

Simon H Tausch

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

651
citations

623734

14
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642732

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34
all docs

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docs citations

34
times ranked

929
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic and biological characteristics of species A rotaviruses detected in common shrews suggest a distinct evolutionary trajectory. <i>Virus Evolution</i> , 2022, 8, veac004.	4.9	7
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	Whole Genome Sequence Analysis of a Prototype Strain of the Novel Putative Rotavirus Species L. <i>Viruses</i> , 2022, 14, 462.	3.3	18
4	Toward an Integrated Genome-Based Surveillance of <i>Salmonella enterica</i> in Germany. <i>Frontiers in Microbiology</i> , 2021, 12, 626941.	3.5	16
5	Outcome of Different Sequencing and Assembly Approaches on the Detection of Plasmids and Localization of Antimicrobial Resistance Genes in Commensal <i>Escherichia coli</i> . <i>Microorganisms</i> , 2021, 9, 598.	3.6	36
6	Species-Specific Quality Control, Assembly and Contamination Detection in Microbial Isolate Sequences with AQUAMIS. <i>Genes</i> , 2021, 12, 644.	2.4	42
7	Decentralized Investigation of Bacterial Outbreaks Based on Hashed cgMLST. <i>Frontiers in Microbiology</i> , 2021, 12, 649517.	3.5	22
8	Comparative genomics of <i>Salmonella enterica</i> subsp. <i>diarizonae</i> serovar 61:k:1,5,(7) reveals lineage-specific host adaptation of ST432. <i>Microbial Genomics</i> , 2021, 7, .	2.0	2
9	What WGS Reveals about <i>Salmonella enterica</i> subsp. <i>enterica</i> in Wildlife in Germany. <i>Microorganisms</i> , 2021, 9, 1911.	3.6	10
10	German-Wide Interlaboratory Study Compares Consistency, Accuracy and Reproducibility of Whole-Genome Short Read Sequencing. <i>Frontiers in Microbiology</i> , 2020, 11, 573972.	3.5	12
11	Reply to Li et al., "GC Content-Associated Sequencing Bias Caused by Library Preparation Method May Infrequently Affect <i>Salmonella</i> Serotype Prediction Using SeqSero" Applied and Environmental Microbiology, 2020, 86, .	3.1	2
12	Proficiency Testing of Metagenomics-Based Detection of Food-Borne Pathogens Using a Complex Artificial Sequencing Dataset. <i>Frontiers in Microbiology</i> , 2020, 11, 575377.	3.5	7
13	First Detection of GES-5-Producing <i>Escherichia coli</i> from Livestock "An Increasing Diversity of Carbapenemases Recognized from German Pig Production. <i>Microorganisms</i> , 2020, 8, 1593.	3.6	13
14	Whole genome sequence analysis of cell culture-adapted rotavirus A strains from chicken. <i>Infection, Genetics and Evolution</i> , 2020, 81, 104275.	2.3	6
15	Typing methods based on whole genome sequencing data. <i>One Health Outlook</i> , 2020, 2, 3.	3.4	90
16	Establishment of a Plasmid-Based Reverse Genetics System for the Cell Culture-Adapted Hepatitis E Virus Genotype 3c Strain 47832c. <i>Pathogens</i> , 2020, 9, 157.	2.8	10
17	Performance and Accuracy of Four Open-Source Tools for <i>In Silico</i> Serotyping of <i>Salmonella</i> spp. Based on Whole-Genome Short-Read Sequencing Data. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	40
18	Complete Genome Sequence of <i>Salmonella enterica</i> subsp. <i>diarizonae</i> Serovar 61:k:1,5,(7) Strain 14-SA00836-0, Isolated from Human Urine. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	6

#	ARTICLE	IF	CITATIONS
19	Fishing in the Soup – Pathogen Detection in Food Safety Using Metabarcoding and Metagenomic Sequencing. <i>Frontiers in Microbiology</i> , 2019, 10, 1805.	3.5	49
20	First complete genome sequence and comparative analysis of <i>Salmonella enterica</i> subsp. <i>diarizonae</i> serovar 61:k:1,5,(7) indicates host adaptation traits to sheep. <i>Gut Pathogens</i> , 2019, 11, 48.	3.4	8
21	Reliable variant calling during runtime of Illumina sequencing. <i>Scientific Reports</i> , 2019, 9, 16502.	3.3	10
22	Distantly Related Rotaviruses in Common Shrews, Germany, 2004–2014. <i>Emerging Infectious Diseases</i> , 2019, 25, 2310-2314.	4.3	34
23	PriLive: privacy-preserving real-time filtering for next-generation sequencing. <i>Bioinformatics</i> , 2018, 34, 2376-2383.	4.1	5
24	Whole Genome Characterization of Orthopoxvirus (OPV) Abatino, a Zoonotic Virus Representing a Putative Novel Clade of Old World Orthopoxviruses. <i>Viruses</i> , 2018, 10, 546.	3.3	17
25	PAIPLINE: pathogen identification in metagenomic and clinical next generation sequencing samples. <i>Bioinformatics</i> , 2018, 34, i715-i721.	4.1	27
26	LiveKraken – real-time metagenomic classification of illumina data. <i>Bioinformatics</i> , 2018, 34, 3750-3752.	4.1	25
27	HiLive: real-time mapping of illumina reads while sequencing. <i>Bioinformatics</i> , 2017, 33, 917-919.	4.1	18
28	An Early American Smallpox Vaccine Based on Horsepox. <i>New England Journal of Medicine</i> , 2017, 377, 1491-1492.	27.0	56
29	Berlin Squirrelpox Virus, a New Poxvirus in Red Squirrels, Berlin, Germany. <i>Emerging Infectious Diseases</i> , 2017, 23, 1726-1729.	4.3	9
30	RAMBO-K: Rapid and Sensitive Removal of Background Sequences from Next Generation Sequencing Data. <i>PLoS ONE</i> , 2015, 10, e0137896.	2.5	18