

Ruth E Timme

List of Publications by Year in descending order

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66
papers

4,009
citations

147801

31
h-index

128289

60
g-index

147
all docs

147
docs citations

147
times ranked

4847
citing authors

#	ARTICLE	IF	CITATIONS
1	Multi-laboratory evaluation of the Illumina iSeq platform for whole genome sequencing of Salmonella, Escherichia coli and Listeria. <i>Microbial Genomics</i> , 2022, 8, .	2.0	3
2	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
3	Use of Whole Genome Sequencing by the Federal Interagency Collaboration for Genomics for Food and Feed Safety in the United States. <i>Journal of Food Protection</i> , 2022, 85, 755-772.	1.7	42
4	Phylogenetic and Biogeographic Patterns of <i>Vibrio parahaemolyticus</i> Strains from North America Inferred from Whole-Genome Sequence Data. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	6
5	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborative's™s Workshop and Follow-On Activities. <i>MSystems</i> , 2021, 6, .	3.8	28
6	Phylogeny of <i>Salmonella enterica</i> subspecies <i>arizonae</i> by whole-genome sequencing reveals high incidence of polyphyly and low phase 1 H antigen variability. <i>Microbial Genomics</i> , 2021, 7, .	2.0	3
7	Salmonella Genomics in Public Health and Food Safety. <i>EcoSal Plus</i> , 2021, 9, eESP00082020.	5.4	23
8	Interpretative Labor and the Bane of Nonstandardized Metadata in Public Health Surveillance and Food Safety. <i>Clinical Infectious Diseases</i> , 2021, 73, 1537-1539.	5.8	13
9	Food Safety Genomics and Connections to One Health and the Clinical Microbiology Laboratory. <i>Clinics in Laboratory Medicine</i> , 2020, 40, 553-563.	1.4	5
10	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
11	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
12	Closed Genome Sequences of 28 Foodborne Pathogens from the CFSAN Verification Set, Determined by a Combination of Long and Short Reads. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	3
13	Whole genome sequencing uses for foodborne contamination and compliance: Discovery of an emerging contamination event in an ice cream facility using whole genome sequencing. <i>Infection, Genetics and Evolution</i> , 2019, 73, 214-220.	2.3	32
14	Phylogenomic Pipeline Validation for Foodborne Pathogen Disease Surveillance. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	20
15	Utilizing the Public GenomeTrakr Database for Foodborne Pathogen Traceback. <i>Methods in Molecular Biology</i> , 2019, 1918, 201-212.	0.9	50
16	Identification of <i>Brucella</i> genus and eight <i>Brucella</i> species by Luminex bead-based suspension array. <i>Food Microbiology</i> , 2018, 70, 113-119.	4.2	11
17	Genomics of foodborne pathogens for microbial food safety. <i>Current Opinion in Biotechnology</i> , 2018, 49, 224-229.	6.6	129
18	Genetic Diversity of <i>Salmonella</i> and <i>Listeria</i> Isolates from Food Facilities. <i>Journal of Food Protection</i> , 2018, 81, 2082-2089.	1.7	41

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19	Salmonella enterica Phylogeny Based on Whole-Genome Sequencing Reveals Two New Clades and Novel Patterns of Horizontally Acquired Genetic Elements. MBio, 2018, 9, .	4.1	71
20	Resistome of carbapenem- and colistin-resistant Klebsiella pneumoniae clinical isolates. PLoS ONE, 2018, 13, e0198526.	2.5	53
21	GenomeTrakr proficiency testing for foodborne pathogen surveillance: an exercise from 2015. Microbial Genomics, 2018, 4, .	2.0	37
22	Singleton Sequence Type 382, an Emerging Clonal Group of Listeria monocytogenes Associated with Three Multistate Outbreaks Linked to Contaminated Stone Fruit, Caramel Apples, and Leafy Green Salad. Journal of Clinical Microbiology, 2017, 55, 931-941.	3.9	56
23	Whole Genome and Core Genome Multilocus Sequence Typing and Single Nucleotide Polymorphism Analyses of Listeria monocytogenes Isolates Associated with an Outbreak Linked to Cheese, United States, 2013. Applied and Environmental Microbiology, 2017, 83, .	3.1	93
24	An analysis of Echinacea chloroplast genomes: Implications for future botanical identification. Scientific Reports, 2017, 7, 216.	3.3	52
25	Development of a Reference Standard Library of Chloroplast Genome Sequences, GenomeTrakrCP. Planta Medica, 2017, 83, 1420-1430.	1.3	19
26	TreeToReads - a pipeline for simulating raw reads from phylogenies. BMC Bioinformatics, 2017, 18, 178.	2.6	16
27	The Public Health Impact of a Publically Available, Environmental Database of Microbial Genomes. Frontiers in Microbiology, 2017, 8, 808.	3.5	48
28	The Rise of Genomics and the Promise of Whole Genome Sequencing for Understanding Microbial Foodborne Pathogens. , 2017, , 333-351.		5
29	Assessing the genome level diversity of Listeria monocytogenes from contaminated ice cream and environmental samples linked to a listeriosis outbreak in the United States. PLoS ONE, 2017, 12, e0171389.	2.5	72
30	Benchmark datasets for phylogenomic pipeline validation, applications for foodborne pathogen surveillance. PeerJ, 2017, 5, e3893.	2.0	61
31	Draft Genome Sequences of 40 Salmonella enterica Serovar Typhimurium Strains Isolated from Humans and Food in Brazil. Genome Announcements, 2016, 4, .	0.8	5
32	Genome Sequences of Multidrug-Resistant, Colistin-Susceptible and -Resistant Klebsiella pneumoniae Clinical Isolates from Pakistan. Genome Announcements, 2016, 4, .	0.8	5
33	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
34	Listeria monocytogenes in Stone Fruits Linked to a Multistate Outbreak: Enumeration of Cells and Whole-Genome Sequencing. Applied and Environmental Microbiology, 2016, 82, 7030-7040.	3.1	83
35	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
36	Genome-Wide Methylation Patterns in Salmonella enterica Subsp. enterica Serovars. PLoS ONE, 2015, 10, e0123639.	2.5	51

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37	Draft Genome Sequences of Histamine-Producing <i>Photobacterium kishitanii</i> and <i>Photobacterium angustum</i> , Isolated from Albacore (<i>Thunnus alalunga</i>) and Yellowfin (<i>Thunnus albacares</i>) Tuna. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
38	Characterization of <i>Vibrio parahaemolyticus</i> clinical strains from Maryland (2012–2013) and comparisons to a locally and globally diverse <i>V. parahaemolyticus</i> strains by whole-genome sequence analysis. <i>Frontiers in Microbiology</i> , 2015, 6, 125.	3.5	40
39	Draft Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Give, Isolated from an Imported Chili Powder Product. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
40	Characterization and evolution of <i>Salmonella</i> CRISPR-Cas systems. <i>Microbiology (United Kingdom)</i> , 2015, 161, 374-386.	1.8	98
41	Whole-Genome Single-Nucleotide-Polymorphism Analysis for Discrimination of <i>Clostridium botulinum</i> Group I Strains. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2125-2132.	3.1	36
42	First Fully Closed Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Cubana Associated with a Food-Borne Outbreak. <i>Genome Announcements</i> , 2014, 2, .	0.8	11
43	Draft Genome Sequences of Clinical <i>Vibrio parahaemolyticus</i> Strains Isolated in Maryland (2010 to 2013). <i>Journal of Clinical Microbiology</i> , 2014, 52, 1074-1081.	0.8	5
44	The evolutionary history and diagnostic utility of the CRISPR-Cas system within <i>Salmonella enterica</i> ssp. <i>enterica</i> . <i>PeerJ</i> , 2014, 2, e340.	2.0	31
45	Development of a Locked Nucleic Acid Real-Time Polymerase Chain Reaction Assay for the Detection of <i>Pinus armandii</i> in Mixed Species Pine Nut Samples Associated with Dysgeusia. <i>Journal of Agricultural and Food Chemistry</i> , 2013, 61, 1060-1066.	5.2	16
46	Genome Sequences of <i>Salmonella enterica</i> Serovar Heidelberg Isolates Isolated in the United States from a Multistate Outbreak of Human <i>Salmonella</i> Infections. <i>Genome Announcements</i> , 2013, 1, .	0.8	22
47	Draft Genome Sequence of a <i>Clostridium botulinum</i> Isolate from Water Used for Cooling at a Plant Producing Low-Acid Canned Foods. <i>Genome Announcements</i> , 2013, 1, .	0.8	1
48	Genome Sequences of Two Emerging Non-O157 Shiga Toxin-Producing <i>Escherichia coli</i> Strains. <i>Genome Announcements</i> , 2013, 1, .	0.8	3
49	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
50	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
51	Complete Genome Sequence of a Multidrug-Resistant <i>Salmonella enterica</i> Serovar Typhimurium var. 5a ⁺ Strain Isolated from Chicken Breast. <i>Genome Announcements</i> , 2013, 1, .	0.8	39
52	On the Evolutionary History, Population Genetics and Diversity among Isolates of <i>Salmonella enteritidis</i> PFGE Pattern JEGX01.0004. <i>PLoS ONE</i> , 2013, 8, e55254.	2.5	146
53	Draft Genome Sequences of 21 <i>Salmonella enterica</i> Serovar Enteritidis Strains. <i>Journal of Bacteriology</i> , 2012, 194, 5994-5995.	2.2	27
54	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

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55	Phylogenetic Analysis of Non-O157 Shiga Toxin-Producing <i>Escherichia coli</i> Strains by Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2012, 50, 4123-4127.	3.9	39
56	Origin of strigolactones in the green lineage. <i>New Phytologist</i> , 2012, 195, 857-871.	7.3	258
57	Broad Phylogenomic Sampling and the Sister Lineage of Land Plants. <i>PLoS ONE</i> , 2012, 7, e29696.	2.5	234
58	Plants. <i>Current Biology</i> , 2011, 21, R417-R422.	3.9	15
59	Unraveling the Evolution of Auxin Signaling. <i>Plant Physiology</i> , 2011, 155, 209-221.	4.8	140
60	Uncovering the evolutionary origin of plant molecular processes: comparison of <i>Coleochaete</i> (<i>Coleochaetales</i>) and <i>Spirogyra</i> (<i>Zygnematales</i>) transcriptomes. <i>BMC Plant Biology</i> , 2010, 10, 96.	3.6	91
61	Multigene Phylogeny of the Green Lineage Reveals the Origin and Diversification of Land Plants. <i>Current Biology</i> , 2010, 20, 2217-2222.	3.9	178
62	PHYLOGENY OF FOUR DINOPHYSIACEAN GENERA (<i>DINOPHYCEAE</i> , <i>DINOPHYSIALES</i>) BASED ON rDNA SEQUENCES FROM SINGLE CELLS AND ENVIRONMENTAL SAMPLES. <i>Journal of Phycology</i> , 2009, 45, 1163-1174.	2.3	33
63	A comparative analysis of the <i>Lactuca</i> and <i>Helianthus</i> (<i>Asteraceae</i>) plastid genomes: identification of divergent regions and categorization of shared repeats. <i>American Journal of Botany</i> , 2007, 94, 302-312.	1.7	258
64	High-resolution phylogeny for <i>Helianthus</i> (<i>Asteraceae</i>) using the 18S-26S ribosomal DNA external transcribed spacer. <i>American Journal of Botany</i> , 2007, 94, 1837-1852.	1.7	89
65	Using MoBloS' scalable genome join to find conserved primer pair candidates between two genomes. <i>Bioinformatics</i> , 2004, 20, i355-i362.	4.1	15
66	Phylogenetic networks: modeling, reconstructibility, and accuracy. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2004, 1, 13-23.	3.0	135