

Samuel K Sheppard

List of Publications by Year in descending order

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118
papers

7,031
citations

66250

44
h-index

84171

75
g-index

142
all docs

142
docs citations

142
times ranked

7187
citing authors

#	ARTICLE	IF	CITATIONS
1	Strain wars and the evolution of opportunistic pathogens. <i>Current Opinion in Microbiology</i> , 2022, 67, 102138.	2.3	9
2	Host ecology regulates interspecies recombination in bacteria of the genus <i>Campylobacter</i> . <i>ELife</i> , 2022, 11, .	2.8	17
3	Stereoselective metabolism of chloramphenicol by bacteria isolated from wastewater, and the importance of stereochemistry in environmental risk assessments for antibiotics. <i>Water Research</i> , 2022, 217, 118415.	5.3	3
4	Signatures of selection in core and accessory genomes indicate different ecological drivers of diversification among <i>Bacillus cereus</i> clades. <i>Molecular Ecology</i> , 2022, 31, 3584-3597.	2.0	4
5	Local accessory gene sharing among Egyptian <i>Campylobacter</i> potentially promotes the spread of antimicrobial resistance. <i>Microbial Genomics</i> , 2022, 8, .	1.0	3
6	Impacts of Antibiotic Residues in the Environment on Bacterial Resistance and Human Health in Eastern China: An Interdisciplinary Mixed-Methods Study Protocol. <i>International Journal of Environmental Research and Public Health</i> , 2022, 19, 8145.	1.2	8
7	A 500-year tale of co-evolution, adaptation, and virulence: <i>Helicobacter pylori</i> in the Americas. <i>ISME Journal</i> , 2021, 15, 78-92.	4.4	23
8	Genome evolution and the emergence of pathogenicity in avian <i>Escherichia coli</i> . <i>Nature Communications</i> , 2021, 12, 765.	5.8	69
9	Stereoselective Bacterial Metabolism of Antibiotics in Environmental Bacteria – A Novel Biochemical Workflow. <i>Frontiers in Microbiology</i> , 2021, 12, 562157.	1.5	4
10	Next-generation microbiology: from comparative genomics to gene function. <i>Genome Biology</i> , 2021, 22, 123.	3.8	29
11	Stress resistance associated with multi-host transmission and enhanced biofilm formation at 42°C among hyper-aerotolerant generalist <i>Campylobacter jejuni</i> . <i>Food Microbiology</i> , 2021, 95, 103706.	2.1	16
12	Genome-wide association study of signature genetic alterations among <i>Pseudomonas aeruginosa</i> cystic fibrosis isolates. <i>PLoS Pathogens</i> , 2021, 17, e1009681.	2.1	7
13	Characterisation of <i>Salmonella enterica</i> clones carrying <i>mcr-1</i> plasmids in meat products and patients in Northern Thailand using long read sequencing. <i>International Journal of Food Microbiology</i> , 2021, 358, 109314.	2.1	7
14	<i>Campylobacter jejuni</i> genotypes are associated with post-infection irritable bowel syndrome in humans. <i>Communications Biology</i> , 2021, 4, 1015.	2.0	24
15	Quantifying bacterial evolution in the wild: A birthday problem for <i>Campylobacter</i> lineages. <i>PLoS Genetics</i> , 2021, 17, e1009829.	1.5	11
16	Machine learning to predict the source of campylobacteriosis using whole genome data. <i>PLoS Genetics</i> , 2021, 17, e1009436.	1.5	21
17	Addressing parachute research and removing barriers for LMIC researchers in <i>Microbial Genomics</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
18	Determining the prevalence, identity and possible origin of bacterial pathogens in soil. <i>Environmental Microbiology</i> , 2020, 22, 5327-5340.	1.8	9

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19	Genome-Wide Identification of Host-Segregating Single-Nucleotide Polymorphisms for Source Attribution of Clinical <i>Campylobacter coli</i> Isolates. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	15
20	Genomic epidemiology of <i>Campylobacter jejuni</i> associated with asymptomatic pediatric infection in the Peruvian Amazon. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008533.	1.3	20
21	Agricultural intensification and the evolution of host specialism in the enteric pathogen <i>Campylobacter jejuni</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 11018-11028.	3.3	50
22	The emergence of plasmid-borne cfr-mediated linezolid resistant-staphylococci in Vietnam. <i>Journal of Global Antimicrobial Resistance</i> , 2020, 22, 462-465.	0.9	7
23	High-resolution sweep metagenomics using fast probabilistic inference. <i>Wellcome Open Research</i> , 2020, 5, 14.	0.9	13
24	Gene pool transmission of multidrug resistance among <i>Campylobacter</i> from livestock, sewage and human disease. <i>Environmental Microbiology</i> , 2019, 21, 4597-4613.	1.8	68
25	PIRATE: A fast and scalable pangenomics toolbox for clustering diverged orthologues in bacteria. <i>GigaScience</i> , 2019, 8, .	3.3	152
26	Phage Predation Shapes the Population Structure of Shiga-Toxigenic <i>Escherichia coli</i> O157:H7 in the UK: An Evolutionary Perspective. <i>Frontiers in Genetics</i> , 2019, 10, 763.	1.1	7
27	Prevalence of faecal carriage of extended-spectrum β -lactamase (ESBL)-producing <i>Escherichia coli</i> in veterinary hospital staff and students. <i>Veterinary Record Open</i> , 2019, 6, e000307.	0.3	26
28	Core genome sequence analysis to characterize <i>Salmonella enterica</i> serovar Rissen ST469 from a swine production chain. <i>International Journal of Food Microbiology</i> , 2019, 304, 68-74.	2.1	15
29	Source attribution of <i>Campylobacter jejuni</i> shows variable importance of chicken and ruminants reservoirs in non-invasive and invasive French clinical isolates. <i>Scientific Reports</i> , 2019, 9, 8098.	1.6	31
30	Genetic Diversity of Composite Enterotoxigenic <i>Staphylococcus epidermidis</i> Pathogenicity Islands. <i>Genome Biology and Evolution</i> , 2019, 11, 3498-3509.	1.1	21
31	Distinct Phenotypic and Genomic Signatures Underlie Contrasting Pathogenic Potential of <i>Staphylococcus epidermidis</i> Clonal Lineages. <i>Frontiers in Microbiology</i> , 2019, 10, 1971.	1.5	32
32	Domestication of <i>Campylobacter jejuni</i> NCTC 11168. <i>Microbial Genomics</i> , 2019, 5, .	1.0	26
33	Piggy: a rapid, large-scale pan-genome analysis tool for intergenic regions in bacteria. <i>GigaScience</i> , 2018, 7, 1-11.	3.3	59
34	Lineage-specific plasmid acquisition and the evolution of specialized pathogens in <i>Bacillus thuringiensis</i> and the <i>Bacillus cereus</i> group. <i>Molecular Ecology</i> , 2018, 27, 1524-1540.	2.0	43
35	Convergent Amino Acid Signatures in Polyphyletic <i>Campylobacter jejuni</i> Subpopulations Suggest Human Niche Tropism. <i>Genome Biology and Evolution</i> , 2018, 10, 763-774.	1.1	12
36	Comparative genomic survey of <i>Bacillus cereus sensu stricto</i> isolates from the dairy production chain in Brazil. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	10

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37	Molecular epidemiology and comparative genomics of <i>Campylobacter concisus</i> strains from saliva, faeces and gut mucosal biopsies in inflammatory bowel disease. <i>Scientific Reports</i> , 2018, 8, 1902.	1.6	35
38	Weak Epistasis May Drive Adaptation in Recombining Bacteria. <i>Genetics</i> , 2018, 208, 1247-1260.	1.2	51
39	Disease-associated genotypes of the commensal skin bacterium <i>Staphylococcus epidermidis</i> . <i>Nature Communications</i> , 2018, 9, 5034.	5.8	115
40	Ruminant and chicken: important sources of campylobacteriosis in France despite a variation of source attribution in 2009 and 2015. <i>Scientific Reports</i> , 2018, 8, 9305.	1.6	43
41	Population genomics of bacterial host adaptation. <i>Nature Reviews Genetics</i> , 2018, 19, 549-565.	7.7	186
42	A GWAS on <i>Helicobacter pylori</i> strains points to genetic variants associated with gastric cancer risk. <i>BMC Biology</i> , 2018, 16, 84.	1.7	55
43	The Potential of Isolation Source to Predict Colonization in Avian Hosts: A Case Study in <i>Campylobacter jejuni</i> Strains From Three Bird Species. <i>Frontiers in Microbiology</i> , 2018, 9, 591.	1.5	18
44	Epistasis analysis uncovers hidden antibiotic resistance-associated fitness costs hampering the evolution of MRSA. <i>Genome Biology</i> , 2018, 19, 94.	3.8	43
45	Trends in fluoroquinolone resistance in <i>Campylobacter</i> . <i>Microbial Genomics</i> , 2018, 4, .	1.0	100
46	Genomic epidemiology of clinical <i>Campylobacter</i> spp. at a single health trust site. <i>Microbial Genomics</i> , 2018, 4, .	1.0	15
47	Phasomelt: an omics™ approach to cataloguing the potential breadth of phase variation in the genus <i>Campylobacter</i> . <i>Microbial Genomics</i> , 2018, 4, .	1.0	17
48	High Resolution Whole Genome Multilocus Sequence Typing (wgMLST) Schemes for <i>Salmonella enterica</i> Weltevreden Epidemiologic Investigations. <i>Microbiology and Biotechnology Letters</i> , 2018, 46, 162-170.	0.2	1
49	Identification and initial characterisation of a protein involved in <i>Campylobacter jejuni</i> cell shape. <i>Microbial Pathogenesis</i> , 2017, 104, 202-211.	1.3	12
50	Genome-Wide Identification of Host-Segregating Epidemiological Markers for Source Attribution in <i>Campylobacter jejuni</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	82
51	Genomic structure and insertion sites of <i>Helicobacter pylori</i> prophages from various geographical origins. <i>Scientific Reports</i> , 2017, 7, 42471.	1.6	34
52	Recombination-Mediated Host Adaptation by Avian <i>Staphylococcus aureus</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 830-842.	1.1	46
53	Local genes for local bacteria: Evidence of allopatry in the genomes of transatlantic <i>Campylobacter</i> populations. <i>Molecular Ecology</i> , 2017, 26, 4497-4508.	2.0	36
54	A Proposal for a Genome Similarity-Based Taxonomy for Plant-Pathogenic Bacteria that Is Sufficiently Precise to Reflect Phylogeny, Host Range, and Outbreak Affiliation Applied to <i>Pseudomonas syringae</i> sensu lato as a Proof of Concept. <i>Phytopathology</i> , 2017, 107, 18-28.	1.1	26

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55	Genomic plasticity and rapid host switching can promote the evolution of generalism: a case study in the zoonotic pathogen <i>Campylobacter</i> . <i>Scientific Reports</i> , 2017, 7, 9650.	1.6	34
56	Comparative Genomics Study of <i>Staphylococcus epidermidis</i> Isolates from Orthopedic-Device-Related Infections Correlated with Patient Outcome. <i>Journal of Clinical Microbiology</i> , 2017, 55, 3089-3103.	1.8	55
57	Genome-wide association of functional traits linked with <i>Campylobacter jejuni</i> survival from farm to fork. <i>Environmental Microbiology</i> , 2017, 19, 361-380.	1.8	88
58	Genome Reduction for Niche Association in <i>Campylobacter Hepaticus</i> , A Cause of Spotty Liver Disease in Poultry. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 354.	1.8	26
59	The Promise of Whole Genome Pathogen Sequencing for the Molecular Epidemiology of Emerging Aquaculture Pathogens. <i>Frontiers in Microbiology</i> , 2017, 8, 121.	1.5	80
60	Genome Comparison of Erythromycin Resistant <i>Campylobacter</i> from Turkeys Identifies Hosts and Pathways for Horizontal Spread of <i>erm(B)</i> Genes. <i>Frontiers in Microbiology</i> , 2017, 8, 2240.	1.5	38
61	Rapid evolution of distinct <i>Helicobacter pylori</i> subpopulations in the Americas. <i>PLoS Genetics</i> , 2017, 13, e1006546.	1.5	73
62	Characterization of nasal methicillin-resistant <i>Staphylococcus aureus</i> isolated from international human and veterinary surgeons. <i>Journal of Medical Microbiology</i> , 2017, 66, 360-370.	0.7	5
63	Combined Analysis of Variation in Core, Accessory and Regulatory Genome Regions Provides a Super-Resolution View into the Evolution of Bacterial Populations. <i>PLoS Genetics</i> , 2016, 12, e1006280.	1.5	177
64	Draft Genome Sequence of an <i>Enterobacter</i> Species Associated with Illnesses and Powdered Infant Formula. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
65	Genomic variations leading to alterations in cell morphology of <i>Campylobacter</i> spp. <i>Scientific Reports</i> , 2016, 6, 38303.	1.6	25
66	Comparative Genomics of <i>Campylobacter fetus</i> from Reptiles and Mammals Reveals Divergent Evolution in Host-Associated Lineages. <i>Genome Biology and Evolution</i> , 2016, 8, 2006-2019.	1.1	25
67	Genetic features of livestock-associated <i>Staphylococcus aureus</i> ST9 isolates from Chinese pigs that carry the <i>Isa(E)</i> gene for quinupristin/dalfopristin resistance. <i>International Journal of Medical Microbiology</i> , 2016, 306, 722-729.	1.5	25
68	Large Sequence Diversity within the Biosynthesis Locus and Common Biochemical Features of <i>Campylobacter coli</i> Lipooligosaccharides. <i>Journal of Bacteriology</i> , 2016, 198, 2829-2840.	1.0	13
69	Phylogenomic approaches to determine the zoonotic potential of Shiga toxin-producing <i>Escherichia coli</i> (STEC) isolated from Zambian dairy cattle. <i>Scientific Reports</i> , 2016, 6, 26589.	1.6	15
70	From <i>Escherich</i> to the <i>Escherichia coli</i> genome. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 634-636.	4.6	20
71	The Landscape of Realized Homologous Recombination in Pathogenic Bacteria. <i>Molecular Biology and Evolution</i> , 2016, 33, 456-471.	3.5	72
72	The impact of host metapopulation structure on the population genetics of colonizing bacteria. <i>Journal of Theoretical Biology</i> , 2016, 396, 53-62.	0.8	13

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73	Rapid host switching in generalist <i>Campylobacter</i> strains erodes the signal for tracing human infections. ISME Journal, 2016, 10, 721-729.	4.4	123
74	Bayesian identification of bacterial strains from sequencing data. Microbial Genomics, 2016, 2, e000075.	1.0	19
75	CLIMB (the Cloud Infrastructure for Microbial Bioinformatics): an online resource for the medical microbiology community. Microbial Genomics, 2016, 2, e000086.	1.0	176
76	Population-genomic insights into emergence, crop adaptation and dissemination of <i>Pseudomonas syringae</i> pathogens. Microbial Genomics, 2016, 2, e000089.	1.0	88
77	Biofilm Morphotypes and Population Structure among <i>Staphylococcus epidermidis</i> from Commensal and Clinical Samples. PLoS ONE, 2016, 11, e0151240.	1.1	49
78	Enhanced biofilm formation and multi-host transmission evolve from divergent genetic backgrounds in <i>Campylobacter jejuni</i> . Environmental Microbiology, 2015, 17, 4779-4789.	1.8	76
79	The Evolution of <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> . Cold Spring Harbor Perspectives in Biology, 2015, 7, a018119.	2.3	119
80	Ecological Overlap and Horizontal Gene Transfer in <i>Staphylococcus aureus</i> and <i>Staphylococcus epidermidis</i> . Genome Biology and Evolution, 2015, 7, 1313-1328.	1.1	130
81	Gene Loss and Lineage-Specific Restriction-Modification Systems Associated with Niche Differentiation in the <i>Campylobacter jejuni</i> Sequence Type 403 Clonal Complex. Applied and Environmental Microbiology, 2015, 81, 3641-3647.	1.4	27
82	Evidence of land-sea transfer of the zoonotic pathogen <i>Campylobacter</i> to a wildlife marine sentinel species. Molecular Ecology, 2015, 24, 208-221.	2.0	25
83	Variation in Siderophore Biosynthetic Gene Distribution and Production across Environmental and Faecal Populations of <i>Escherichia coli</i> . PLoS ONE, 2015, 10, e0117906.	1.1	58
84	A phylogeny-based sampling strategy and power calculator informs genome-wide associations study design for microbial pathogens. Genome Medicine, 2014, 6, 101.	3.6	30
85	Efficient Inference of Recombination Hot Regions in Bacterial Genomes. Molecular Biology and Evolution, 2014, 31, 1593-1605.	3.5	62
86	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. Molecular Ecology, 2014, 23, 2442-2451.	2.0	131
87	Prevalence and risk factors of <i>Campylobacter</i> infection in broiler flocks from southern Spain. Preventive Veterinary Medicine, 2014, 114, 106-113.	0.7	43
88	A Reference Pan-Genome Approach to Comparative Bacterial Genomics: Identification of Novel Epidemiological Markers in Pathogenic <i>Campylobacter</i> . PLoS ONE, 2014, 9, e92798.	1.1	122
89	Widespread acquisition of antimicrobial resistance among <i>Campylobacter</i> isolates from UK retail poultry and evidence for clonal expansion of resistant lineages. BMC Microbiology, 2013, 13, 160.	1.3	57
90	Evidence for Phenotypic Plasticity among Multihost <i>Campylobacter jejuni</i> and <i>C. coli</i> Lineages, Obtained Using Ribosomal Multilocus Sequence Typing and Raman Spectroscopy. Applied and Environmental Microbiology, 2013, 79, 965-973.	1.4	24

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91	Operationalising Factors That Explain the Emergence of Infectious Diseases: A Case Study of the Human Campylobacteriosis Epidemic. PLoS ONE, 2013, 8, e79331.	1.1	17
92	Genome-wide association study identifies vitamin B ₅ biosynthesis as a host specificity factor in <i>Campylobacter</i> . Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 11923-11927.	3.3	267
93	Progressive genome-wide introgression in agricultural <i>Campylobacter coli</i> . Molecular Ecology, 2013, 22, 1051-1064.	2.0	128
94	Elucidating the Aetiology of Human <i>Campylobacter coli</i> Infections. PLoS ONE, 2013, 8, e64504.	1.1	40
95	<i>Campylobacter</i> epidemiology: a descriptive study reviewing 1 million cases in England and Wales between 1989 and 2011. BMJ Open, 2012, 2, e001179.	0.8	108
96	Ribosomal multilocus sequence typing: universal characterization of bacteria from domain to strain. Microbiology (United Kingdom), 2012, 158, 1005-1015.	0.7	497
97	Molecular Evidence for the Thriving of <i>Campylobacter jejuni</i> ST-4526 in Japan. PLoS ONE, 2012, 7, e48394.	1.1	42
98	A Gene-By-Gene Approach to Bacterial Population Genomics: Whole Genome MLST of <i>Campylobacter</i> . Genes, 2012, 3, 261-277.	1.0	135
99	<i>Campylobacter</i> populations in wild and domesticated Mallard ducks (<i>Anas</i>). Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 4	1.0	68
100	Niche segregation and genetic structure of <i>Campylobacter jejuni</i> populations from wild and agricultural host species. Molecular Ecology, 2011, 20, 3484-3490.	2.0	105
101	Temporal Variation and Host Association in the <i>Campylobacter</i> Population in a Longitudinal Ruminant Farm Study. Applied and Environmental Microbiology, 2011, 77, 6579-6586.	1.4	37
102	Introgression in the genus <i>Campylobacter</i> : generation and spread of mosaic alleles. Microbiology (United Kingdom), 2011, 157, 1066-1074.	0.7	47
103	Comparison of <i>Campylobacter</i> populations isolated from a free-range broiler flock before and after slaughter. International Journal of Food Microbiology, 2010, 137, 259-264.	2.1	32
104	Evolution of an Agriculture-Associated Disease Causing <i>Campylobacter coli</i> Clade: Evidence from National Surveillance Data in Scotland. PLoS ONE, 2010, 5, e15708.	1.1	75
105	Host Association of <i>Campylobacter</i> Genotypes Transcends Geographic Variation. Applied and Environmental Microbiology, 2010, 76, 5269-5277.	1.4	116
106	Environmental Factors Determining the Epidemiology and Population Genetic Structure of the <i>Bacillus cereus</i> Group in the Field. PLoS Pathogens, 2010, 6, e1000905.	2.1	94
107	Where Does <i>Campylobacter</i> Come From? A Molecular Odyssey. Advances in Experimental Medicine and Biology, 2010, 659, 47-56.	0.8	10
108	<i>Campylobacter</i> Excreted into the Environment by Animal Sources: Prevalence, Concentration Shed, and Host Association. Foodborne Pathogens and Disease, 2009, 6, 1161-1170.	0.8	81

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109	Spatiotemporal Homogeneity of <i>Campylobacter</i> Subtypes from Cattle and Sheep across Northeastern and Southwestern Scotland. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6275-6281.	1.4	32
110	Attribution of <i>Campylobacter</i> Infections in Northeast Scotland to Specific Sources by Use of Multilocus Sequence Typing. <i>Journal of Infectious Diseases</i> , 2009, 199, 1205-1208.	1.9	117
111	<i>Campylobacter</i> genotypes from food animals, environmental sources and clinical disease in Scotland 2005/6. <i>International Journal of Food Microbiology</i> , 2009, 134, 96-103.	2.1	158
112	<i>Campylobacter</i> Genotyping to Determine the Source of Human Infection. <i>Clinical Infectious Diseases</i> , 2009, 48, 1072-1078.	2.9	358
113	<i>Campylobacter</i> infection of broiler chickens in a free-range environment. <i>Environmental Microbiology</i> , 2008, 10, 2042-2050.	1.8	89
114	Convergence of <i>Campylobacter</i> Species: Implications for Bacterial Evolution. <i>Science</i> , 2008, 320, 237-239.	6.0	231
115	The significance of facultative scavenging in generalist predator nutrition: detecting decayed prey in the guts of predators using PCR. <i>Molecular Ecology</i> , 2005, 14, 4147-4158.	2.0	102
116	Effects of soil improvement treatments on bacterial community structure and soil processes in an upland grassland soil. <i>FEMS Microbiology Ecology</i> , 2003, 46, 11-22.	1.3	38
117	Whole-genome characterisation of multidrug resistant monophasic variants of <i>Salmonella</i> Typhimurium from pig production in Thailand. <i>PeerJ</i> , 0, 8, e9700.	0.9	13
118	High-resolution sweep metagenomics using fast probabilistic inference. <i>Wellcome Open Research</i> , 0, 5, 14.	0.9	14