. Epidemics, 2022, , 100576.	3.0	3
144	Response to Comment on "Impacts of the Cretaceous Terrestrial Revolution and KPg Extinction on Mammal Diversification― Science, 2012, 337, 34-34.	12.6	2

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145	Species-specific diversification. Nature Ecology and Evolution, 2019, 3, 1003-1004.	7.8	2
146	Mathematical Models for the Epidemiology and Evolution of Mycobacterium tuberculosis. Advances in Experimental Medicine and Biology, 2017, 1019, 281-307.	1.6	1