Errol Strain

List of Publications by Year
in descending order

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	A Multidrug-Resistant *Salmonella* Infantis Clone is Spreading and Recombining in the United States. Microbial Drug Resistance, 2021, 27, 792-799.	2.0	44
2	Survey of *Salmonella* in raw tree nuts at retail in the United States. Journal of Food Science, 2021, 86, 495-504.	3.1	6
3	GalaxyTrakr: a distributed analysis tool for public health whole genome sequence data accessible to non-bioinformaticians. BMC Genomics, 2021, 22, 114.	2.8	38
4	Evaluating the accuracy of Listeria monocytogenes assemblies from quasimetagenomic samples using long and short reads. BMC Genomics, 2021, 22, 389.	2.8	9
5	Genomic Drivers of Multidrug-Resistant *Shigella* Affecting Vulnerable Patient Populations in the United States and Abroad. MBio, 2021, 12, .	4.1	19
6	Gen-FS coordinated proficiency test data for genomic foodborne pathogen surveillance, 2017 and 2018 exercises. Scientific Data, 2020, 7, 402.	5.3	13
7	Optimizing open data to support one health: best practices to ensure interoperability of genomic data from bacterial pathogens. One Health Outlook, 2020, 2, 20.	3.4	50
8	Quasimetagenomic source tracking of Listeria monocytogenes from naturally contaminated ice cream. BMC Infectious Diseases, 2020, 20, 83.	2.9	26
9	Genomic diversity of Salmonella enterica isolated from papaya samples collected during multiple outbreaks in 2017. Microbiology (United Kingdom), 2020, 166, 453-459.	1.8	1
10	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
11	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
12	Phylogenomic Pipeline Validation for Foodborne Pathogen Disease Surveillance. Journal of Clinical Microbiology, 2019, 57, .	3.9	20
13	Within-species contamination of bacterial whole-genome sequence data has a greater influence on clustering analyses than between-species contamination. Genome Biology, 2019, 20, 286.	8.8	16
14	Genetic Diversity of Salmonella and Listeria Isolates from Food Facilities. Journal of Food Protection, 2018, 81, 2082-2089.	1.7	41
15	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
16	Interpreting Whole-Genome Sequence Analyses of Foodborne Bacteria for Regulatory Applications and Outbreak Investigations. Frontiers in Microbiology, 2018, 9, 1482.	3.5	210
17	GenomeTrakr proficiency testing for foodborne pathogen surveillance: an exercise from 2015. Microbial Genomics, 2018, 4, .	2.0	37
18	Enumeration and characterization of Listeria monocytogenes in novelty ice cream samples manufactured on a specific production line linked to a listeriosis outbreak. Food Control, 2017, 82, 1-7.	5.5	13

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19	TreeToReads - a pipeline for simulating raw reads from phylogenies. BMC Bioinformatics, 2017, 18, 178.	2.6	16
20	The Public Health Impact of a Publically Available, Environmental Database of Microbial Genomes. Frontiers in Microbiology, 2017, 8, 808.	3.5	48
21	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
22	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
23	Prevalence and Level of Listeria monocytogenes in Ice Cream Linked to a Listeriosis Outbreak in the United States. Journal of Food Protection, 2016, 79, 1828-1832.	1.7	49
24	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 Salmonella Samples. PLoS ONE, 2016, 11, e0166162.	2.5	13
25	Infectious Dose of *Listeria monocytogenes* in Outbreak Linked to Ice Cream, United States, 2015. Emerging Infectious Diseases, 2016, 22, 2113-2119.	4.3	97
26	Implementation of Nationwide Real-time Whole-genome Sequencing to Enhance Listeriosis Outbreak Detection and Investigation. Clinical Infectious Diseases, 2016, 63, 380-386.	5.8	330
27	Practical Value of Food Pathogen Traceability through Building a Whole-Genome Sequencing Network and Database. Journal of Clinical Microbiology, 2016, 54, 1975-1983.	3.9	278
28	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
29	Ecological prevalence, genetic diversity, and epidemiological aspects of Salmonella isolated from tomato agricultural regions of the Virginia Eastern Shore. Frontiers in Microbiology, 2015, 6, 415.	3.5	77
30	Proficiency testing for bacterial whole genome sequencing: an end-user survey of current capabilities, requirements and priorities. BMC Infectious Diseases, 2015, 15, 174.	2.9	62
31	Outbreak of Salmonella Newport infections linked to cucumbers--United States, 2014. Morbidity and Mortality Weekly Report, 2015, 64, 144-7.	15.1	48
32	Notes from the field: listeriosis associated with stone fruit--United States, 2014. Morbidity and Mortality Weekly Report, 2015, 64, 282-3.	15.1	46
33	Rapid Whole-Genome Sequencing for Surveillance of *Salmonella enterica* Serovar Enteritidis. Emerging Infectious Diseases, 2014, 20, 1306-1314.	4.3	155
34	Genetic Diversity of *Salmonella* Pathogenicity Islands SPI-5 and SPI-6 in *Salmonella* Newport. Foodborne Pathogens and Disease, 2014, 11, 798-807.	1.8	13
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	The evolutionary history and diagnostic utility of the CRISPR-Cas system within *Salmonella enterica* ssp. *enterica*. PeerJ, 2014, 2, e340.	2.0	31

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37	An evaluation of alternative methods for constructing phylogenies from whole genome sequence data: a case study with *Salmonella*. PeerJ, 2014, 2, e620.	2.0	45
38	Fully Assembled Genome Sequence for Salmonella enterica subsp. enterica Serovar Javiana CFSAN001992. Genome Announcements, 2013, 1, e0008113.	0.8	8
39	Phylogenetic Diversity of the Enteric Pathogen Salmonella enterica subsp. enterica Inferred from Genome-Wide Reference-Free SNP Characters. Genome Biology and Evolution, 2013, 5, 2109-2123.	2.5	139
40	On the Evolutionary History, Population Genetics and Diversity among Isolates of Salmonella Enteritidis PFGE Pattern JEGX01.0004. PLoS ONE, 2013, 8, e55254.	2.5	146
41	Co-Enriching Microflora Associated with Culture Based Methods to Detect Salmonella from Tomato Phyllosphere. PLoS ONE, 2013, 8, e73079.	2.5	49
42	Phylogenetics and Differentiation of Salmonella Newport Lineages by Whole Genome Sequencing. PLoS ONE, 2013, 8, e55687.	2.5	63
43	Draft Genome Sequences of 21 Salmonella enterica Serovar Enteritidis Strains. Journal of Bacteriology, 2012, 194, 5994-5995.	2.2	27
44	Draft Genome Sequences of Eight Salmonella enterica Serotype Newport Strains from Diverse Hosts and Locations. Journal of Bacteriology, 2012, 194, 5146-5146.	2.2	10
45	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
46	High resolution clustering of Salmonella enterica serovar Montevideo strains using a next-generation sequencing approach. BMC Genomics, 2012, 13, 32.	2.8	140
47	Identification of a Salmonellosis Outbreak by Means of Molecular Sequencing. New England Journal of Medicine, 2011, 364, 981-982.	27.0	155
48	Genomic Analysis of Closely Related Astroviruses. Journal of Virology, 2008, 82, 5099-5103.	3.4	67
49	CFSAN SNP Pipeline: an automated method for constructing SNP matrices from next-generation sequence data. PeerJ Computer Science, 0, 1, e20.	4.5	254