

# Francesc Coll

## List of Publications by Year in descending order

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Version: 2024-02-01

54  
papers

3,345  
citations

201674

27  
h-index

168389

53  
g-index

57  
all docs

57  
docs citations

57  
times ranked

4232  
citing authors

#	ARTICLE	IF	CITATIONS
1	A robust SNP barcode for typing <i>Mycobacterium tuberculosis</i> complex strains. <i>Nature Communications</i> , 2014, 5, 4812.	12.8	531
2	Rapid determination of anti-tuberculosis drug resistance from whole-genome sequences. <i>Genome Medicine</i> , 2015, 7, 51.	8.2	323
3	Genome-wide analysis of multi- and extensively drug-resistant <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2018, 50, 307-316.	21.4	271
4	Large-scale whole genome sequencing of <i>M. tuberculosis</i> provides insights into transmission in a high prevalence area. <i>ELife</i> , 2015, 4, .	6.0	198
5	Recurrence due to Relapse or Reinfection With <i>Mycobacterium tuberculosis</i> : A Whole-Genome Sequencing Approach in a Large, Population-Based Cohort With a High HIV Infection Prevalence and Active Follow-up. <i>Journal of Infectious Diseases</i> , 2015, 211, 1154-1163.	4.0	149
6	One Health Genomic Surveillance of <i>Escherichia coli</i> Demonstrates Distinct Lineages and Mobile Genetic Elements in Isolates from Humans versus Livestock. <i>MBio</i> , 2019, 10, .	4.1	130
7	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
8	Longitudinal genomic surveillance of MRSA in the UK reveals transmission patterns in hospitals and the community. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	103
9	<i>Mycobacterium tuberculosis</i> whole genome sequencing and protein structure modelling provides insights into anti-tuberculosis drug resistance. <i>BMC Medicine</i> , 2016, 14, 31.	5.5	102
10	Complex Routes of Nosocomial Vancomycin-Resistant <i>Enterococcus faecium</i> Transmission Revealed by Genome Sequencing. <i>Clinical Infectious Diseases</i> , 2017, 64, 886-893.	5.8	93
11	SpolPred: rapid and accurate prediction of <i>Mycobacterium tuberculosis</i> spoligotypes from short genomic sequences. <i>Bioinformatics</i> , 2012, 28, 2991-2993.	4.1	80
12	PolyTB: A genomic variation map for <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2014, 94, 346-354.	1.9	79
13	Genomic expression catalogue of a global collection of BCG vaccine strains show evidence for highly diverged metabolic and cell-wall adaptations. <i>Scientific Reports</i> , 2015, 5, 15443.	3.3	78
14	Elucidating Emergence and Transmission of Multidrug-Resistant Tuberculosis in Treatment Experienced Patients by Whole Genome Sequencing. <i>PLoS ONE</i> , 2013, 8, e83012.	2.5	75
15	Definition of a genetic relatedness cutoff to exclude recent transmission of methicillin-resistant <i>Staphylococcus aureus</i> : a genomic epidemiology analysis. <i>Lancet Microbe</i> , The, 2020, 1, e328-e335.	7.3	75
16	Recombination in <i>pe/ppe</i> genes contributes to genetic variation in <i>Mycobacterium tuberculosis</i> lineages. <i>BMC Genomics</i> , 2016, 17, 151.	2.8	62
17	Whole Genome Sequencing Based Characterization of Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Isolates from Pakistan. <i>PLoS ONE</i> , 2015, 10, e0117771.	2.5	59
18	Imputation-Based Population Genetics Analysis of <i>Plasmodium falciparum</i> Malaria Parasites. <i>PLoS Genetics</i> , 2015, 11, e1005131.	3.5	53

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19	Quantifying acquisition and transmission of <i>Enterococcus faecium</i> using genomic surveillance. <i>Nature Microbiology</i> , 2021, 6, 103-111.	13.3	53
20	Unraveling <i>Mycobacterium tuberculosis</i> genomic diversity and evolution in Lisbon, Portugal, a highly drug resistant setting. <i>BMC Genomics</i> , 2014, 15, 991.	2.8	52
21	Genomic identification of cryptic susceptibility to penicillins and $\beta$ -lactamase inhibitors in methicillin-resistant <i>Staphylococcus aureus</i> . <i>Nature Microbiology</i> , 2019, 4, 1680-1691.	13.3	47
22	Systematic Surveillance Detects Multiple Silent Introductions and Household Transmission of Methicillin-Resistant <i>Staphylococcus aureus</i> USA300 in the East of England. <i>Journal of Infectious Diseases</i> , 2016, 214, 447-453.	4.0	45
23	Evolution of mobile genetic element composition in an epidemic methicillin-resistant <i>Staphylococcus aureus</i> : temporal changes correlated with frequent loss and gain events. <i>BMC Genomics</i> , 2017, 18, 684.	2.8	43
24	Detection of vancomycin-resistant <i>Enterococcus faecium</i> hospital-adapted lineages in municipal wastewater treatment plants indicates widespread distribution and release into the environment. <i>Genome Research</i> , 2019, 29, 626-634.	5.5	40
25	Defining nosocomial transmission of <i>Escherichia coli</i> and antimicrobial resistance genes: a genomic surveillance study. <i>Lancet Microbe</i> , The, 2021, 2, e472-e480.	7.3	39
26	Transient Silencing of Antibiotic Resistance by Mutation Represents a Significant Potential Source of Unanticipated Therapeutic Failure. <i>MBio</i> , 2019, 10, .	4.1	39
27	Mathematical modelling for antibiotic resistance control policy: do we know enough?. <i>BMC Infectious Diseases</i> , 2019, 19, 1011.	2.9	37
28	Sharing of carbapenemase-encoding plasmids between Enterobacteriaceae in UK sewage uncovered by MinION sequencing. <i>Microbial Genomics</i> , 2017, 3, e000114.	2.0	33
29	Transmission of methicillin-resistant <i>Staphylococcus aureus</i> in long-term care facilities and their related healthcare networks. <i>Genome Medicine</i> , 2016, 8, 102.	8.2	30
30	Some Synonymous and Nonsynonymous <i>gyrA</i> Mutations in <i>Mycobacterium tuberculosis</i> Lead to Systematic False-Positive Fluoroquinolone Resistance Results with the Hain GenoType MTBDR Assays. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	29
31	Genomic Surveillance of Methicillin-resistant <i>Staphylococcus aureus</i> : A Mathematical Early Modeling Study of Cost-effectiveness. <i>Clinical Infectious Diseases</i> , 2020, 70, 1613-1619.	5.8	27
32	Rapid feedback on hospital onset SARS-CoV-2 infections combining epidemiological and sequencing data. <i>ELife</i> , 2021, 10, .	6.0	26
33	Genomic surveillance reveals low prevalence of livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> in the East of England. <i>Scientific Reports</i> , 2017, 7, 7406.	3.3	25
34	Role of Alanine Racemase Mutations in <i>Mycobacterium tuberculosis</i> Cycloserine Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	24
35	PhyTB: Phylogenetic tree visualisation and sample positioning for <i>M. tuberculosis</i> . <i>BMC Bioinformatics</i> , 2015, 16, 155.	2.6	23
36	Revised Interpretation of the Hain Lifescience GenoType MTBC To Differentiate <i>Mycobacterium canettii</i> and Members of the <i>Mycobacterium tuberculosis</i> Complex. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	20

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37	The draft genome of <i>Mycobacterium aurum</i> , a potential model organism for investigating drugs against <i>Mycobacterium tuberculosis</i> and <i>Mycobacterium leprae</i> . <i>International Journal of Mycobacteriology</i> , 2015, 4, 207-216.	0.6	19
38	Prospective genomic surveillance of methicillin-resistant <i>Staphylococcus aureus</i> (MRSA) associated with bloodstream infection, England, 1 October 2012 to 30 September 2013. <i>Eurosurveillance</i> , 2019, 24, .	7.0	19
39	Population-based analysis of ocular <i>Chlamydia trachomatis</i> in trachoma-endemic West African communities identifies genomic markers of disease severity. <i>Genome Medicine</i> , 2018, 10, 15.	8.2	18
40	Investigation of a Cluster of Sequence Type 22 Methicillin-Resistant <i>Staphylococcus aureus</i> Transmission in a Community Setting. <i>Clinical Infectious Diseases</i> , 2017, 65, 2069-2077.	5.8	11
41	rPinecone: Define sub-lineages of a clonal expansion via a phylogenetic tree. <i>Microbial Genomics</i> , 2019, 5, .	2.0	10
42	<i>Mycobacterium tuberculosis</i> lineage 1 genetic diversity in Pará, Brazil, suggests common ancestry with east-African isolates potentially linked to historical slave trade. <i>Infection, Genetics and Evolution</i> , 2019, 73, 337-341.	2.3	9
43	Turkish and Japanese <i>Mycobacterium tuberculosis</i> sublineages share a remote common ancestor. <i>Infection, Genetics and Evolution</i> , 2016, 45, 461-473.	2.3	8
44	Feasibility of informing syndrome-level empiric antibiotic recommendations using publicly available antibiotic resistance datasets. <i>Wellcome Open Research</i> , 2019, 4, 140.	1.8	6
45	A proportion of mutations fixed in the genomes of in vitro selected isogenic drug-resistant <i>Mycobacterium tuberculosis</i> mutants can be detected as minority variants in the parent culture. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-7.	1.8	5
46	Local Persistence of Novel MRSA Lineage after Hospital Ward Outbreak, Cambridge, UK, 2011–2013. <i>Emerging Infectious Diseases</i> , 2016, 22, 1658-1659.	4.3	4
47	Ferric Citrate Regulator FecR Is Translocated across the Bacterial Inner Membrane via a Unique Twin-Arginine Transport-Dependent Mechanism. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	4
48	Defining metrics for whole-genome sequence analysis of MRSA in clinical practice. <i>Microbial Genomics</i> , 2020, 6, .	2.0	4
49	Feasibility of informing syndrome-level empiric antibiotic recommendations using publicly available antibiotic resistance datasets. <i>Wellcome Open Research</i> , 2019, 4, 140.	1.8	4
50	PowerBacGWAS: a computational pipeline to perform power calculations for bacterial genome-wide association studies. <i>Communications Biology</i> , 2022, 5, 266.	4.4	4
51	Characterization of genomic variations in SNPs of PE_PGRS genes reveals deletions and insertions in extensively drug resistant (XDR) <i>M. tuberculosis</i> strains from Pakistan. <i>International Journal of Mycobacteriology</i> , 2015, 4, 73-79.	0.6	3
52	Whole genome sequencing-based characterization of extensively drug resistant (XDR) strains of <i>Mycobacterium tuberculosis</i> from Pakistan. <i>International Journal of Mycobacteriology</i> , 2015, 4, 11-12.	0.6	1
53	Ocular chlamydial genomic variants and disease severity in trachoma: a cross-sectional population-based genome-wide association study. <i>Lancet, The</i> , 2016, 387, S63.	13.7	0
54	Key variables affecting genetic distance calculations in genomic epidemiology. <i>Lancet Microbe, The</i> , 2021, 2, e486-e487.	7.3	0