

Stephan C Schuster

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

7,607
citations

218677
26
h-index

85541
71
g-index

88
all docs

88
docs citations

88
times ranked

13957
citing authors

#	ARTICLE	IF	CITATIONS
1	Airborne SARS-CoV-2 surveillance in hospital environment using high-flowrate air samplers and its comparison to surface sampling. <i>Indoor Air</i> , 2022, 32, .	4.3	27
2	Vertical stratification of the air microbiome in the lower troposphere. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	13
3	Short-range contributions of local sources to ambient air. , 2022, 1, .		1
4	Integrative multiomics analysis reveals host-microbe-metabolite interplays associated with the aging process in Singaporeans. <i>Gut Microbes</i> , 2022, 14, 2070392.	9.8	6
5	Insights into bear evolution from a Pleistocene polar bear genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	11
6	The genomic characterisation and comparison of <i>Bacillus cereus</i> strains isolated from indoor air. <i>Gut Pathogens</i> , 2021, 13, 6.	3.4	9
7	Human ACE2 receptor polymorphisms and altered susceptibility to SARS-CoV-2. <i>Communications Biology</i> , 2021, 4, 475.	4.4	126
8	Experimental parameters defining ultra-low biomass bioaerosol analysis. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 37.	6.4	27
9	Effective design of barrier enclosure to contain aerosol emissions from COVID-19 patients. <i>Indoor Air</i> , 2021, 31, 1639-1644.	4.3	12
10	Genomic and Phenotypic Characterization of <i>Chloracidobacterium</i> Isolates Provides Evidence for Multiple Species. <i>Frontiers in Microbiology</i> , 2021, 12, 704168.	3.5	3
11	A synbiotic intervention modulates meta-omics signatures of gut redox potential and acidity in elective caesarean born infants. <i>BMC Microbiology</i> , 2021, 21, 191.	3.3	13
12	Evolutionary and phylogenetic insights from a nuclear genome sequence of the extinct, giant, subfossil koala lemur <i>Megaladapis edwardsi</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	12
13	Periodontitis associates with species-specific gene expression of the oral microbiota. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 76.	6.4	18
14	Coronavirus viability in surgical plume and methods for safe disposal: a preclinical model. <i>British Journal of Surgery</i> , 2021, , .	0.3	0
15	Imputation Performance in Latin American Populations: Improving Rare Variants Representation With the Inclusion of Native American Genomes. <i>Frontiers in Genetics</i> , 2021, 12, 719791.	2.3	7
16	A compromised developmental trajectory of the infant gut microbiome and metabolome in atopic eczema. <i>Gut Microbes</i> , 2020, 12, 1801964.	9.8	51
17	Taxonomic composition and seasonal dynamics of the air microbiome in West Siberia. <i>Scientific Reports</i> , 2020, 10, 21515.	3.3	10
18	Environmental fungal sensitisation associates with poorer clinical outcomes in COPD. <i>European Respiratory Journal</i> , 2020, 56, 2000418.	6.7	44

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19	Longitudinal assessment of antibiotic resistance gene profiles in gut microbiomes of infants at risk of eczema. <i>BMC Infectious Diseases</i> , 2020, 20, 312.	2.9	11
20	Detection of air and surface contamination by SARS-CoV-2 in hospital rooms of infected patients. <i>Nature Communications</i> , 2020, 11, 2800.	12.8	703
21	Whole-Genome Sequencing of <i>Aspergillus terreus</i> Species Complex. <i>Mycopathologia</i> , 2020, 185, 405-408.	3.1	7
22	Complete genome of <i>Enterobacter sichuanensis</i> strain SGAir0282 isolated from air in Singapore. <i>Gut Pathogens</i> , 2020, 12, 12.	3.4	1
23	Metagenomics Reveals a Core Macrolide Resistome Related to Microbiota in Chronic Respiratory Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 202, 433-447.	5.6	58
24	Complete Genome Sequence of <i>Penicillium oxalicum</i> Strain SGAir0226 Isolated from Outdoor Tropical Air in Singapore. <i>Mycopathologia</i> , 2020, 185, 591-594.	3.1	3
25	Systematic evaluation of library preparation methods and sequencing platforms for high-throughput whole genome bisulfite sequencing. <i>Scientific Reports</i> , 2019, 9, 10383.	3.3	57
26	Complete Genome Sequence of <i>Citricoccus</i> sp. Strain SGAir0253, Isolated from Indoor Air in Singapore. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
27	Complete Genome Sequence of <i>Microbacterium</i> sp. Strain SGAir0570, Isolated from Tropical Air Collected in Singapore. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
28	NARD: whole-genome reference panel of 1779 Northeast Asians improves imputation accuracy of rare and low-frequency variants. <i>Genome Medicine</i> , 2019, 11, 64.	8.2	28
29	Genome Sequence of the Tropical Atmosphere Bacterium <i>Pontibacter</i> sp. Strain SGAir0037. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0
30	Complete Genome Sequence of <i>Agrococcus</i> sp. Strain SGAir0287, Isolated from Tropical Air Collected in Singapore. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0
31	Pleiotropic Effects of c-di-GMP Content in <i>Pseudomonas syringae</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	28
32	Complete Genome Sequence of <i>Micrococcus luteus</i> Strain SGAir0127, Isolated from Indoor Air Samples from Singapore. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	7
33	Whole-Genome Sequence of <i>Bacillus megaterium</i> Strain SGAir0080, Isolated from an Indoor Air Sample. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
34	Complete Genome Sequence of <i>Curtobacterium</i> sp. Strain SGAir0471, Isolated from Singapore Air Samples. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	0
35	Neurogenesis and longevity signaling in young germ-free mice transplanted with the gut microbiota of old mice. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	122
36	Complete Genome Sequence of <i>Brachybacterium</i> sp. Strain SGAir0954, Isolated from Singapore Air. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4

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37	Microbial communities in the tropical air ecosystem follow a precise diel cycle. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23299-23308.	7.1	99
38	Complete Genome Sequence of <i>Lysinibacillus</i> sp. Strain SGAir0095, Isolated from Tropical Air Samples Collected in Singapore. Microbiology Resource Announcements, 2019, 8, .	0.6	2
39	Complete Genome Sequence of <i>Streptomyces</i> sp. Strain SGAir0924, an Actinobacterium Isolated from Outdoor Air in Singapore. Microbiology Resource Announcements, 2019, 8, .	0.6	2
40	Complete Genome Sequence of <i>Nissabacter</i> sp. Strain SGAir0207, Isolated from an Air Sample Collected in Singapore. Microbiology Resource Announcements, 2019, 8, .	0.6	1
41	Complete Genome Sequence of <i>Pseudomonas</i> sp. Strain SGAir0191, Isolated from Tropical Air Collected in Singapore. Microbiology Resource Announcements, 2019, 8, .	0.6	0
42	Complete Genome Sequence of <i>Brevundimonas</i> sp. Strain SGAir0440, Isolated from Indoor Air in Singapore. Microbiology Resource Announcements, 2019, 8, .	0.6	0
43	Complete Genome Sequence of <i>Enterococcus faecalis</i> Strain SGAir0397, Isolated from a Tropical Air Sample Collected in Singapore. Microbiology Resource Announcements, 2019, 8, .	0.6	0
44	Complete Genome Sequence of <i>Rhodococcus</i> sp. Strain SGAir0479, Isolated from Indoor Air Collected in Singapore. Microbiology Resource Announcements, 2019, 8, .	0.6	1
45	623. Dynamic Nature of the Gut Resistome Among Infants in Singapore. Open Forum Infectious Diseases, 2018, 5, S227-S228.	0.9	1
46	Repurposing the anticancer drug cisplatin with the aim of developing novel <i>Pseudomonas aeruginosa</i> infection control agents. Beilstein Journal of Organic Chemistry, 2018, 14, 3059-3069.	2.2	25
47	Complete Genome Sequence of <i>Acinetobacter indicus</i> Type Strain SGAir0564 Isolated from Tropical Air Collected in Singapore. Genome Announcements, 2018, 6, .	0.8	2
48	Genome Sequence of <i>Bacillus velezensis</i> SGAir0473, Isolated from Tropical Air Collected in Singapore. Genome Announcements, 2018, 6, .	0.8	7
49	Complete Genome Sequence of <i>Lelliottia nimipressuralis</i> Type Strain SGAir0187, Isolated from Tropical Air Collected in Singapore. Genome Announcements, 2018, 6, .	0.8	5
50	Complete Genome Sequence of the Bacterium <i>Serratia marcescens</i> SGAir0764, Isolated from Singapore Air. Genome Announcements, 2018, 6, .	0.8	1
51	Complete Genome Sequence of <i>Pseudomonas stutzeri</i> Type Strain SGAir0442, Isolated from Singapore Air Samples. Genome Announcements, 2018, 6, .	0.8	1
52	Complete Genome Sequence of <i>Acinetobacter schindleri</i> SGAir0122 Isolated from Singapore Air. Genome Announcements, 2018, 6, .	0.8	2
53	Complete Genome Sequence of <i>Staphylococcus haemolyticus</i> Type Strain SGAir0252. Genome Announcements, 2018, 6, .	0.8	4
54	Whole-genome analysis of <i>Mustela erminea</i> finds that pulsed hybridization impacts evolution at high altitudes. Communications Biology, 2018, 1, 51.	4.4	24

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55	Characterization of a novel multidrug resistance plasmid pSGB23 isolated from <i>Salmonella enterica</i> subspecies <i>enterica</i> serovar Saintpaul. <i>Gut Pathogens</i> , 2018, 10, 20.	3.4	6
56	Genome Sequence of <i>Geobacillus thermoleovorans</i> SGAir0734, Isolated from Singapore Air. <i>Genome Announcements</i> , 2018, 6, .	0.8	4
57	Genome Sequence of <i>Pantoea ananatis</i> SGAir0210, Isolated from Outdoor Air in Singapore. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
58	Acquisition of resistance to carbapenem and macrolide-mediated quorum sensing inhibition by <i>Pseudomonas aeruginosa</i> via ICETn43716385. <i>Communications Biology</i> , 2018, 1, 57.	4.4	29
59	Long-read sequencing uncovers the adaptive topography of a carnivorous plant genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4435-E4441.	7.1	95
60	Metagenomic and metatranscriptomic analysis of saliva reveals disease-associated microbiota in patients with periodontitis and dental caries. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 23.	6.4	109
61	The rapid <i>in vivo</i> evolution of <i>Pseudomonas aeruginosa</i> in ventilator-associated pneumonia patients leads to attenuated virulence. <i>Open Biology</i> , 2017, 7, 170029.	3.6	50
62	The microbiomes of blowflies and houseflies as bacterial transmission reservoirs. <i>Scientific Reports</i> , 2017, 7, 16324.	3.3	115
63	Complete Genome Sequence of <i>Bacillus altitudinis</i> Type Strain SGAir0031 Isolated from Tropical Air Collected in Singapore. <i>Genome Announcements</i> , 2017, 5, .	0.8	9
64	Development of novel genic microsatellite markers from transcriptome sequencing in sugar maple (<i>Acer saccharum</i> Marsh.). <i>BMC Research Notes</i> , 2017, 10, 369.	1.4	9
65	Genome Sequence of <i>Prosthecochloris</i> sp. Strain HL-130-GSB, from the Phylum Chlorobi. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
66	Large-scale mitogenomics enables insights into <i>Schizophora</i> (Diptera) radiation and population diversity. <i>Scientific Reports</i> , 2016, 6, 21762.	3.3	66
67	Mitogenomes reveal diversity of the European Lyme borreliosis vector <i>Ixodes ricinus</i> in Italy. <i>Molecular Phylogenetics and Evolution</i> , 2016, 101, 194-202.	2.7	26
68	Data characterizing the chloroplast genomes of extinct and endangered Hawaiian endemic mints (Lamiaceae) and their close relatives. <i>Data in Brief</i> , 2016, 7, 900-922.	1.0	4
69	Horizontal gene transfer is more frequent with increased heterotrophy and contributes to parasite adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7010-E7019.	7.1	85
70	The quest to resolve recent radiations: Plastid phylogenomics of extinct and endangered Hawaiian endemic mints (Lamiaceae). <i>Molecular Phylogenetics and Evolution</i> , 2016, 99, 16-33.	2.7	47
71	In silico analyses of metagenomes from human atherosclerotic plaque samples. <i>Microbiome</i> , 2015, 3, 38.	11.1	87
72	Draft Genome Sequence of <i>Thauera</i> sp. Strain SWB20, Isolated from a Singapore Wastewater Treatment Facility Using Gel Microdroplets. <i>Genome Announcements</i> , 2015, 3, .	0.8	5

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73	Comparative and population mitogenomic analyses of Madagascar's extinct, giant "subfossil" lemurs. <i>Journal of Human Evolution</i> , 2015, 79, 45-54.	2.6	86
74	Khoisan hunter-gatherers have been the largest population throughout most of modern-human demographic history. <i>Nature Communications</i> , 2014, 5, 5692.	12.8	65
75	Whole Genome Sequencing and Analysis of Plant Growth Promoting Bacteria Isolated from the Rhizosphere of Plantation Crops Coconut, Cocoa and Arecanut. <i>PLoS ONE</i> , 2014, 9, e104259.	2.5	97
76	Multispecies diel transcriptional oscillations in open ocean heterotrophic bacterial assemblages. <i>Science</i> , 2014, 345, 207-212.	12.6	245
77	A mutation burst during the acute phase of <i>Helicobacter pylori</i> infection in humans and rhesus macaques. <i>Nature Communications</i> , 2014, 5, 4165.	12.8	81
78	Integrative analysis of environmental sequences using MEGAN4. <i>Genome Research</i> , 2011, 21, 1552-1560.	5.5	1,245
79	Simultaneous Assessment of Soil Microbial Community Structure and Function through Analysis of the Meta-Transcriptome. <i>PLoS ONE</i> , 2008, 3, e2527.	2.5	667
80	MEGAN analysis of metagenomic data. <i>Genome Research</i> , 2007, 17, 377-386.	5.5	2,764
81	Detection of air and surface contamination by SARS-CoV-2 in hospital rooms of infected patients. , 0, .		1