Simon H Tausch

List of Publications by Year
in descending order

30 papers	651 citations	623734 14 h-index
34 all docs	34 docs citations	34 times ranked

642732 23 g-index
929 citing authors

#	Article	IF	Citations
1	Typing methods based on whole genome sequencing data. One Health Outlook, 2020, 2, 3.	3.4	90
2	An Early American Smallpox Vaccine Based on Horsepox. New England Journal of Medicine, 2017, 377, 1491-1492.	27.0	56
3	Fishing in the Soup â€" Pathogen Detection in Food Safety Using Metabarcoding and Metagenomic Sequencing. Frontiers in Microbiology, 2019, 10, 1805.	3.5	49
4	Species-Specific Quality Control, Assembly and Contamination Detection in Microbial Isolate Sequences with AQUAMIS. Genes, 2021, 12, 644.	2.4	42
5	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. Applied and Environmental Microbiology, 2020, 86, .	3.1	40
6	Outcome of Different Sequencing and Assembly Approaches on the Detection of Plasmids and Localization of Antimicrobial Resistance Genes in Commensal Escherichia coli. Microorganisms, 2021, 9, 598.	3.6	36
7	Distantly Related Rotaviruses in Common Shrews, Germany, 2004â€"2014. Emerging Infectious Diseases, 2019, 25, 2310-2314.	4.3	34
8	PAIPline: pathogen identification in metagenomic and clinical next generation sequencing samples. Bioinformatics, 2018, 34, i715-i721.	4.1	27
9	LiveKrakenâ€"â€"real-time metagenomic classification of illumina data. Bioinformatics, 2018, 34, 3750-3752.	4.1	25
10	Decentralized Investigation of Bacterial Outbreaks Based on Hashed cgMLST. Frontiers in Microbiology, 2021, 12, 649517.	3.5	22
11	HiLive: real-time mapping of illumina reads while sequencing. Bioinformatics, 2017, 33, 917-319.	4.1	18
12	RAMBO-K: Rapid and Sensitive Removal of Background Sequences from Next Generation Sequencing Data. PLoS ONE, 2015, 10, e0137896.	2.5	18
13	Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package. GigaScience, 2022, 11, .	6.4	18
14	Whole Genome Sequence Analysis of a Prototype Strain of the Novel Putative Rotavirus Species L. Viruses, 2022, 14, 462.	3.3	18
15	Whole Genome Characterization of Orthopoxvirus (OPV) Abatino, a Zoonotic Virus Representing a Putative Novel Clade of Old World Orthopoxviruses. Viruses, 2018, 10, 546.	3.3	17
16	Toward an Integrated Genome-Based Surveillance of Salmonella enterica in Germany. Frontiers in Microbiology, 2021, 12, 626941.	3.5	16
17	First Detection of GES-5-Producing Escherichia coli from Livestockâ€"An Increasing Diversity of Carbapenemases Recognized from German Pig Production. Microorganisms, 2020, 8, 1593.	3.6	13
18	German-Wide Interlaboratory Study Compares Consistency, Accuracy and Reproducibility of Whole-Genome Short Read Sequencing. Frontiers in Microbiology, 2020, 11, 573972.	3.5	12

#	ARTICLE	IF	CITATIONS
19	Reliable variant calling during runtime of Illumina sequencing. Scientific Reports, 2019, 9, 16502.	3.3	10
20	Establishment of a Plasmid-Based Reverse Genetics System for the Cell Culture-Adapted Hepatitis E Virus Genotype 3c Strain 47832c. Pathogens, 2020, 9, 157.	2.8	10
21	What WGS Reveals about Salmonella enterica subsp. enterica in Wildlife in Germany. Microorganisms, 2021, 9, 1911.	3.6	10
22	Berlin Squirrelpox Virus, a New Poxvirus in Red Squirrels, Berlin, Germany. Emerging Infectious Diseases, 2017, 23, 1726-1729.	4.3	9
23	First complete genome sequence and comparative analysis of Salmonella enterica subsp. diarizonae serovar 61:ꝅ:1,5,(7) indicates host adaptation traits to sheep. Gut Pathogens, 2019, 11, 48.	3.4	8
24	Proficiency Testing of Metagenomics-Based Detection of Food-Borne Pathogens Using a Complex Artificial Sequencing Dataset. Frontiers in Microbiology, 2020, 11, 575377.	3.5	7
25	Genetic and biological characteristics of species A rotaviruses detected in common shrews suggest a distinct evolutionary trajectory. Virus Evolution, 2022, 8, veac004.	4.9	7
26	Whole genome sequence analysis of cell culture-adapted rotavirus A strains from chicken. Infection, Genetics and Evolution, 2020, 81, 104275.	2.3	6
27	Complete Genome Sequence of Salmonella enterica subsp. <i>diarizonae</i> Serovar 61:ꝅ:1,5,(7) Strain 14-SA00836-0, Isolated from Human Urine. Microbiology Resource Announcements, 2020, 9, .	0.6	6
28	PriLive: privacy-preserving real-time filtering for next-generation sequencing. Bioinformatics, 2018, 34, 2376-2383.	4.1	5
29	Reply to Li et al., â€œGC Content-Associated Sequencing Bias Caused by Library Preparation Method May Infrequently Affect Salmonella Serotype Prediction Using SeqSero2â€. Applied and Environmental Microbiology, 2020, 86, .	3.1	2
30	Comparative genomics of Salmonella enterica subsp. diarizonae serovar 61:ꝅ:1,5,(7) reveals lineage-specific host adaptation of ST432. Microbial Genomics, 2021, 7, .	2.0	2