

# Iñaki Comas

## List of Publications by Year in descending order

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Version: 2024-02-01

130  
papers

9,271  
citations

93792

39  
h-index

56606

87  
g-index

151  
all docs

151  
docs citations

151  
times ranked

10621  
citing authors

#	ARTICLE	IF	CITATIONS
1	Recurrences of multidrug-resistant tuberculosis: Strains involved, within-host diversity, and fine-tuned allocation of reinfections. <i>Transboundary and Emerging Diseases</i> , 2022, 69, 327-336.	1.3	6
2	Immunological response against SARS-CoV-2 following full-dose administration of Comirnaty® COVID-19 vaccine in nursing home residents. <i>Clinical Microbiology and Infection</i> , 2022, 28, 279-284.	2.8	17
3	Systematic Genomic and Clinical Analysis of Severe Acute Respiratory Syndrome Coronavirus 2 Reinfections and Recurrences Involving the Same Strain. <i>Emerging Infectious Diseases</i> , 2022, 28, 86-95.	2.0	8
4	Severe Acute Respiratory Syndrome Coronavirus 2 Adaptive Immunity in Nursing Home Residents Following a Third Dose of the Comirnaty Coronavirus Disease 2019 Vaccine. <i>Clinical Infectious Diseases</i> , 2022, 75, e865-e868.	2.9	12
5	SARS-CoV-2 adaptive immunity in nursing home residents up to eight months after two doses of the Comirnaty® COVID-19 vaccine. <i>Journal of Infection</i> , 2022, 84, 834-872.	1.7	2
6	SNPs in Genes Related to DNA Damage Repair in Mycobacterium Tuberculosis: Their Association with Type 2 Diabetes Mellitus and Drug Resistance. <i>Genes</i> , 2022, 13, 609.	1.0	3
7	The 2021 WHO catalogue of Mycobacterium tuberculosis complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273.	3.4	114
8	SARS-CoV-2 Delta variant breakthrough infections in nursing home residents at midterm after Comirnaty® COVID-19 vaccination. <i>Journal of Medical Virology</i> , 2022, 94, 3776-3782.	2.5	6
9	Gene evolutionary trajectories in <i>Mycobacterium tuberculosis</i> reveal temporal signs of selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2113600119.	3.3	13
10	SARS-CoV-2 Omicron BA.1 variant breakthrough infections in nursing home residents after an homologous third dose of the Comirnaty® COVID-19 vaccine: Looking for correlates of protection. <i>Journal of Medical Virology</i> , 2022, 94, 4216-4223.	2.5	15
11	Whole genome sequencing analysis to evaluate the influence of T2DM on polymorphisms associated with drug resistance in <i>M. tuberculosis</i> . <i>BMC Genomics</i> , 2022, 23, .	1.2	1
12	Fine-grain population structure and transmission patterns of Mycobacterium tuberculosis in southern Mozambique, a high TB/HIV burden area. <i>Microbial Genomics</i> , 2022, 8, .	1.0	4
13	The structural role of SARS-CoV-2 genetic background in the emergence and success of spike mutations: The case of the spike A222V mutation. <i>PLoS Pathogens</i> , 2022, 18, e1010631.	2.1	11
14	B-type natriuretic peptide over N-terminal pro-brain natriuretic peptide to predict incident atrial fibrillation after cryptogenic stroke. <i>European Journal of Neurology</i> , 2021, 28, 540-547.	1.7	20
15	Whole genomic sequencing based genotyping reveals a specific X3 sublineage restricted to Mexico and related with multidrug resistance. <i>Scientific Reports</i> , 2021, 11, 1870.	1.6	8
16	Local adaptation in populations of Mycobacterium tuberculosis endemic to the Indian Ocean Rim. <i>F1000Research</i> , 2021, 10, 60.	0.8	13
17	Epidemiological, clinical and genomic snapshot of the first 100 B.1.1.7 SARS-CoV-2 cases in Madrid. <i>Journal of Travel Medicine</i> , 2021, 28, .	1.4	3
18	Whole-genome sequencing for TB source investigations: principles of ethical precision public health. <i>International Journal of Tuberculosis and Lung Disease</i> , 2021, 25, 222-227.	0.6	1

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19	Local adaptation in populations of Mycobacterium tuberculosis endemic to the Indian Ocean Rim. <i>F1000Research</i> , 2021, 10, 60.	0.8	21
20	Overlapping prison/community tuberculosis outbreaks in Costa Rica revealed by alternative analysis of suboptimal material. <i>Transboundary and Emerging Diseases</i> , 2021, , .	1.3	0
21	Integrative transnational analysis to dissect tuberculosis transmission events along the migratory route from Africa to Europe. <i>Journal of Travel Medicine</i> , 2021, 28, .	1.4	7
22	Genomic analyses of Mycobacterium tuberculosis from human lung resections reveal a high frequency of polyclonal infections. <i>Nature Communications</i> , 2021, 12, 2716.	5.8	25
23	Proper Assignment of Reactivation in a COVID-19 Recurrence Initially Interpreted as a Reinfection. <i>Journal of Infectious Diseases</i> , 2021, 224, 788-792.	1.9	5
24	SplitStrains, a tool to identify and separate mixed Mycobacterium tuberculosis infections from WGS data. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
25	Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. <i>Nature</i> , 2021, 595, 707-712.	13.7	363
26	Heterogeneous Streptomycin Resistance Level Among Mycobacterium tuberculosis Strains From the Same Transmission Cluster. <i>Frontiers in Microbiology</i> , 2021, 12, 659545.	1.5	10
27	Different Within-Host Viral Evolution Dynamics in Severely Immunosuppressed Cases with Persistent SARS-CoV-2. <i>Biomedicines</i> , 2021, 9, 808.	1.4	28
28	Overlapping of Independent SARS-CoV-2 Nosocomial Transmissions in a Complex Outbreak. <i>MSphere</i> , 2021, 6, e0038921.	1.3	9
29	Host Genetic Analysis Should Be Mandatory for Proper Classification of COVID-19 Reinfections. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab402.	0.4	1
30	The Sputum Microbiome in Pulmonary Tuberculosis and Its Association With Disease Manifestations: A Cross-Sectional Study. <i>Frontiers in Microbiology</i> , 2021, 12, 633396.	1.5	9
31	The first wave of the COVID-19 epidemic in Spain was associated with early introductions and fast spread of a dominating genetic variant. <i>Nature Genetics</i> , 2021, 53, 1405-1414.	9.4	35
32	Complete Analysis of the Epidemiological Scenario around a SARS-CoV-2 Reinfection: Previous Infection Events and Subsequent Transmission. <i>MSphere</i> , 2021, 6, e0059621.	1.3	4
33	Expanded tracking of a Beijing Mycobacterium tuberculosis strain involved in an outbreak in France. <i>Travel Medicine and Infectious Disease</i> , 2021, 44, 102167.	1.5	2
34	An evolutionary functional genomics approach identifies novel candidate regions involved in isoniazid resistance in Mycobacterium tuberculosis. <i>Communications Biology</i> , 2021, 4, 1322.	2.0	5
35	Evolutionary and Phenotypic Characterization of Two Spike Mutations in European Lineage 20E of SARS-CoV-2. <i>MBio</i> , 2021, 12, e0231521.	1.8	6
36	A Genomic Snapshot of the SARS-CoV-2 Pandemic in the Balearic Islands. <i>Frontiers in Microbiology</i> , 2021, 12, 803827.	1.5	3

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37	SARS-CoV-2 Outbreak on a Spanish Mink Farm: Epidemiological, Molecular, and Pathological Studies. <i>Frontiers in Veterinary Science</i> , 2021, 8, 805004.	0.9	14
38	Accuracy of an amplicon-sequencing nanopore approach to identify variants in tuberculosis drug-resistance-associated genes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
39	Towards next-generation diagnostics for tuberculosis: identification of novel molecular targets by large-scale comparative genomics. <i>Bioinformatics</i> , 2020, 36, 985-989.	1.8	13
40	Characterization of Polymorphisms Associated with Multidrug-Resistant Tuberculosis by Whole Genomic Sequencing: A Preliminary Report from Mexico. <i>Microbial Drug Resistance</i> , 2020, 26, 732-740.	0.9	4
41	Uso de las tecnologías de secuenciación masiva para el diagnóstico y epidemiología de enfermedades infecciosas. <i>Enfermedades Infecciosas Y Microbiología Clínica</i> , 2020, 38, 32-38.	0.3	1
42	Whole-genome sequencing of <i>Mycobacterium tuberculosis</i> directly from clinical samples for high-resolution genomic epidemiology and drug resistance surveillance: an observational study. <i>Lancet Microbe</i> , The, 2020, 1, e175-e183.	3.4	42
43	Glucocorticoid-dependent transcription in skin requires epidermal expression of the glucocorticoid receptor and is modulated by the mineralocorticoid receptor. <i>Scientific Reports</i> , 2020, 10, 18954.	1.6	4
44	<i>Mycobacterium tuberculosis</i> clinical isolates carry mutational signatures of host immune environments. <i>Science Advances</i> , 2020, 6, eaba4901.	4.7	33
45	GenomeMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 2450-2460.	3.5	25
46	Contaminant DNA in bacterial sequencing experiments is a major source of false genetic variability. <i>BMC Biology</i> , 2020, 18, 24.	1.7	53
47	Specificity and mutagenesis bias of the mycobacterial alternative mismatch repair analyzed by mutation accumulation studies. <i>Science Advances</i> , 2020, 6, eaay4453.	4.7	30
48	Screening of inmates transferred to Spain reveals a Peruvian prison as a reservoir of persistent <i>Mycobacterium tuberculosis</i> MDR strains and mixed infections. <i>Scientific Reports</i> , 2020, 10, 2704.	1.6	12
49	<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
50	Geographical and temporal distribution of SARS-CoV-2 clades in the WHO European Region, January to June 2020. <i>Eurosurveillance</i> , 2020, 25, .	3.9	186
51	Tuberculosis in Liberia: high multidrug-resistance burden, transmission and diversity modelled by multiple importation events. <i>Microbial Genomics</i> , 2020, 6, .	1.0	11
52	The Future of TB Resistance Diagnosis: The Essentials on Whole Genome Sequencing and Rapid Testing Methods. <i>Archivos De Bronconeumologia</i> , 2019, 55, 421-426.	0.4	0
53	The Future of TB Resistance Diagnosis: The Essentials on Whole Genome Sequencing and Rapid Testing Methods. <i>Archivos De Bronconeumologia</i> , 2019, 55, 421-426.	0.4	7
54	Development and application of affordable SNP typing approaches to genotype <i>Mycobacterium tuberculosis</i> complex strains in low and high burden countries. <i>Scientific Reports</i> , 2019, 9, 15343.	1.6	8

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55	High-resolution mapping of tuberculosis transmission: Whole genome sequencing and phylogenetic modelling of a cohort from Valencia Region, Spain. <i>PLoS Medicine</i> , 2019, 16, e1002961.	3.9	62
56	Influence of Gut Microbiota on Progression to Tuberculosis Generated by High Fat Diet-Induced Obesity in C3HeB/FeJ Mice. <i>Frontiers in Immunology</i> , 2019, 10, 2464.	2.2	26
57	Genome-wide mutational biases fuel transcriptional diversity in the <i>Mycobacterium tuberculosis</i> complex. <i>Nature Communications</i> , 2019, 10, 3994.	5.8	33
58	Evolutionary Dissection of the Dot/Icm System Based on Comparative Genomics of 58 <i>Legionella</i> Species. <i>Genome Biology and Evolution</i> , 2019, 11, 2619-2632.	1.1	12
59	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
60	Whole genomic sequencing as a tool for diagnosis of drug and multidrug-resistance tuberculosis in an endemic region in Mexico. <i>PLoS ONE</i> , 2019, 14, e0213046.	1.1	20
61	Genomic determinants of speciation and spread of the <i>Mycobacterium tuberculosis</i> complex. <i>Science Advances</i> , 2019, 5, eaaw3307.	4.7	61
62	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019, 35, 3240-3249.	1.8	38
63	Cryptic Resistance Mutations Associated With Misdiagnoses of Multidrug-Resistant Tuberculosis. <i>Journal of Infectious Diseases</i> , 2019, 220, 316-320.	1.9	19
64	Simplified Model to Survey Tuberculosis Transmission in Countries Without Systematic Molecular Epidemiology Programs. <i>Emerging Infectious Diseases</i> , 2019, 25, 507-514.	2.0	5
65	Large genomics datasets shed light on the evolution of the <i>Mycobacterium tuberculosis</i> complex. <i>Infection, Genetics and Evolution</i> , 2019, 72, 10-15.	1.0	11
66	Application of machine learning techniques to tuberculosis drug resistance analysis. <i>Bioinformatics</i> , 2019, 35, 2276-2282.	1.8	71
67	Antibiotic resistance prediction for <i>Mycobacterium tuberculosis</i> from genome sequence data with Mykrobe. <i>Wellcome Open Research</i> , 2019, 4, 191.	0.9	103
68	Whole genome sequencing-based analysis of tuberculosis (TB) in migrants: rapid tools for cross-border surveillance and to distinguish between recent transmission in the host country and new importations. <i>Eurosurveillance</i> , 2019, 24, .	3.9	22
69	Tuberculosis of the elbow: A rare form of presentation of extrapulmonary tuberculosis. <i>Enfermedades Infecciosas Y Microbiología Clínica</i> , 2019, 37, 550-551.	0.3	1
70	Gene expression models based on a reference laboratory strain are poor predictors of <i>Mycobacterium tuberculosis</i> complex transcriptional diversity. <i>Scientific Reports</i> , 2018, 8, 3813.	1.6	14
71	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018, 379, 1403-1415.	13.9	405
72	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

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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	TB Transmission: Closing the Gaps. <i>EBioMedicine</i> , 2018, 34, 4-5.	2.7	1
75	The Troika Host-Pathogen-Extrinsic Factors in Tuberculosis: Modulating Inflammation and Clinical Outcomes. <i>Frontiers in Immunology</i> , 2018, 8, 1948.	2.2	24
76	Mycobacterium tuberculosis Acquires Limited Genetic Diversity in Prolonged Infections, Reactivations and Transmissions Involving Multiple Hosts. <i>Frontiers in Microbiology</i> , 2018, 8, 2661.	1.5	12
77	Whole-genome sequence analysis of the Mycobacterium avium complex and proposal of the transfer of Mycobacterium yongonense to Mycobacterium intracellulare subsp. yongonense subsp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 1998-2005.	0.8	25
78	The effect size of type 2 diabetes mellitus on tuberculosis drug resistance and adverse treatment outcomes. <i>Tuberculosis</i> , 2017, 103, 83-91.	0.8	33
79	The Evolution of Antibiotic Resistance. , 2017, , 257-284.		3
80	Genomic Epidemiology of Tuberculosis. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1019, 79-93.	0.8	21
81	A novel strategy based on genomics and specific PCR reveals how a multidrug-resistant Mycobacterium tuberculosis strain became prevalent in Equatorial Guinea 15 years after its emergence. <i>Clinical Microbiology and Infection</i> , 2017, 23, 92-97.	2.8	11
82	A standardised method for interpreting the association between mutations and phenotypic drug resistance in Mycobacterium tuberculosis. <i>European Respiratory Journal</i> , 2017, 50, 1701354.	3.1	273
83	In-Depth Characterization and Functional Analysis of Clonal Variants in a Mycobacterium tuberculosis Strain Prone to Microevolution. <i>Frontiers in Microbiology</i> , 2017, 8, 694.	1.5	11
84	Draft Genome Sequence of Mycobacterium brumae ATCC 51384. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
85	New Genome-Wide Algorithm Identifies Novel In-Vivo Expressed Mycobacterium Tuberculosis Antigens Inducing Human T-Cell Responses with Classical and Unconventional Cytokine Profiles. <i>Scientific Reports</i> , 2016, 6, 37793.	1.6	69
86	Subtle genotypic changes can be observed soon after diagnosis in Mycobacterium tuberculosis infection. <i>International Journal of Medical Microbiology</i> , 2016, 306, 401-405.	1.5	5
87	Genomic Analysis of Bacterial Outbreaks. , 2016, , 203-232.		0
88	Urgent Implementation in a Hospital Setting of a Strategy To Rule Out Secondary Cases Caused by Imported Extensively Drug-Resistant Mycobacterium tuberculosis Strains at Diagnosis. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2969-2974.	1.8	15
89	Mycobacterium tuberculosis lineage 4 comprises globally distributed and geographically restricted sublineages. <i>Nature Genetics</i> , 2016, 48, 1535-1543.	9.4	326
90	Legionella effectors reflect strength in diversity. <i>Nature Genetics</i> , 2016, 48, 115-116.	9.4	1

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91	Ultrafast Assessment of the Presence of a High-Risk <i>Mycobacterium tuberculosis</i> Strain in a Population. <i>Journal of Clinical Microbiology</i> , 2016, 54, 779-781.	1.8	18
92	Phylogenetic analysis of vitamin B12-related metabolism in <i>Mycobacterium tuberculosis</i> . <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 6.	1.6	27
93	Draft Genome Sequences of <i>Mycobacterium setense</i> Type Strain DSM-45070 and the Nonpathogenic Strain <i>Manresensis</i> , Isolated from the Bank of the Cardener River in Manresa, Catalonia, Spain. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
94	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
95	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
96	Persistent Infection by a <i>Mycobacterium tuberculosis</i> Strain That Was Theorized To Have Advantageous Properties, as It Was Responsible for a Massive Outbreak. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3423-3429.	1.8	21
97	Fast and low-cost decentralized surveillance of transmission of tuberculosis based on strain-specific PCRs tailored from whole genome sequencing data: a pilot study. <i>Clinical Microbiology and Infection</i> , 2015, 21, 249.e1-249.e9.	2.8	22
98	Comment on: Characterization of the <i>embB</i> gene in <i>Mycobacterium tuberculosis</i> 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, 2298-2299.	1.3	8
99	Whole Genome Sequencing Analysis of Inpatient Microevolution in <i>Mycobacterium tuberculosis</i> : Potential Impact on the Inference of Tuberculosis Transmission. <i>Journal of Infectious Diseases</i> , 2014, 209, 98-108.	1.9	120
100	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. <i>Nature</i> , 2014, 514, 494-497.	13.7	506
101	Recombination drives genome evolution in outbreak-related <i>Legionella pneumophila</i> isolates. <i>Nature Genetics</i> , 2014, 46, 1205-1211.	9.4	76
102	Genetic diversity within <i>Mycobacterium tuberculosis</i> complex impacts on the accuracy of genotypic pyrazinamide drug-susceptibility assay. <i>Tuberculosis</i> , 2014, 94, 451-453.	0.8	11
103	Evaluation of Customised Lineage-Specific Sets of MIRU-VNTR Loci for Genotyping <i>Mycobacterium tuberculosis</i> Complex Isolates in Ghana. <i>PLoS ONE</i> , 2014, 9, e92675.	1.1	19
104	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
105	Genome-wide Mapping of Transcriptional Start Sites Defines an Extensive Leaderless Transcriptome in <i>Mycobacterium tuberculosis</i> . <i>Cell Reports</i> , 2013, 5, 1121-1131.	2.9	283
106	<i>Mycobacterial</i> Lineages Causing Pulmonary and Extrapulmonary Tuberculosis, Ethiopia. <i>Emerging Infectious Diseases</i> , 2013, 19, 460-463.	2.0	215
107	Novel <i>Mycobacterium tuberculosis</i> Complex Isolate from a Wild Chimpanzee. <i>Emerging Infectious Diseases</i> , 2013, 19, 969-976.	2.0	100
108	Mapping of Genotype-Phenotype Diversity among Clinical Isolates of <i>Mycobacterium tuberculosis</i> by Sequence-Based Transcriptional Profiling. <i>Genome Biology and Evolution</i> , 2013, 5, 1849-1862.	1.1	69

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109	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, 1326-1336.	3.5	43
110	Vacunes i evolució: Per què és important entendre la diversitat genètica dels patògens?. <i>Mètode Revista De Difusió De La Investigació De La Universitat De València</i> , 2013, .	0.0	0
111	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
112	Two New Rapid SNP-Typing Methods for Classifying Mycobacterium tuberculosis Complex into the Main Phylogenetic Lineages. <i>PLoS ONE</i> , 2012, 7, e41253.	1.1	120
113	Long-Range Transcriptional Control of an Operon Necessary for Virulence-Critical ESX-1 Secretion in Mycobacterium tuberculosis. <i>Journal of Bacteriology</i> , 2012, 194, 2307-2320.	1.0	36
114	Whole-genome sequencing of rifampicin-resistant Mycobacterium tuberculosis strains identifies compensatory mutations in RNA polymerase genes. <i>Nature Genetics</i> , 2012, 44, 106-110.	9.4	475
115	The Evolution of Antibiotic Resistance. , 2011, , 305-337.		6
116	A role for systems epidemiology in tuberculosis research. <i>Trends in Microbiology</i> , 2011, 19, 492-500.	3.5	71
117	Human Macrophage Responses to Clinical Isolates from the Mycobacterium tuberculosis Complex Discriminate between Ancient and Modern Lineages. <i>PLoS Pathogens</i> , 2011, 7, e1001307.	2.1	258
118	Quantifying Nonvertical Inheritance in the Evolution of Legionella pneumophila. <i>Molecular Biology and Evolution</i> , 2011, 28, 985-1001.	3.5	47
119	Sequence-Based Analysis Uncovers an Abundance of Non-Coding RNA in the Total Transcriptome of Mycobacterium tuberculosis. <i>PLoS Pathogens</i> , 2011, 7, e1002342.	2.1	210
120	Human T cell epitopes of Mycobacterium tuberculosis are evolutionarily hyperconserved. <i>Nature Genetics</i> , 2010, 42, 498-503.	9.4	642
121	Evolutionary Trajectories of Beta-Lactamase CTX-M-1 Cluster Enzymes: Predicting Antibiotic Resistance. <i>PLoS Pathogens</i> , 2010, 6, e1000735.	2.1	100
122	The Past and Future of Tuberculosis Research. <i>PLoS Pathogens</i> , 2009, 5, e1000600.	2.1	130
123	Genotyping of Genetically Monomorphic Bacteria: DNA Sequencing in Mycobacterium tuberculosis Highlights the Limitations of Current Methodologies. <i>PLoS ONE</i> , 2009, 4, e7815.	1.1	377
124	Unraveling the evolutionary history of the phosphoryl-transfer chain of the phosphoenolpyruvate:phosphotransferase system through phylogenetic analyses and genome context. <i>BMC Evolutionary Biology</i> , 2008, 8, 147.	3.2	23
125	Evolution of Snake Venom Disintegrins by Positive Darwinian Selection. <i>Molecular Biology and Evolution</i> , 2008, 25, 2391-2407.	3.5	131
126	From Phylogenetics to Phylogenomics: The Evolutionary Relationships of Insect Endosymbiotic $\beta$ -Proteobacteria as a Test Case. <i>Systematic Biology</i> , 2007, 56, 1-16.	2.7	52



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127	Phylogenetic signal and functional categories in Proteobacteria genomes. BMC Evolutionary Biology, 2007, 7, S7.	3.2	12
128	The Evolutionary Origin of Xanthomonadales Genomes and the Nature of the Horizontal Gene Transfer Process. Molecular Biology and Evolution, 2006, 23, 2049-2057.	3.5	44
129	Validating viral quasispecies with digital organisms: a re-examination of the critical mutation rate. BMC Evolutionary Biology, 2005, 5, 5.	3.2	21
130	Horizontal Gene Transfer in the Molecular Evolution of Mannose PTS Transporters. Molecular Biology and Evolution, 2005, 22, 1673-1685.	3.5	50