

# Juliana Pfrimer Falcão

## List of Publications by Year in descending order

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81  
papers

1,527  
citations

331670

21  
h-index

345221

36  
g-index

82  
all docs

82  
docs citations

82  
times ranked

1912  
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole genome sequencing analyses revealed that <i>Salmonella enterica</i> serovar Dublin strains from Brazil belonged to two predominant clades. <i>Scientific Reports</i> , 2022, 12, .	3.3	7
2	Comparison of cell invasion, macrophage survival and inflammatory cytokines profiles between <i>Salmonella enterica</i> serovars Enteritidis and Dublin from Brazil. <i>Journal of Applied Microbiology</i> , 2021, 130, 2123-2131.	3.1	5
3	Antimicrobial Resistance Profiles and Phylogenetic Analysis of <i>Campylobacter jejuni</i> Strains Isolated in Brazil by Whole Genome Sequencing. <i>Microbial Drug Resistance</i> , 2021, 27, 660-669.	2.0	11
4	Phenotypic analyses of <i>Salmonella enterica</i> serovar Enteritidis strains isolated in the pre- and post-epidemic period in Brazil. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 173-183.	2.0	2
5	Genetic diversity assessed using PFGE, MLP and MLST in <i>Candida</i> spp. candidemia isolates obtained from a Brazilian hospital. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 503-516.	2.0	3
6	<i>Campylobacter coli</i> strains from Brazil can invade phagocytic and epithelial cells and induce IL-8 secretion. <i>Brazilian Journal of Microbiology</i> , 2021, 52, 859-867.	2.0	1
7	Insights about the epidemiology of <i>Salmonella Typhimurium</i> isolates from different sources in Brazil using comparative genomics. <i>Gut Pathogens</i> , 2021, 13, 27.	3.4	6
8	Draft Genome Sequences of 80 <i>Salmonella enterica</i> Serovar Infantis Strains Isolated from Food, Environmental, Human, and Veterinary Sources in Brazil. <i>Microbiology Resource Announcements</i> , 2021, 10, e0031321.	0.6	5
9	<i>Salmonella Typhimurium</i> ST313 isolated in Brazil revealed to be more invasive and inflammatory in murine colon compared to ST19 strains. <i>Journal of Microbiology</i> , 2021, 59, 861-870.	2.8	5
10	Analysis of the antimicrobial resistance gene frequency in whole-genome sequenced <i>Vibrio</i> from Latin American countries. <i>Journal of Medical Microbiology</i> , 2021, 70, .	1.8	3
11	Phylogenetic relationship and genomic characterization of <i>Salmonella Typhimurium</i> strains isolated from swine in Brazil. <i>Infection, Genetics and Evolution</i> , 2021, 93, 104977.	2.3	11
12	<i>Campylobacter coli</i> isolated in Brazil typed by core genome Multilocus Sequence Typing shows high genomic diversity in a global context. <i>Infection, Genetics and Evolution</i> , 2021, 95, 105018.	2.3	3
13	Genomic characterization and antimicrobial resistance profiles of <i>Salmonella enterica</i> serovar Infantis isolated from food, humans and veterinary-related sources in Brazil. <i>Journal of Applied Microbiology</i> , 2021, , .	3.1	4
14	Phylogenetic analysis revealed that <i>Salmonella Typhimurium</i> ST313 isolated from humans and food in Brazil presented a high genomic similarity. <i>Brazilian Journal of Microbiology</i> , 2020, 51, 53-64.	2.0	4
15	High similarity and high frequency of virulence genes among <i>Salmonella</i> Dublin strains isolated over a 33-year period in Brazil. <i>Brazilian Journal of Microbiology</i> , 2020, 51, 497-509.	2.0	7
16	Virulence traits and expression of <i>bstA</i> , <i>fliC</i> and <i>sopE2</i> in <i>Salmonella</i> Dublin strains isolated from humans and animals in Brazil. <i>Infection, Genetics and Evolution</i> , 2020, 80, 104193.	2.3	6
17	Molecular typing of <i>Campylobacter jejuni</i> strains: comparison among four different techniques. <i>Brazilian Journal of Microbiology</i> , 2020, 51, 519-525.	2.0	7
18	Analysis of Resistance Gene Prevalence in Whole-Genome Sequenced <i>Enterobacteriales</i> from Brazil. <i>Microbial Drug Resistance</i> , 2020, 26, 594-604.	2.0	6

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19	Molecular Epidemiology and Resistance Profile of <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> Strains Isolated from Different Sources in Brazil. <i>Microbial Drug Resistance</i> , 2020, 26, 1516-1525.	2.0	11
20	A high number of multidrug-resistant and predominant genetically related cluster of <i>Shigella flexneri</i> strains isolated over 34 years in Brazil. <i>Brazilian Journal of Microbiology</i> , 2020, 51, 1563-1571.	2.0	3
21	Phenotypic and genotypic characterization of <i>Salmonella</i> Typhimurium isolates from humans and foods in Brazil. <i>PLoS ONE</i> , 2020, 15, e0237886.	2.5	9
22	Partial Correlation Between Phenotypic and Genotypic Antimicrobial Resistance of <i>Salmonella enterica</i> Serovar Enteritidis Strains from Brazil. <i>Microbial Drug Resistance</i> , 2020, 26, 1466-1471.	2.0	4
23	Heart failure developed after myocardial infarction does not affect gut microbiota composition in the rat. <i>American Journal of Physiology - Renal Physiology</i> , 2019, 317, G342-G348.	3.4	7
24	Molecular characterization of multidrug-resistant Shiga toxin-producing <i>Escherichia coli</i> harboring antimicrobial resistance genes obtained from a farmhouse. <i>Pathogens and Global Health</i> , 2019, 113, 268-274.	2.3	16
25	Genotypic Resistance to Quinolone and Tetracycline in <i>Salmonella</i> Dublin Strains Isolated from Humans and Animals in Brazil. <i>Microbial Drug Resistance</i> , 2019, 25, 143-151.	2.0	13
26	High survival rates of <i>Campylobacter coli</i> under different stress conditions suggest that more rigorous food control measures might be needed in Brazil. <i>Food Microbiology</i> , 2018, 73, 327-333.	4.2	20
27	Draft Genome Sequences of 20 <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Typhimurium Strains Isolated from Swine in Santa Catarina, Brazil. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
28	Draft Genome Sequences of 116 <i>Campylobacter jejuni</i> Strains Isolated from Humans, Animals, Food, and the Environment in Brazil. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
29	<i>Yersinia enterocolitica</i> in a Brazilian pork production chain: Tracking of contamination routes, virulence and antimicrobial resistance. <i>International Journal of Food Microbiology</i> , 2018, 276, 5-9.	4.7	29
30	Genetic diversity, antimicrobial resistance, plasmid profile and frequency of the Vi antigen in <i>Salmonella</i> Dublin strains isolated in Brazil. <i>Zoonoses and Public Health</i> , 2018, 65, e34-e43.	2.2	6
31	Draft Genome Sequences of 112 <i>Salmonella enterica</i> Serovar Dublin Strains Isolated from Humans and Animals in Brazil. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
32	IncU plasmid harbouring blaCTX-M-8 in multidrug-resistant <i>Shigella sonnei</i> in Brazil. <i>Journal of Global Antimicrobial Resistance</i> , 2018, 14, 99-100.	2.2	0
33	Changing of the Genomic Pattern of <i>Salmonella</i> Enteritidis Strains Isolated in Brazil Over a 48 year-period revealed by Whole Genome SNP Analyses. <i>Scientific Reports</i> , 2018, 8, 10478.	3.3	18
34	Phylogenetic and antimicrobial resistance gene analysis of <i>Salmonella</i> Typhimurium strains isolated in Brazil by whole genome sequencing. <i>PLoS ONE</i> , 2018, 13, e0201882.	2.5	48
35	Genotypic diversity and presence of $\beta$ -lactamase encoding genes in <i>Pseudomonas aeruginosa</i> isolated from Brazilian soils. <i>Applied Soil Ecology</i> , 2018, 129, 94-97.	4.3	4
36	Virulence-related genes, adhesion and invasion of some <i>Yersinia enterocolitica</i> -like strains suggests its pathogenic potential. <i>Microbial Pathogenesis</i> , 2017, 104, 72-77.	2.9	16

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37	Immune Response Against Salmonella Enteritidis Is Unsettled by HIV Infection. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1057, 29-39.	1.6	1
38	Antimicrobial resistance and plasmid replicons in <i>Yersinia enterocolitica</i> strains isolated in Brazil in 30 years. <i>Brazilian Journal of Infectious Diseases</i> , 2017, 21, 477-480.	0.6	16
39	Multilocus sequence typing of <i>Salmonella Typhimurium</i> reveals the presence of the highly invasive ST313 in Brazil. <i>Infection, Genetics and Evolution</i> , 2017, 51, 41-44.	2.3	41
40	Molecular characterization of <i>Salmonella Typhimurium</i> isolated in Brazil by CRISPR-MVLST. <i>Journal of Microbiological Methods</i> , 2017, 133, 55-61.	1.6	22
41	Molecular typing and occurrence of beta-lactam resistance genes of <i>Shigella sonnei</i> strains isolated from 1983 to 2014 in the São Paulo state of Brazil. <i>Microbiology and Immunology</i> , 2017, 61, 547-553.	1.4	0
42	Draft Genome Sequences of 256 <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Enteritidis Strains Isolated from Humans, Food, Chickens, and Farm Environments in Brazil. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
43	Prevalence of <i>gyrA</i> Mutations in Nalidixic Acid-Resistant Strains of <i>Salmonella</i> Enteritidis Isolated from Humans, Food, Chickens, and the Farm Environment in Brazil. <i>Microbial Drug Resistance</i> , 2017, 23, 421-428.	2.0	31
44	Draft Genome Sequences of <i>Yersinia frederiksenii</i> , <i>Yersinia intermedia</i> , and <i>Yersinia kristensenii</i> Strains from Brazil. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
45	Pathogenic potential and genotypic diversity of <i>Campylobacter jejuni</i> : a neglected food-borne pathogen in Brazil. <i>Journal of Medical Microbiology</i> , 2017, 66, 350-359.	1.8	23
46	Draft Genome Sequences of 40 <i>Salmonella enterica</i> Serovar Typhimurium Strains Isolated from Humans and Food in Brazil. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
47	Virulence-associated genes, antimicrobial resistance and molecular typing of <i>Salmonella</i> Typhimurium strains isolated from swine from 2000 to 2012 in Brazil. <i>Journal of Applied Microbiology</i> , 2016, 120, 1677-1690.	3.1	31
48	<i>In vitro</i> and <i>ex vivo</i> infection models help assess the molecular aspects of the interaction of <i>Trichophyton rubrum</i> with the host milieu. <i>Medical Mycology</i> , 2016, 54, 420-427.	0.7	38
49	Genotyping of <i>Campylobacter coli</i> strains isolated in Brazil suggests possible contamination amongst environmental, human, animal and food sources. <i>Journal of Medical Microbiology</i> , 2016, 65, 80-90.	1.8	25
50	Molecular and phenotypic characterization of strains of <i>Shigella sonnei</i> isolated over 31 years suggests the circulation of two prevalent subtypes in São Paulo State, Brazil. <i>Journal of Medical Microbiology</i> , 2016, 65, 666-677.	1.8	10
51	Rapid and efficient differentiation of <i>Yersinia</i> species using high-resolution melting analysis. <i>Journal of Microbiological Methods</i> , 2015, 115, 6-12.	1.6	5
52	Genotypic diversity and pathogenic potential of <i>Yersinia enterocolitica</i> biotype 2 strains isolated in Brazil. <i>Journal of Applied Microbiology</i> , 2015, 118, 1058-1067.	3.1	8
53	Comparison of four molecular methods to type <i>Salmonella</i> Enteritidis strains. <i>Apmis</i> , 2015, 123, 422-426.	2.0	20
54	Phenotypic and genetic features of enteropathogenic <i>Escherichia coli</i> isolates from diarrheal children in the Ribeirão Preto metropolitan area, São Paulo State, Brazil. <i>Apmis</i> , 2015, 123, 128-135.	2.0	11

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55	Genotypic diversity, pathogenic potential and the resistance profile of <i>Salmonella</i> Typhimurium strains isolated from humans and food from 1983 to 2013 in Brazil. <i>Journal of Medical Microbiology</i> , 2015, 64, 1395-1407.	1.8	20
56	YERSINIA   Introduction. , 2014, , 831-837.		1
57	Characterization of <i>Salmonella</i> Enteritidis strains isolated from poultry and farm environments in Brazil. <i>Epidemiology and Infection</i> , 2014, 142, 1403-1410.	2.1	22
58	Pathogenic potential and genetic diversity of environmental and clinical isolates of <i>Pseudomonas aeruginosa</i> . <i>Apmis</i> , 2014, 122, 92-100.	2.0	32
59	Pulsed-Field Gel Electrophoresis characterization of <i>Listeria monocytogenes</i> isolates from cheese manufacturing plants in São Paulo, Brazil. <i>International Journal of Food Microbiology</i> , 2014, 173, 21-29.	4.7	53
60	Parallel independent evolution of pathogenicity within the genus <i>Yersinia</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6768-6773.	7.1	154
61	A novel high-resolution melting analysis-based method for <i>Yersinia enterocolitica</i> genotyping. <i>Journal of Microbiological Methods</i> , 2014, 106, 129-134.	1.6	3
62	Genotyping of <i>Yersinia enterocolitica</i> biotype 1A strains from clinical and nonclinical origins by pulsed-field gel electrophoresis. <i>Canadian Journal of Microbiology</i> , 2014, 60, 419-424.	1.7	6
63	Genotypic diversity and virulence markers of <i>Yersinia enterocolitica</i> biotype 1A strains isolated from clinical and non-clinical origins. <i>Apmis</i> , 2014, 122, 215-222.	2.0	43
64	Multilocus sequence analysis and 16S rRNA gene sequencing reveal that <i>Yersinia frederiksenii</i> sensu lato is <i>Yersinia massiliensis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 3124-3129.	1.7	5
65	Molecular epidemiology and virulence markers of <i>Salmonella</i> Infantis isolated over 25 years in São Paulo State, Brazil. <i>Infection, Genetics and Evolution</i> , 2013, 19, 145-151.	2.3	38
66	MLVA typing reveals higher genetic homogeneity among <i>S. Enteritidis</i> strains isolated from food, humans and chickens in Brazil in comparison to the North American Strains. <i>International Journal of Food Microbiology</i> , 2013, 162, 174-181.	4.7	17
67	Molecular typing of <i>Yersinia pseudotuberculosis</i> strains isolated from livestock in Brazil. <i>Genetics and Molecular Research</i> , 2013, 12, 4869-4878.	0.2	2
68	Genetic diversity, virulence genes and antimicrobial resistance of <i>Salmonella</i> Enteritidis isolated from food and humans over a 24-year period in Brazil. <i>Food Microbiology</i> , 2012, 32, 254-264.	4.2	99
69	A novel high-resolution melting analysis-based method for <i>Yersinia pseudotuberculosis</i> genotyping. <i>Journal of Microbiological Methods</i> , 2012, 91, 329-335.	1.6	11
70	Pathogenic Potential of the <i>Yersinia massiliensis</i> Species. <i>Advances in Experimental Medicine and Biology</i> , 2012, 954, 223-228.	1.6	3
71	Population structure of the <i>Yersinia pseudotuberculosis</i> complex according to multilocus sequence typing. <i>Environmental Microbiology</i> , 2011, 13, 3114-3127.	3.8	84
72	Emended description of <i>Yersinia massiliensis</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2011, 61, 1094-1097.	1.7	18

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73	Transcriptional profiling reveals the expression of novel genes in response to various stimuli in the human dermatophyte <i>Trichophyton rubrum</i> . <i>BMC Microbiology</i> , 2010, 10, 39.	3.3	49
74	Evaluation of four molecular typing methodologies as tools for determining taxonomy relations and for identifying species among <i>Yersinia</i> isolates. <i>Journal of Microbiological Methods</i> , 2010, 82, 141-150.	1.6	29
75	Molecular typing and virulence markers of <i>Yersinia enterocolitica</i> strains from human, animal and food origins isolated between 1968 and 2000 in Brazil. <i>Journal of Medical Microbiology</i> , 2006, 55, 1539-1548.	1.8	98
76	Virulence characteristics and epidemiology of <i>Yersinia enterocolitica</i> and <i>Yersinia</i> other than <i>Y. pseudotuberculosis</i> and <i>Y. pestis</i> isolated from water and sewage. <i>Journal of Applied Microbiology</i> , 2004, 96, 1230-1236.	3.1	51
77	Ice as a vehicle for diarrheagenic <i>Escherichia coli</i> . <i>International Journal of Food Microbiology</i> , 2004, 91, 99-103.	4.7	21
78	Cell-to-cell signaling in intestinal pathogens. <i>Current Issues in Intestinal Microbiology</i> , 2004, 5, 9-17.	2.5	20
79	<i>Yersinia</i> spp. in the Environment: Epidemiology and Virulence Characteristics. , 2003, 529, 341-343.		2
80	A Virulence Study of <i>Yersinia enterocolitica</i> O:3 Isolated from Sick Humans and Animals in Brazil Using PCR and Phenotypic Tests. , 2003, 529, 317-319.		1
81	Microbiological quality of ice used to refrigerate foods. <i>Food Microbiology</i> , 2002, 19, 269-276.	4.2	43