

# Josefina Campos

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7855322/publications.pdf>

Version: 2024-02-01

26  
papers

1,297  
citations

840776

11  
h-index

552781

26  
g-index

28  
all docs

28  
docs citations

28  
times ranked

2047  
citing authors

#	ARTICLE	IF	CITATIONS
1	Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package. <i>GigaScience</i> , 2022, 11, .	6.4	18
2	Five-year microevolution of a multidrug-resistant <i>Mycobacterium tuberculosis</i> strain within a patient with inadequate compliance to treatment. <i>BMC Infectious Diseases</i> , 2021, 21, 394.	2.9	3
3	Genomic contextualisation of ancient DNA molecular data from an Argentinian fifth pandemic <i>Vibrio cholerae</i> infection. <i>Microbial Genomics</i> , 2021, 7, .	2.0	0
4	A genomic snapshot of <i>Salmonella enterica</i> serovar Typhi in Colombia. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009755.	3.0	7
5	A rapid and simple protocol for concentration of SARS-CoV-2 from sewage. <i>Journal of Virological Methods</i> , 2021, 297, 114272.	2.1	6
6	Genomic Epidemiology of Azithromycin-Nonsusceptible <i>Neisseria gonorrhoeae</i> , Argentina, 2005–2019. <i>Emerging Infectious Diseases</i> , 2021, 27, 2369-2378.	4.3	7
7	Emergence of colistin resistance in <i>Klebsiella pneumoniae</i> ST15 disseminating blaKPC-2 in a novel genetic platform. <i>Journal of Global Antimicrobial Resistance</i> , 2021, , .	2.2	3
8	Reply to Baba and Kanamori. <i>Clinical Infectious Diseases</i> , 2020, 71, 1353-1355.	5.8	0
9	Genomics of the Argentinian cholera epidemic elucidate the contrasting dynamics of epidemic and endemic <i>Vibrio cholerae</i> . <i>Nature Communications</i> , 2020, 11, 4918.	12.8	12
10	“Super-Spreaders” and Person-to-Person Transmission of Andes Virus in Argentina. <i>New England Journal of Medicine</i> , 2020, 383, 2230-2241.	27.0	52
11	Multidrug-Resistant CTX-M and CMY-2 Producing <i>Escherichia coli</i> Isolated from Healthy Household Dogs from the Great Metropolitan Area, Costa Rica. <i>Microbial Drug Resistance</i> , 2020, 26, 1421-1428.	2.0	7
12	Surveillance of <i>Salmonella enterica</i> serovar Typhi in Colombia, 2012–2015. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008040.	3.0	6
13	OXA-48 Carbapenemase in <i>Klebsiella pneumoniae</i> Sequence Type 307 in Ecuador. <i>Microorganisms</i> , 2020, 8, 435.	3.6	4
14	PulseNet Latin America and the Caribbean Network: Present and Future. <i>Foodborne Pathogens and Disease</i> , 2019, 16, 489-497.	1.8	11
15	Phylogeographic Analysis Reveals Multiple International transmission Events Have Driven the Global Emergence of <i>Escherichia coli</i> O157:H7. <i>Clinical Infectious Diseases</i> , 2019, 69, 428-437.	5.8	26
16	Emergence of azithromycin resistance mediated by the mph (A) gene in <i>Salmonella Typhimurium</i> clinical isolates in Latin America. <i>Journal of Global Antimicrobial Resistance</i> , 2018, 13, 237-239.	2.2	9
17	Genomic analysis of the first isolate of KPC-2-producing <i>Klebsiella pneumoniae</i> from Uruguay. <i>Journal of Global Antimicrobial Resistance</i> , 2018, 15, 109-110.	2.2	9
18	Draft Genome Sequence of <i>Lactobacillus helveticus</i> ATCC 12046. <i>Genome Announcements</i> , 2018, 6, .	0.8	1

#	ARTICLE	IF	CITATIONS
19	Whole genome sequencing of <i>Shigella sonnei</i> through PulseNet Latin America and Caribbean: advancing global surveillance of foodborne illnesses. <i>Clinical Microbiology and Infection</i> , 2017, 23, 845-853.	6.0	37
20	Integrated view of <i>Vibrio cholerae</i> in the Americas. <i>Science</i> , 2017, 358, 789-793.	12.6	128
21	PulseNet International: Vision for the implementation of whole genome sequencing (WGS) for global food-borne disease surveillance. <i>Eurosurveillance</i> , 2017, 22, .	7.0	307
22	Distinct <i>Salmonella</i> Enteritidis lineages associated with enterocolitis in high-income settings and invasive disease in low-income settings. <i>Nature Genetics</i> , 2016, 48, 1211-1217.	21.4	191
23	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of <i>Salmonella</i> Typhi identifies inter- and intracontinental transmission events. <i>Nature Genetics</i> , 2015, 47, 632-639.	21.4	403
24	Multiple-locus variable-number tandem repeat analysis of <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Dublin. <i>Journal of Applied Microbiology</i> , 2014, 116, 1044-1054.	3.1	11
25	Diagnosis of an outbreak of <i>Salmonella</i> Typhimurium in chinchillas ( <i>Chinchilla lanigera</i> ) by pulsed-field gel electrophoresis. <i>Revista Argentina De Microbiologia</i> , 2014, 46, 205-209.	0.7	2
26	Building PulseNet Latin America and Caribbean <i>Salmonella</i> regional database: First conclusions of genetic subtypes of <i>S. Typhi</i> , <i>S. Typhimurium</i> and <i>S. Enteritidis</i> circulating in six countries of the region. <i>Food Research International</i> , 2012, 45, 1030-1036.	6.2	21