

# Errol Strain

## List of Publications by Year in descending order

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Version: 2024-02-01

49  
papers

3,180  
citations

172457

29  
h-index

206112

48  
g-index

49  
all docs

49  
docs citations

49  
times ranked

2728  
citing authors

#	ARTICLE	IF	CITATIONS
1	Implementation of Nationwide Real-time Whole-genome Sequencing to Enhance Listeriosis Outbreak Detection and Investigation. <i>Clinical Infectious Diseases</i> , 2016, 63, 380-386.	5.8	330
2	Practical Value of Food Pathogen Traceability through Building a Whole-Genome Sequencing Network and Database. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1975-1983.	3.9	278
3	CFSAN SNP Pipeline: an automated method for constructing SNP matrices from next-generation sequence data. <i>PeerJ Computer Science</i> , 0, 1, e20.	4.5	254
4	Interpreting Whole-Genome Sequence Analyses of Foodborne Bacteria for Regulatory Applications and Outbreak Investigations. <i>Frontiers in Microbiology</i> , 2018, 9, 1482.	3.5	210
5	Identification of a Salmonellosis Outbreak by Means of Molecular Sequencing. <i>New England Journal of Medicine</i> , 2011, 364, 981-982.	27.0	155
6	Rapid Whole-Genome Sequencing for Surveillance of <i>Salmonella enterica</i> Serovar Enteritidis. <i>Emerging Infectious Diseases</i> , 2014, 20, 1306-1314.	4.3	155
7	On the Evolutionary History, Population Genetics and Diversity among Isolates of <i>Salmonella</i> Enteritidis PFGE Pattern JEGX01.0004. <i>PLoS ONE</i> , 2013, 8, e55254.	2.5	146
8	High resolution clustering of <i>Salmonella enterica</i> serovar Montevideo strains using a next-generation sequencing approach. <i>BMC Genomics</i> , 2012, 13, 32.	2.8	140
9	Phylogenetic Diversity of the Enteric Pathogen <i>Salmonella enterica</i> subsp. <i>enterica</i> Inferred from Genome-Wide Reference-Free SNP Characters. <i>Genome Biology and Evolution</i> , 2013, 5, 2109-2123.	2.5	139
10	Infectious Dose of <i>Listeria monocytogenes</i> in Outbreak Linked to Ice Cream, United States, 2015. <i>Emerging Infectious Diseases</i> , 2016, 22, 2113-2119.	4.3	97
11	Ecological prevalence, genetic diversity, and epidemiological aspects of <i>Salmonella</i> isolated from tomato agricultural regions of the Virginia Eastern Shore. <i>Frontiers in Microbiology</i> , 2015, 6, 415.	3.5	77
12	Genomic Analysis of Closely Related Astroviruses. <i>Journal of Virology</i> , 2008, 82, 5099-5103.	3.4	67
13	Phylogenetics and Differentiation of <i>Salmonella</i> Newport Lineages by Whole Genome Sequencing. <i>PLoS ONE</i> , 2013, 8, e55687.	2.5	63
14	Proficiency testing for bacterial whole genome sequencing: an end-user survey of current capabilities, requirements and priorities. <i>BMC Infectious Diseases</i> , 2015, 15, 174.	2.9	62
15	Optimizing open data to support one health: best practices to ensure interoperability of genomic data from bacterial pathogens. <i>One Health Outlook</i> , 2020, 2, 20.	3.4	50
16	Co-Enriching Microflora Associated with Culture Based Methods to Detect <i>Salmonella</i> from Tomato Phyllosphere. <i>PLoS ONE</i> , 2013, 8, e73079.	2.5	49
17	Prevalence and Level of <i>Listeria monocytogenes</i> in Ice Cream Linked to a Listeriosis Outbreak in the United States. <i>Journal of Food Protection</i> , 2016, 79, 1828-1832.	1.7	49
18	The Public Health Impact of a Publically Available, Environmental Database of Microbial Genomes. <i>Frontiers in Microbiology</i> , 2017, 8, 808.	3.5	48

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19	Outbreak of Salmonella Newport infections linked to cucumbers--United States, 2014. Morbidity and Mortality Weekly Report, 2015, 64, 144-7.	15.1	48
20	Notes from the field: listeriosis associated with stone fruit--United States, 2014. Morbidity and Mortality Weekly Report, 2015, 64, 282-3.	15.1	46
21	An evaluation of alternative methods for constructing phylogenies from whole genome sequence data: a case study with <i>Salmonella</i> . PeerJ, 2014, 2, e620.	2.0	45
22	A Multidrug-Resistant <i>Salmonella</i> Infantis Clone is Spreading and Recombining in the United States. Microbial Drug Resistance, 2021, 27, 792-799.	2.0	44
23	Genetic Diversity of Salmonella and Listeria Isolates from Food Facilities. Journal of Food Protection, 2018, 81, 2082-2089.	1.7	41
24	Prevalence of Salmonella in Cashews, Hazelnuts, Macadamia Nuts, Pecans, Pine Nuts, and Walnuts in the United States. Journal of Food Protection, 2017, 80, 459-466.	1.7	40
25	Whole Genome DNA Sequence Analysis of Salmonella subspecies enterica serotype Tennessee obtained from related peanut butter foodborne outbreaks.. PLoS ONE, 2016, 11, e0146929.	2.5	40
26	Phylogenetic Analysis of Non-O157 Shiga Toxin-Producing Escherichia coli Strains by Whole-Genome Sequencing. Journal of Clinical Microbiology, 2012, 50, 4123-4127.	3.9	39
27	GalaxyTrakr: a distributed analysis tool for public health whole genome sequence data accessible to non-bioinformaticians. BMC Genomics, 2021, 22, 114.	2.8	38
28	GenomeTrakr proficiency testing for foodborne pathogen surveillance: an exercise from 2015. Microbial Genomics, 2018, 4, .	2.0	37
29	Survey of Foodborne Pathogens, Aerobic Plate Counts, Total Coliform Counts, and Escherichia coli Counts in Leafy Greens, Sprouts, and Melons Marketed in the United States. Journal of Food Protection, 2018, 81, 400-411.	1.7	34
30	Whole genome sequencing uses for foodborne contamination and compliance: Discovery of an emerging contamination event in an ice cream facility using whole genome sequencing. Infection, Genetics and Evolution, 2019, 73, 214-220.	2.3	32
31	Prevalence of Salmonella in 11 Spices Offered for Sale from Retail Establishments and in Imported Shipments Offered for Entry to the United States. Journal of Food Protection, 2017, 80, 1791-1805.	1.7	31
32	The evolutionary history and diagnostic utility of the CRISPR-Cas system within <i>Salmonella enterica</i> ssp. <i>enterica</i> . PeerJ, 2014, 2, e340.	2.0	31
33	GenomeGraphR: A user-friendly open-source web application for foodborne pathogen whole genome sequencing data integration, analysis, and visualization. PLoS ONE, 2019, 14, e0213039.	2.5	29
34	Draft Genome Sequences of 21 Salmonella enterica Serovar Enteritidis Strains. Journal of Bacteriology, 2012, 194, 5994-5995.	2.2	27
35	Genetic Diversity and Evolution of Salmonella enterica Serovar Enteritidis Strains with Different Phage Types. Journal of Clinical Microbiology, 2014, 52, 1490-1500.	3.9	26
36	Quasimetagenomic source tracking of Listeria monocytogenes from naturally contaminated ice cream. BMC Infectious Diseases, 2020, 20, 83.	2.9	26

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37	Phylogenomic Pipeline Validation for Foodborne Pathogen Disease Surveillance. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	20
38	Genomic Drivers of Multidrug-Resistant <i>Shigella</i> Affecting Vulnerable Patient Populations in the United States and Abroad. <i>MBio</i> , 2021, 12, .	4.1	19
39	TreeToReads - a pipeline for simulating raw reads from phylogenies. <i>BMC Bioinformatics</i> , 2017, 18, 178.	2.6	16
40	Within-species contamination of bacterial whole-genome sequence data has a greater influence on clustering analyses than between-species contamination. <i>Genome Biology</i> , 2019, 20, 286.	8.8	16
41	Genetic Diversity of <i>Salmonella</i> Pathogenicity Islands SPI-5 and SPI-6 in <i>Salmonella</i> Newport. <i>Foodborne Pathogens and Disease</i> , 2014, 11, 798-807.	1.8	13
42	Real-Time Pathogen Detection in the Era of Whole-Genome Sequencing and Big Data: Comparison of k-mer and Site-Based Methods for Inferring the Genetic Distances among Tens of Thousands of <i>Salmonella</i> Samples. <i>PLoS ONE</i> , 2016, 11, e0166162.	2.5	13
43	Enumeration and characterization of <i>Listeria monocytogenes</i> in novelty ice cream samples manufactured on a specific production line linked to a listeriosis outbreak. <i>Food Control</i> , 2017, 82, 1-7.	5.5	13
44	Gen-FS coordinated proficiency test data for genomic foodborne pathogen surveillance, 2017 and 2018 exercises. <i>Scientific Data</i> , 2020, 7, 402.	5.3	13
45	Draft Genome Sequences of Eight <i>Salmonella enterica</i> Serotype Newport Strains from Diverse Hosts and Locations. <i>Journal of Bacteriology</i> , 2012, 194, 5146-5146.	2.2	10
46	Evaluating the accuracy of <i>Listeria monocytogenes</i> assemblies from quasimetagenomic samples using long and short reads. <i>BMC Genomics</i> , 2021, 22, 389.	2.8	9
47	Fully Assembled Genome Sequence for <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Javiana CFSAN001992. <i>Genome Announcements</i> , 2013, 1, e0008113.	0.8	8
48	Survey of <i>Salmonella</i> in raw tree nuts at retail in the United States. <i>Journal of Food Science</i> , 2021, 86, 495-504.	3.1	6
49	Genomic diversity of <i>Salmonella enterica</i> isolated from papaya samples collected during multiple outbreaks in 2017. <i>Microbiology (United Kingdom)</i> , 2020, 166, 453-459.	1.8	1