

# Laura PÃ©rez-Lago

## List of Publications by Year in descending order

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Version: 2024-02-01

50  
papers

1,125  
citations

567281

15  
h-index

434195

31  
g-index

52  
all docs

52  
docs citations

52  
times ranked

2374  
citing authors

#	ARTICLE	IF	CITATIONS
1	Spread of a SARS-CoV-2 variant through Europe in the summer of 2020. <i>Nature</i> , 2021, 595, 707-712.	27.8	363
2	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
3	Current knowledge and pending challenges in zoonosis caused by <i>Mycobacterium bovis</i> : A review. <i>Research in Veterinary Science</i> , 2014, 97, S94-S100.	1.9	69
4	Systematic Survey of Clonal Complexity in Tuberculosis at a Populational Level and Detailed Characterization of the Isolates Involved. <i>Journal of Clinical Microbiology</i> , 2011, 49, 4131-4137.	3.9	52
5	Characterization of Microevolution Events in <i>Mycobacterium tuberculosis</i> Strains Involved in Recent Transmission Clusters. <i>Journal of Clinical Microbiology</i> , 2011, 49, 3771-3776.	3.9	35
6	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
7	A Case-Control Study of Real-Life Experience with Ceftolozane-Tazobactam in Patients with Hematologic Malignancy and <i>Pseudomonas aeruginosa</i> Infection. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	34
8	Different Within-Host Viral Evolution Dynamics in Severely Immunosuppressed Cases with Persistent SARS-CoV-2. <i>Biomedicines</i> , 2021, 9, 808.	3.2	28
9	Inference of Active Viral Replication in Cases with Sustained Positive Reverse Transcription-PCR Results for SARS-CoV-2. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	3.9	27
10	Differences in gene expression between clonal variants of <i>Mycobacterium tuberculosis</i> emerging as a result of microevolution. <i>International Journal of Medical Microbiology</i> , 2013, 303, 674-677.	3.6	26
11	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
12	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.	3.9	21
13	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.	3.9	18
14	The Structure of Phage $\Phi$ 29 Transcription Regulator p4-DNA Complex Reveals an N-Hook Motif for DNA Binding. <i>Molecular Cell</i> , 2006, 22, 73-81.	9.7	15
15	Novel dimeric structure of phage $\Phi$ 29-encoded protein p56: insights into uracil-DNA glycosylase inhibition. <i>Nucleic Acids Research</i> , 2011, 39, 9779-9788.	14.5	15
16	Co-infection with Drug-Susceptible and Reactivated Latent Multidrug-Resistant <i>Mycobacterium tuberculosis</i> . <i>Emerging Infectious Diseases</i> , 2015, 21, 2098-2100.	4.3	15
17	Urgent Implementation in a Hospital Setting of a Strategy To Rule Out Secondary Cases Caused by Imported Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Strains at Diagnosis. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2969-2974.	3.9	15
18	A precise DNA bend angle is essential for the function of the phage $\Phi$ 29 transcriptional regulator. <i>Nucleic Acids Research</i> , 2005, 33, 126-134.	14.5	14

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19	The Evolution of Genotyping Strategies To Detect, Analyze, and Control Transmission of Tuberculosis. <i>Microbiology Spectrum</i> , 2018, 6, .	3.0	14
20	Unmasking subtle differences in the infectivity of microevolved <i>Mycobacterium tuberculosis</i> variants coinfecting the same patient. <i>International Journal of Medical Microbiology</i> , 2013, 303, 693-696.	3.6	13
21	Characterization of <i>Bacillus subtilis</i> uracil-DNA glycosylase and its inhibition by phage $\Phi$ 29 protein p56. <i>Molecular Microbiology</i> , 2011, 80, 1657-1666.	2.5	12
22	<i>Mycobacterium tuberculosis</i> Acquires Limited Genetic Diversity in Prolonged Infections, Reactivations and Transmissions Involving Multiple Hosts. <i>Frontiers in Microbiology</i> , 2018, 8, 2661.	3.5	12
23	Different dynamics of mean SARS-CoV-2 RT-PCR Ct values between the first and second COVID-19 waves in the Madrid population. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 3103-3106.	3.0	12
24	In-Depth Characterization and Functional Analysis of Clonal Variants in a <i>Mycobacterium tuberculosis</i> Strain Prone to Microevolution. <i>Frontiers in Microbiology</i> , 2017, 8, 694.	3.5	11
25	A <i>Mycobacterium tuberculosis</i> Beijing strain persists at high rates and extends its geographic boundaries 20 years after importation. <i>Scientific Reports</i> , 2019, 9, 4687.	3.3	11
26	DNA sequence-specific recognition by a transcriptional regulator requires indirect readout of A-tracts. <i>Nucleic Acids Research</i> , 2007, 35, 3252-3261.	14.5	10
27	Trends of Two Epidemic Multidrug-Resistant Strains of <i>Mycobacterium tuberculosis</i> in Argentina Disclosed by Tailored Molecular Strategy. <i>American Journal of Tropical Medicine and Hygiene</i> , 2019, 101, 1308-1311.	1.4	9
28	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
29	Detection of Minority Variants and Mixed Infections in <i>Mycobacterium tuberculosis</i> by Direct Whole-Genome Sequencing on Noncultured Specimens Using a Specific-DNA Capture Strategy. <i>MSphere</i> , 2021, 6, e0074421.	2.9	8
30	Diagnostic performance of Anyplex II MTB/MDR/XDR for detection of resistance to first and second line drugs in <i>Mycobacterium tuberculosis</i> . <i>Journal of Microbiological Methods</i> , 2017, 139, 74-78.	1.6	7
31	Optimizing and accelerating the assignation of lineages in <i>Mycobacterium tuberculosis</i> using novel alternative single-tube assays. <i>PLoS ONE</i> , 2017, 12, e0186956.	2.5	7
32	Exportation of MDR TB to Europe from Setting with Actively Transmitted Persistent Strains in Peru. <i>Emerging Infectious Diseases</i> , 2019, 25, 596-598.	4.3	7
33	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
34	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
35	SARS-CoV-2 superinfection and reinfection with three different strains. <i>Transboundary and Emerging Diseases</i> , 2021, , .	3.0	6
36	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

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37	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
38	Homologies and Divergences in the Transcription Regulatory System of Two Related <i>Bacillus subtilis</i> Phages. <i>Journal of Bacteriology</i> , 2005, 187, 6403-6409.	2.2	4
39	Functional Specificity of a Protein-DNA Complex Mediated by Two Arginines Bound to the Minor Groove. <i>Journal of Bacteriology</i> , 2012, 194, 4727-4735.	2.2	4
40	Dynamic and complex <i>Mycobacterium tuberculosis</i> microevolution unrevealed by standard genotyping. <i>Tuberculosis</i> , 2012, 92, 232-235.	1.9	4
41	Genetic features shared by <i>Mycobacterium tuberculosis</i> strains involved in microevolution events. <i>Infection, Genetics and Evolution</i> , 2013, 16, 326-329.	2.3	3
42	Clonal Complexity in <i>Mycobacterium tuberculosis</i> Can Hamper Diagnostic Procedures. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1388-1395.	3.9	3
43	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
44	Probable long-term prevalence for a predominant <i>Mycobacterium tuberculosis</i> clone of a Beijing genotype in Colon, Panama. <i>Transboundary and Emerging Diseases</i> , 2021, 68, 2229-2238.	3.0	2
45	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
46	Equatorial Guinea, a multidrug-resistant tuberculosis hotspot in Central Africa. <i>European Respiratory Journal</i> , 2017, 49, 1600952.	6.7	1
47	A deletion hampering appropriate typing of <i>Mycobacterium africanum</i> . <i>Tuberculosis</i> , 2017, 103, 24-27.	1.9	0
48	Overlapping prison/community tuberculosis outbreaks in Costa Rica revealed by alternative analysis of suboptimal material. <i>Transboundary and Emerging Diseases</i> , 2021, , .	3.0	0
49	High within-host diversity found from direct genotyping on post-mortem tuberculosis specimens in a high-burden setting. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1518.e5-1518.e9.	6.0	0
50	Insights into the Complexity of a Dormant <i>Mycobacterium tuberculosis</i> Cluster Once Transmission Is Resumed. <i>Microbiology Spectrum</i> , 2022, 10, e0138121.	3.0	0