

# Stephan C Schuster

## List of Publications by Year in descending order

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Version: 2024-02-01

81  
papers

7,607  
citations

218592

26  
h-index

85498

71  
g-index

88  
all docs

88  
docs citations

88  
times ranked

13957  
citing authors

#	ARTICLE	IF	CITATIONS
1	MEGAN analysis of metagenomic data. <i>Genome Research</i> , 2007, 17, 377-386.	2.4	2,764
2	Integrative analysis of environmental sequences using MEGAN4. <i>Genome Research</i> , 2011, 21, 1552-1560.	2.4	1,245
3	Detection of air and surface contamination by SARS-CoV-2 in hospital rooms of infected patients. <i>Nature Communications</i> , 2020, 11, 2800.	5.8	703
4	Simultaneous Assessment of Soil Microbial Community Structure and Function through Analysis of the Meta-Transcriptome. <i>PLoS ONE</i> , 2008, 3, e2527.	1.1	667
5	Multispecies diel transcriptional oscillations in open ocean heterotrophic bacterial assemblages. <i>Science</i> , 2014, 345, 207-212.	6.0	245
6	Human ACE2 receptor polymorphisms and altered susceptibility to SARS-CoV-2. <i>Communications Biology</i> , 2021, 4, 475.	2.0	126
7	Neurogenesis and longevity signaling in young germ-free mice transplanted with the gut microbiota of old mice. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	122
8	The microbiomes of blowflies and houseflies as bacterial transmission reservoirs. <i>Scientific Reports</i> , 2017, 7, 16324.	1.6	115
9	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.	2.9	109
10	Microbial communities in the tropical air ecosystem follow a precise diel cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 23299-23308.	3.3	99
11	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.	1.1	97
12	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.	3.3	95
13	In silico analyses of metagenomes from human atherosclerotic plaque samples. <i>Microbiome</i> , 2015, 3, 38.	4.9	87
14	Comparative and population mitogenomic analyses of Madagascar's extinct, giant "subfossil" lemurs. <i>Journal of Human Evolution</i> , 2015, 79, 45-54.	1.3	86
15	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.	3.3	85
16	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.	5.8	81
17	Large-scale mitogenomics enables insights into <i>Schizophora</i> (Diptera) radiation and population diversity. <i>Scientific Reports</i> , 2016, 6, 21762.	1.6	66
18	Khoisan hunter-gatherers have been the largest population throughout most of modern-human demographic history. <i>Nature Communications</i> , 2014, 5, 5692.	5.8	65

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19	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.	2.5	58
20	Systematic evaluation of library preparation methods and sequencing platforms for high-throughput whole genome bisulfite sequencing. <i>Scientific Reports</i> , 2019, 9, 10383.	1.6	57
21	A compromised developmental trajectory of the infant gut microbiome and metabolome in atopic eczema. <i>Gut Microbes</i> , 2020, 12, 1801964.	4.3	51
22	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.	1.5	50
23	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.	1.2	47
24	Environmental fungal sensitisation associates with poorer clinical outcomes in COPD. <i>European Respiratory Journal</i> , 2020, 56, 2000418.	3.1	44
25	Acquisition of resistance to carbapenem and macrolide-mediated quorum sensing inhibition by <i>Pseudomonas aeruginosa</i> via ICE <sub>Tn43716385</sub> . <i>Communications Biology</i> , 2018, 1, 57.	2.0	29
26	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.	3.6	28
27	Pleiotropic Effects of c-di-GMP Content in <i>Pseudomonas syringae</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	28
28	Experimental parameters defining ultra-low biomass bioaerosol analysis. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 37.	2.9	27
29	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, .	2.0	27
30	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.	1.2	26
31	Repurposing the anticancer drug cisplatin with the aim of developing novel <i>Pseudomonas aeruginosa</i> infection control agents. <i>Beilstein Journal of Organic Chemistry</i> , 2018, 14, 3059-3069.	1.3	25
32	Whole-genome analysis of <i>Mustela erminea</i> finds that pulsed hybridization impacts evolution at high latitudes. <i>Communications Biology</i> , 2018, 1, 51.	2.0	24
33	Periodontitis associates with species-specific gene expression of the oral microbiota. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 76.	2.9	18
34	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.	1.3	13
35	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, .	3.3	13
36	Effective design of barrier enclosure to contain aerosol emissions from COVID-19 patients. <i>Indoor Air</i> , 2021, 31, 1639-1644.	2.0	12

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37	Evolutionary and phylogenetic insights from a nuclear genome sequence of the extinct, giant, <i>Megaladapis edwardsi</i> . Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	12
38	Longitudinal assessment of antibiotic resistance gene profiles in gut microbiomes of infants at risk of eczema. BMC Infectious Diseases, 2020, 20, 312.	1.3	11
39	Insights into bear evolution from a Pleistocene polar bear genome. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	11
40	Taxonomic composition and seasonal dynamics of the air microbiome in West Siberia. Scientific Reports, 2020, 10, 21515.	1.6	10
41	Complete Genome Sequence of <i>Bacillus altitudinis</i> Type Strain SGAir0031 Isolated from Tropical Air Collected in Singapore. Genome Announcements, 2017, 5, .	0.8	9
42	Development of novel genic microsatellite markers from transcriptome sequencing in sugar maple ( <i>Acer saccharum</i> Marsh.). BMC Research Notes, 2017, 10, 369.	0.6	9
43	The genomic characterisation and comparison of <i>Bacillus cereus</i> strains isolated from indoor air. Gut Pathogens, 2021, 13, 6.	1.6	9
44	Genome Sequence of <i>Bacillus velezensis</i> SGAir0473, Isolated from Tropical Air Collected in Singapore. Genome Announcements, 2018, 6, .	0.8	7
45	Complete Genome Sequence of <i>Micrococcus luteus</i> Strain SGAir0127, Isolated from Indoor Air Samples from Singapore. Microbiology Resource Announcements, 2019, 8, .	0.3	7
46	Whole-Genome Sequencing of <i>Aspergillus terreus</i> Species Complex. Mycopathologia, 2020, 185, 405-408.	1.3	7
47	Imputation Performance in Latin American Populations: Improving Rare Variants Representation With the Inclusion of Native American Genomes. Frontiers in Genetics, 2021, 12, 719791.	1.1	7
48	Characterization of a novel multidrug resistance plasmid pSGB23 isolated from <i>Salmonella enterica</i> subspecies <i>enterica</i> serovar Saintpaul. Gut Pathogens, 2018, 10, 20.	1.6	6
49	Integrative multiomics analysis reveals host-microbe-metabolite interplays associated with the aging process in Singaporeans. Gut Microbes, 2022, 14, 2070392.	4.3	6
50	Draft Genome Sequence of <i>Thauera</i> sp. Strain SWB20, Isolated from a Singapore Wastewater Treatment Facility Using Gel Microdroplets. Genome Announcements, 2015, 3, .	0.8	5
51	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
52	Data characterizing the chloroplast genomes of extinct and endangered Hawaiian endemic mints (Lamiaceae) and their close relatives. Data in Brief, 2016, 7, 900-922.	0.5	4
53	Complete Genome Sequence of <i>Staphylococcus haemolyticus</i> Type Strain SGAir0252. Genome Announcements, 2018, 6, .	0.8	4
54	Genome Sequence of <i>Geobacillus thermoleovorans</i> SGAir0734, Isolated from Singapore Air. Genome Announcements, 2018, 6, .	0.8	4

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55	Complete Genome Sequence of <i>Brachybacterium</i> sp. Strain SGAir0954, Isolated from Singapore Air. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	4
56	Genome Sequence of <i>Prosthecochloris</i> sp. Strain HL-130-GSB, from the Phylum Chlorobi. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
57	Whole-Genome Sequence of <i>Bacillus megaterium</i> Strain SGAir0080, Isolated from an Indoor Air Sample. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	3
58	Complete Genome Sequence of <i>Penicillium oxalicum</i> Strain SGAir0226 Isolated from Outdoor Tropical Air in Singapore. <i>Mycopathologia</i> , 2020, 185, 591-594.	1.3	3
59	Genomic and Phenotypic Characterization of <i>Chloracidobacterium</i> Isolates Provides Evidence for Multiple Species. <i>Frontiers in Microbiology</i> , 2021, 12, 704168.	1.5	3
60	Complete Genome Sequence of <i>Acinetobacter indicus</i> Type Strain SGAir0564 Isolated from Tropical Air Collected in Singapore. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
61	Complete Genome Sequence of <i>Acinetobacter schindleri</i> SGAir0122 Isolated from Singapore Air. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
62	Genome Sequence of <i>Pantoea ananatis</i> SGAir0210, Isolated from Outdoor Air in Singapore. <i>Genome Announcements</i> , 2018, 6, .	0.8	2
63	Complete Genome Sequence of <i>Microbacterium</i> sp. Strain SGAir0570, Isolated from Tropical Air Collected in Singapore. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
64	Complete Genome Sequence of <i>Lysinibacillus</i> sp. Strain SGAir0095, Isolated from Tropical Air Samples Collected in Singapore. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
65	Complete Genome Sequence of <i>Streptomyces</i> sp. Strain SGAir0924, an Actinobacterium Isolated from Outdoor Air in Singapore. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	2
66	623. Dynamic Nature of the Gut Resistome Among Infants in Singapore. <i>Open Forum Infectious Diseases</i> , 2018, 5, S227-S228.	0.4	1
67	Complete Genome Sequence of the Bacterium <i>Serratia marcescens</i> SGAir0764, Isolated from Singapore Air. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
68	Complete Genome Sequence of <i>Pseudomonas stutzeri</i> Type Strain SGAir0442, Isolated from Singapore Air Samples. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
69	Complete Genome Sequence of <i>Citricoccus</i> sp. Strain SGAir0253, Isolated from Indoor Air in Singapore. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1
70	Complete genome of <i>Enterobacter sichuanensis</i> strain SGAir0282 isolated from air in Singapore. <i>Gut Pathogens</i> , 2020, 12, 12.	1.6	1
71	Detection of air and surface contamination by SARS-CoV-2 in hospital rooms of infected patients. , 0, .		1
72	Complete Genome Sequence of <i>Nissabacter</i> sp. Strain SGAir0207, Isolated from an Air Sample Collected in Singapore. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	1

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73	Complete Genome Sequence of <i>Rhodococcus</i> sp. Strain SGAir0479, Isolated from Indoor Air Collected in Singapore. Microbiology Resource Announcements, 2019, 8, .	0.3	1
74	Short-range contributions of local sources to ambient air. , 2022, 1, .		1
75	Genome Sequence of the Tropical Atmosphere Bacterium <i>Pontibacter</i> sp. Strain SGAir0037. Microbiology Resource Announcements, 2019, 8, .	0.3	0
76	Complete Genome Sequence of <i>Agrococcus</i> sp. Strain SGAir0287, Isolated from Tropical Air Collected in Singapore. Microbiology Resource Announcements, 2019, 8, .	0.3	0
77	Complete Genome Sequence of <i>Curtobacterium</i> sp. Strain SGAir0471, Isolated from Singapore Air Samples. Microbiology Resource Announcements, 2019, 8, .	0.3	0
78	Coronavirus viability in surgical plume and methods for safe disposal: a preclinical model. British Journal of Surgery, 2021, , .	0.1	0
79	Complete Genome Sequence of <i>Pseudomonas</i> sp. Strain SGAir0191, Isolated from Tropical Air Collected in Singapore. Microbiology Resource Announcements, 2019, 8, .	0.3	0
80	Complete Genome Sequence of <i>Brevundimonas</i> sp. Strain SGAir0440, Isolated from Indoor Air in Singapore. Microbiology Resource Announcements, 2019, 8, .	0.3	0
81	Complete Genome Sequence of <i>Enterococcus faecalis</i> Strain SGAir0397, Isolated from a Tropical Air Sample Collected in Singapore. Microbiology Resource Announcements, 2019, 8, .	0.3	0