

# Iñaki Comas

## List of Publications by Year in descending order

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130  
papers

9,271  
citations

81900

39  
h-index

49909

87  
g-index

151  
all docs

151  
docs citations

151  
times ranked

9772  
citing authors

#	ARTICLE	IF	CITATIONS
1	Out-of-Africa migration and Neolithic coexpansion of <i>Mycobacterium tuberculosis</i> with modern humans. <i>Nature Genetics</i> , 2013, 45, 1176-1182.	21.4	900
2	Human T cell epitopes of <i>Mycobacterium tuberculosis</i> are evolutionarily hyperconserved. <i>Nature Genetics</i> , 2010, 42, 498-503.	21.4	642
3	Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. <i>Nature</i> , 2014, 514, 494-497.	27.8	506
4	Whole-genome sequencing of rifampicin-resistant <i>Mycobacterium tuberculosis</i> strains identifies compensatory mutations in RNA polymerase genes. <i>Nature Genetics</i> , 2012, 44, 106-110.	21.4	475
5	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018, 379, 1403-1415.	27.0	405
6	Genotyping of Genetically Monomorphic Bacteria: DNA Sequencing in <i>Mycobacterium tuberculosis</i> Highlights the Limitations of Current Methodologies. <i>PLoS ONE</i> , 2009, 4, e7815.	2.5	377
7	Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. <i>Nature</i> , 2021, 595, 707-712.	27.8	363
8	<i>Mycobacterium tuberculosis</i> lineage 4 comprises globally distributed and geographically restricted sublineages. <i>Nature Genetics</i> , 2016, 48, 1535-1543.	21.4	326
9	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.	6.4	283
10	A standardised method for interpreting the association between mutations and phenotypic drug resistance in <i>Mycobacterium tuberculosis</i> . <i>European Respiratory Journal</i> , 2017, 50, 1701354.	6.7	273
11	Human Macrophage Responses to Clinical Isolates from the <i>Mycobacterium tuberculosis</i> Complex Discriminate between Ancient and Modern Lineages. <i>PLoS Pathogens</i> , 2011, 7, e1001307.	4.7	258
12	Whole genome sequencing of <i>Mycobacterium tuberculosis</i> : current standards and open issues. <i>Nature Reviews Microbiology</i> , 2019, 17, 533-545.	28.6	237
13	Mycobacterial Lineages Causing Pulmonary and Extrapulmonary Tuberculosis, Ethiopia. <i>Emerging Infectious Diseases</i> , 2013, 19, 460-463.	4.3	215
14	Sequence-Based Analysis Uncovers an Abundance of Non-Coding RNA in the Total Transcriptome of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002342.	4.7	210
15	Geographical and temporal distribution of SARS-CoV-2 clades in the WHO European Region, January to June 2020. <i>Eurosurveillance</i> , 2020, 25, .	7.0	186
16	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.	7.1	142
17	Evolution of Snake Venom Disintegrins by Positive Darwinian Selection. <i>Molecular Biology and Evolution</i> , 2008, 25, 2391-2407.	8.9	131
18	The Past and Future of Tuberculosis Research. <i>PLoS Pathogens</i> , 2009, 5, e1000600.	4.7	130

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19	Two New Rapid SNP-Typing Methods for Classifying <i>Mycobacterium tuberculosis</i> Complex into the Main Phylogenetic Lineages. <i>PLoS ONE</i> , 2012, 7, e41253.	2.5	120
20	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.	4.0	120
21	The 2021 WHO catalogue of <i>Mycobacterium tuberculosis</i> complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273.	7.3	114
22	Antibiotic resistance prediction for <i>Mycobacterium tuberculosis</i> from genome sequence data with Mykrobe. Wellcome Open Research, 2019, 4, 191.	1.8	103
23	Evolutionary Trajectories of Beta-Lactamase CTX-M-1 Cluster Enzymes: Predicting Antibiotic Resistance. <i>PLoS Pathogens</i> , 2010, 6, e1000735.	4.7	100
24	Novel <i>Mycobacterium tuberculosis</i> Complex Isolate from a Wild Chimpanzee. <i>Emerging Infectious Diseases</i> , 2013, 19, 969-976.	4.3	100
25	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.	3.9	94
26	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.	7.8	83
27	Recombination drives genome evolution in outbreak-related <i>Legionella pneumophila</i> isolates. <i>Nature Genetics</i> , 2014, 46, 1205-1211.	21.4	76
28	Integrating standardized whole genome sequence analysis with a global <i>Mycobacterium tuberculosis</i> antibiotic resistance knowledgebase. <i>Scientific Reports</i> , 2018, 8, 15382.	3.3	75
29	A role for systems epidemiology in tuberculosis research. <i>Trends in Microbiology</i> , 2011, 19, 492-500.	7.7	71
30	Application of machine learning techniques to tuberculosis drug resistance analysis. <i>Bioinformatics</i> , 2019, 35, 2276-2282.	4.1	71
31	The Genome of <i>Mycobacterium Africanum</i> West African 2 Reveals a Lineage-Specific Locus and Genome Erosion Common to the <i>M. tuberculosis</i> Complex. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1552.	3.0	69
32	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.	2.5	69
33	New Genome-Wide Algorithm Identifies Novel In-Vivo Expressed <i>Mycobacterium Tuberculosis</i> Antigens Inducing Human T-Cell Responses with Classical and Unconventional Cytokine Profiles. <i>Scientific Reports</i> , 2016, 6, 37793.	3.3	69
34	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.	8.4	62
35	Genomic determinants of speciation and spread of the <i>Mycobacterium tuberculosis</i> complex. <i>Science Advances</i> , 2019, 5, eaaw3307.	10.3	61
36	Contaminant DNA in bacterial sequencing experiments is a major source of false genetic variability. <i>BMC Biology</i> , 2020, 18, 24.	3.8	53

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37	From Phylogenetics to Phylogenomics: The Evolutionary Relationships of Insect Endosymbiotic $\beta$ -Proteobacteria as a Test Case. <i>Systematic Biology</i> , 2007, 56, 1-16.	5.6	52
38	<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.	12.8	52
39	Horizontal Gene Transfer in the Molecular Evolution of Mannose PTS Transporters. <i>Molecular Biology and Evolution</i> , 2005, 22, 1673-1685.	8.9	50
40	Quantifying Nonvertical Inheritance in the Evolution of <i>Legionella pneumophila</i> . <i>Molecular Biology and Evolution</i> , 2011, 28, 985-1001.	8.9	47
41	The Evolutionary Origin of Xanthomonadales Genomes and the Nature of the Horizontal Gene Transfer Process. <i>Molecular Biology and Evolution</i> , 2006, 23, 2049-2057.	8.9	44
42	Evidence for Diversifying Selection in a Set of <i>Mycobacterium tuberculosis</i> Genes in Response to Antibiotic- and Nonantibiotic-Related Pressure. <i>Molecular Biology and Evolution</i> , 2013, 30, 1326-1336.	8.9	43
43	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.	7.3	42
44	DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . <i>Bioinformatics</i> , 2019, 35, 3240-3249.	4.1	38
45	Long-Range Transcriptional Control of an Operon Necessary for Virulence-Critical ESX-1 Secretion in <i>Mycobacterium tuberculosis</i> . <i>Journal of Bacteriology</i> , 2012, 194, 2307-2320.	2.2	36
46	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.	21.4	35
47	The effect size of type 2 diabetes mellitus on tuberculosis drug resistance and adverse treatment outcomes. <i>Tuberculosis</i> , 2017, 103, 83-91.	1.9	33
48	Genome-wide mutational biases fuel transcriptional diversity in the <i>Mycobacterium tuberculosis</i> complex. <i>Nature Communications</i> , 2019, 10, 3994.	12.8	33
49	<i>Mycobacterium tuberculosis</i> clinical isolates carry mutational signatures of host immune environments. <i>Science Advances</i> , 2020, 6, eaba4901.	10.3	33
50	Specificity and mutagenesis bias of the mycobacterial alternative mismatch repair analyzed by mutation accumulation studies. <i>Science Advances</i> , 2020, 6, eaay4453.	10.3	30
51	Different Within-Host Viral Evolution Dynamics in Severely Immunosuppressed Cases with Persistent SARS-CoV-2. <i>Biomedicines</i> , 2021, 9, 808.	3.2	28
52	Phylogenetic analysis of vitamin B12-related metabolism in <i>Mycobacterium tuberculosis</i> . <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 6.	3.5	27
53	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.	4.8	26
54	GenomeMap: Within-Species Genome-Wide dN/dS Estimation from over 10,000 Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 2450-2460.	8.9	25

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55	Genomic analyses of Mycobacterium tuberculosis from human lung resections reveal a high frequency of polyclonal infections. <i>Nature Communications</i> , 2021, 12, 2716.	12.8	25
56	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.	1.7	25
57	The Troika Host-Pathogen-Extrinsic Factors in Tuberculosis: Modulating Inflammation and Clinical Outcomes. <i>Frontiers in Immunology</i> , 2018, 8, 1948.	4.8	24
58	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
59	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.	6.0	22
60	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, .	7.0	22
61	Validating viral quasispecies with digital organisms: a re-examination of the critical mutation rate. <i>BMC Evolutionary Biology</i> , 2005, 5, 5.	3.2	21
62	Persistent Infection by a Mycobacterium tuberculosis 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.	3.9	21
63	Genomic Epidemiology of Tuberculosis. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1019, 79-93.	1.6	21
64	Local adaptation in populations of Mycobacterium tuberculosis endemic to the Indian Ocean Rim. <i>F1000Research</i> , 2021, 10, 60.	1.6	21
65	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.	2.5	20
66	B-type natriuretic peptide over N-terminal pro-B-type natriuretic peptide to predict incident atrial fibrillation after cryptogenic stroke. <i>European Journal of Neurology</i> , 2021, 28, 540-547.	3.3	20
67	Cryptic Resistance Mutations Associated With Misdiagnoses of Multidrug-Resistant Tuberculosis. <i>Journal of Infectious Diseases</i> , 2019, 220, 316-320.	4.0	19
68	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.	2.5	19
69	Ultrafast Assessment of the Presence of a High-Risk Mycobacterium tuberculosis Strain in a Population. <i>Journal of Clinical Microbiology</i> , 2016, 54, 779-781.	3.9	18
70	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.	6.0	17
71	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.	3.9	15
72	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.	5.0	15

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73	Gene expression models based on a reference laboratory strain are poor predictors of Mycobacterium tuberculosis complex transcriptional diversity. <i>Scientific Reports</i> , 2018, 8, 3813.	3.3	14
74	SARS-CoV-2 Outbreak on a Spanish Mink Farm: Epidemiological, Molecular, and Pathological Studies. <i>Frontiers in Veterinary Science</i> , 2021, 8, 805004.	2.2	14
75	Towards next-generation diagnostics for tuberculosis: identification of novel molecular targets by large-scale comparative genomics. <i>Bioinformatics</i> , 2020, 36, 985-989.	4.1	13
76	Local adaptation in populations of Mycobacterium tuberculosis endemic to the Indian Ocean Rim. <i>F1000Research</i> , 2021, 10, 60.	1.6	13
77	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.	7.1	13
78	Phylogenetic signal and functional categories in Proteobacteria genomes. <i>BMC Evolutionary Biology</i> , 2007, 7, S7.	3.2	12
79	Mycobacterium tuberculosis Acquires Limited Genetic Diversity in Prolonged Infections, Reactivations and Transmissions Involving Multiple Hosts. <i>Frontiers in Microbiology</i> , 2018, 8, 2661.	3.5	12
80	Evolutionary Dissection of the Dot/Icm System Based on Comparative Genomics of 58 Legionella Species. <i>Genome Biology and Evolution</i> , 2019, 11, 2619-2632.	2.5	12
81	Screening of inmates transferred to Spain reveals a Peruvian prison as a reservoir of persistent Mycobacterium tuberculosis MDR strains and mixed infections. <i>Scientific Reports</i> , 2020, 10, 2704.	3.3	12
82	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.	5.8	12
83	Genetic diversity within Mycobacterium tuberculosis complex impacts on the accuracy of genotypic pyrazinamide drug-susceptibility assay. <i>Tuberculosis</i> , 2014, 94, 451-453.	1.9	11
84	Draft Genome Sequences of Mycobacterium setense Type Strain DSM-45070 and the Nonpathogenic Strain Manresensis, Isolated from the Bank of the Cardener River in Manresa, Catalonia, Spain. <i>Genome Announcements</i> , 2015, 3, .	0.8	11
85	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.	6.0	11
86	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.	3.5	11
87	Large genomics datasets shed light on the evolution of the Mycobacterium tuberculosis complex. <i>Infection, Genetics and Evolution</i> , 2019, 72, 10-15.	2.3	11
88	Tuberculosis in Liberia: high multidrug-resistance burden, transmission and diversity modelled by multiple importation events. <i>Microbial Genomics</i> , 2020, 6, .	2.0	11
89	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.	4.7	11
90	Heterogeneous Streptomycin Resistance Level Among Mycobacterium tuberculosis Strains From the Same Transmission Cluster. <i>Frontiers in Microbiology</i> , 2021, 12, 659545.	3.5	10

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91	Overlapping of Independent SARS-CoV-2 Nosocomial Transmissions in a Complex Outbreak. <i>MSphere</i> , 2021, 6, e0038921.	2.9	9
92	The Sputum Microbiome in Pulmonary Tuberculosis and Its Association With Disease Manifestations: A Cross-Sectional Study. <i>Frontiers in Microbiology</i> , 2021, 12, 633396.	3.5	9
93	Comment on: Characterization of the embB 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.	3.0	8
94	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.	3.3	8
95	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.	3.3	8
96	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.	4.3	8
97	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.	0.8	7
98	Integrative transnational analysis to dissect tuberculosis transmission events along the migratory route from Africa to Europe. <i>Journal of Travel Medicine</i> , 2021, 28, .	3.0	7
99	SplitStrains, a tool to identify and separate mixed <i>Mycobacterium tuberculosis</i> infections from WGS data. <i>Microbial Genomics</i> , 2021, 7, .	2.0	7
100	Accuracy of an amplicon-sequencing nanopore approach to identify variants in tuberculosis drug-resistance-associated genes. <i>Microbial Genomics</i> , 2021, 7, .	2.0	7
101	The Evolution of Antibiotic Resistance. , 2011, , 305-337.		6
102	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.	3.0	6
103	Evolutionary and Phenotypic Characterization of Two Spike Mutations in European Lineage 20E of SARS-CoV-2. <i>MBio</i> , 2021, 12, e0231521.	4.1	6
104	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.	5.0	6
105	Subtle genotypic changes can be observed soon after diagnosis in <i>Mycobacterium tuberculosis</i> infection. <i>International Journal of Medical Microbiology</i> , 2016, 306, 401-405.	3.6	5
106	Simplified Model to Survey Tuberculosis Transmission in Countries Without Systematic Molecular Epidemiology Programs. <i>Emerging Infectious Diseases</i> , 2019, 25, 507-514.	4.3	5
107	Proper Assignment of Reactivation in a COVID-19 Recurrence Initially Interpreted as a Reinfection. <i>Journal of Infectious Diseases</i> , 2021, 224, 788-792.	4.0	5
108	An evolutionary functional genomics approach identifies novel candidate regions involved in isoniazid resistance in <i>Mycobacterium tuberculosis</i> . <i>Communications Biology</i> , 2021, 4, 1322.	4.4	5

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109	Draft Genome Sequence of <i>Mycobacterium brumae</i> ATCC 51384. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
110	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.	2.0	4
111	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.	3.3	4
112	Complete Analysis of the Epidemiological Scenario around a SARS-CoV-2 Reinfection: Previous Infection Events and Subsequent Transmission. <i>MSphere</i> , 2021, 6, e0059621.	2.9	4
113	Fine-grain population structure and transmission patterns of <i>Mycobacterium tuberculosis</i> in southern Mozambique, a high TB/HIV burden area. <i>Microbial Genomics</i> , 2022, 8, .	2.0	4
114	The Evolution of Antibiotic Resistance. , 2017, , 257-284.		3
115	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, .	3.0	3
116	A Genomic Snapshot of the SARS-CoV-2 Pandemic in the Balearic Islands. <i>Frontiers in Microbiology</i> , 2021, 12, 803827.	3.5	3
117	SNPs in Genes Related to DNA Damage Repair in <i>Mycobacterium Tuberculosis</i> : Their Association with Type 2 Diabetes Mellitus and Drug Resistance. <i>Genes</i> , 2022, 13, 609.	2.4	3
118	Expanded tracking of a Beijing <i>Mycobacterium tuberculosis</i> strain involved in an outbreak in France. <i>Travel Medicine and Infectious Disease</i> , 2021, 44, 102167.	3.0	2
119	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.	3.3	2
120	<i>Legionella</i> effectors reflect strength in diversity. <i>Nature Genetics</i> , 2016, 48, 115-116.	21.4	1
121	TB Transmission: Closing the Gaps. <i>EBioMedicine</i> , 2018, 34, 4-5.	6.1	1
122	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.	0.5	1
123	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.	1.2	1
124	Host Genetic Analysis Should Be Mandatory for Proper Classification of COVID-19 Reinfections. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab402.	0.9	1
125	Tuberculosis of the elbow: A rare form of presentation of extrapulmonary tuberculosis. <i>Enfermedades Infecciosas Y Microbiología Clínica</i> , 2019, 37, 550-551.	0.5	1
126	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, .	2.8	1



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127	Genomic Analysis of Bacterial Outbreaks. , 2016, , 203-232.		0
128	The Future of TB Resistance Diagnosis: The Essentials on Whole Genome Sequencing and Rapid Testing Methods. Archivos De Bronconeumologia, 2019, 55, 421-426.	0.8	0
129	Overlapping prison/community tuberculosis outbreaks in Costa Rica revealed by alternative analysis of suboptimal material. Transboundary and Emerging Diseases, 2021, , .	3.0	0
130	Vacunes i evoluci3: Per qu4 s important entendre la diversitat gen2tica dels pat2gens?. M4tode Revista De Difusi4 De La Investigaci4 De La Universitat De Val4ncia, 2013, .	0.0	0