

Stephen D Bentley

List of Publications by Year in descending order

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Version: 2024-02-01

104
papers

11,997
citations

41344

49
h-index

33894

99
g-index

119
all docs

119
docs citations

119
times ranked

10225
citing authors

#	ARTICLE	IF	CITATIONS
1	Rapid phylogenetic analysis of large samples of recombinant bacterial whole genome sequences using Gubbins. <i>Nucleic Acids Research</i> , 2015, 43, e15-e15.	14.5	1,834
2	Rapid Pneumococcal Evolution in Response to Clinical Interventions. <i>Science</i> , 2011, 331, 430-434.	12.6	828
3	Genetic Analysis of the Capsular Biosynthetic Locus from All 90 Pneumococcal Serotypes. <i>PLoS Genetics</i> , 2006, 2, e31.	3.5	661
4	Producing polished prokaryotic pangenomes with the Panaroo pipeline. <i>Genome Biology</i> , 2020, 21, 180.	8.8	419
5	Dense genomic sampling identifies highways of pneumococcal recombination. <i>Nature Genetics</i> , 2014, 46, 305-309.	21.4	371
6	Population genomics of post-vaccine changes in pneumococcal epidemiology. <i>Nature Genetics</i> , 2013, 45, 656-663.	21.4	364
7	Structure and dynamics of the pan-genome of <i>Streptococcus pneumoniae</i> and closely related species. <i>Genome Biology</i> , 2010, 11, R107.	8.8	321
8	Genome-wide association study identifies vitamin B ₅ biosynthesis as a host specificity factor in <i>Campylobacter</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 11923-11927.	7.1	267
9	Description and Nomenclature of <i>Neisseria meningitidis</i> Capsule Locus. <i>Emerging Infectious Diseases</i> , 2013, 19, 566-573.	4.3	259
10	Fast and flexible bacterial genomic epidemiology with PopPUNK. <i>Genome Research</i> , 2019, 29, 304-316.	5.5	258
11	pyseer: a comprehensive tool for microbial pangenome-wide association studies. <i>Bioinformatics</i> , 2018, 34, 4310-4312.	4.1	208
12	Comprehensive Identification of Single Nucleotide Polymorphisms Associated with Beta-lactam Resistance within Pneumococcal Mosaic Genes. <i>PLoS Genetics</i> , 2014, 10, e1004547.	3.5	205
13	RhierBAPS: An R implementation of the population clustering algorithm hierBAPS. <i>Wellcome Open Research</i> , 2018, 3, 93.	1.8	198
14	Genomic epidemiology of <i>Neisseria gonorrhoeae</i> with reduced susceptibility to cefixime in the USA: a retrospective observational study. <i>Lancet Infectious Diseases</i> , The, 2014, 14, 220-226.	9.1	193
15	Methicillin-resistant <i>Staphylococcus aureus</i> emerged long before the introduction of methicillin into clinical practice. <i>Genome Biology</i> , 2017, 18, 130.	8.8	193
16	Whole-Genome Sequencing for Routine Pathogen Surveillance in Public Health: a Population Snapshot of Invasive <i>Staphylococcus aureus</i> in Europe. <i>MBio</i> , 2016, 7, .	4.1	192
17	Sequence element enrichment analysis to determine the genetic basis of bacterial phenotypes. <i>Nature Communications</i> , 2016, 7, 12797.	12.8	190
18	Genomic Epidemiology of Gonococcal Resistance to Extended-Spectrum Cephalosporins, Macrolides, and Fluoroquinolones in the United States, 2000–2013. <i>Journal of Infectious Diseases</i> , 2016, 214, 1579-1587.	4.0	186

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19	Inferring patient to patient transmission of <i>Mycobacterium tuberculosis</i> from whole genome sequencing data. <i>BMC Infectious Diseases</i> , 2013, 13, 110.	2.9	180
20	Detection of recombination events in bacterial genomes from large population samples. <i>Nucleic Acids Research</i> , 2012, 40, e6-e6.	14.5	179
21	Bayesian inference of ancestral dates on bacterial phylogenetic trees. <i>Nucleic Acids Research</i> , 2018, 46, e134-e134.	14.5	174
22	Diversification of bacterial genome content through distinct mechanisms over different timescales. <i>Nature Communications</i> , 2014, 5, 5471.	12.8	173
23	Fast hierarchical Bayesian analysis of population structure. <i>Nucleic Acids Research</i> , 2019, 47, 5539-5549.	14.5	173
24	Role of Conjugative Elements in the Evolution of the Multidrug-Resistant Pandemic Clone <i>Streptococcus pneumoniae</i> Spain23F ^{ST81} . <i>Journal of Bacteriology</i> , 2009, 191, 1480-1489.	2.2	168
25	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. <i>EBioMedicine</i> , 2019, 43, 338-346.	6.1	168
26	Pneumococcal lineages associated with serotype replacement and antibiotic resistance in childhood invasive pneumococcal disease in the post-PCV13 era: an international whole-genome sequencing study. <i>Lancet Infectious Diseases</i> , The, 2019, 19, 759-769.	9.1	165
27	Improved Detection of Nasopharyngeal Cocolonization by Multiple Pneumococcal Serotypes by Use of Latex Agglutination or Molecular Serotyping by Microarray. <i>Journal of Clinical Microbiology</i> , 2011, 49, 1784-1789.	3.9	134
28	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. <i>Molecular Ecology</i> , 2014, 23, 2442-2451.	3.9	131
29	Horizontal DNA Transfer Mechanisms of Bacteria as Weapons of Intragenomic Conflict. <i>PLoS Biology</i> , 2016, 14, e1002394.	5.6	127
30	Genomic signatures of human and animal disease in the zoonotic pathogen <i>Streptococcus suis</i> . <i>Nature Communications</i> , 2015, 6, 6740.	12.8	124
31	Frequency-dependent selection in vaccine-associated pneumococcal population dynamics. <i>Nature Ecology and Evolution</i> , 2017, 1, 1950-1960.	7.8	121
32	Atlas of group A streptococcal vaccine candidates compiled using large-scale comparative genomics. <i>Nature Genetics</i> , 2019, 51, 1035-1043.	21.4	120
33	Phylogeographic variation in recombination rates within a global clone of methicillin-resistant <i>Staphylococcus aureus</i> . <i>Genome Biology</i> , 2012, 13, R126.	9.6	118
34	Evidence for Soft Selective Sweeps in the Evolution of Pneumococcal Multidrug Resistance and Vaccine Escape. <i>Genome Biology and Evolution</i> , 2014, 6, 1589-1602.	2.5	112
35	Phase-variable methylation and epigenetic regulation by type I restriction modification systems. <i>FEMS Microbiology Reviews</i> , 2017, 41, S3-S15.	8.6	110
36	A High-Resolution View of Genome-Wide Pneumococcal Transformation. <i>PLoS Pathogens</i> , 2012, 8, e1002745.	4.7	98

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37	Genome-wide identification of lineage and locus specific variation associated with pneumococcal carriage duration. <i>ELife</i> , 2017, 6, .	6.0	95
38	Heterogeneity in the Frequency and Characteristics of Homologous Recombination in Pneumococcal Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004300.	3.5	84
39	Joint sequencing of human and pathogen genomes reveals the genetics of pneumococcal meningitis. <i>Nature Communications</i> , 2019, 10, 2176.	12.8	83
40	Dominant Role of Nucleotide Substitution in the Diversification of Serotype 3 Pneumococci over Decades and during a Single Infection. <i>PLoS Genetics</i> , 2013, 9, e1003868.	3.5	81
41	Selective and Genetic Constraints on Pneumococcal Serotype Switching. <i>PLoS Genetics</i> , 2015, 11, e1005095.	3.5	78
42	Variable recombination dynamics during the emergence, transmission and "disarming" of a multidrug-resistant pneumococcal clone. <i>BMC Biology</i> , 2014, 12, 49.	3.8	75
43	Global emergence and population dynamics of divergent serotype 3 CC180 pneumococci. <i>PLoS Pathogens</i> , 2018, 14, e1007438.	4.7	74
44	Defining the Estimated Core Genome of Bacterial Populations Using a Bayesian Decision Model. <i>PLoS Computational Biology</i> , 2014, 10, e1003788.	3.2	72
45	Apparent nosocomial adaptation of <i>Enterococcus faecalis</i> predates the modern hospital era. <i>Nature Communications</i> , 2021, 12, 1523.	12.8	69
46	Diverse evolutionary patterns of pneumococcal antigens identified by pangenome-wide immunological screening. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E357-E366.	7.1	68
47	SeroBA: rapid high-throughput serotyping of <i>Streptococcus pneumoniae</i> from whole genome sequence data. <i>Microbial Genomics</i> , 2018, 4, .	2.0	68
48	Population genomic datasets describing the post-vaccine evolutionary epidemiology of <i>Streptococcus pneumoniae</i> . <i>Scientific Data</i> , 2015, 2, 150058.	5.3	67
49	Pneumococcal Capsule Synthesis Locus <i>cps</i> as Evolutionary Hotspot with Potential to Generate Novel Serotypes by Recombination. <i>Molecular Biology and Evolution</i> , 2017, 34, 2537-2554.	8.9	65
50	Global Phylogenomic Analysis of Nonencapsulated <i>Streptococcus pneumoniae</i> Reveals a Deep-Branching Classic Lineage That Is Distinct from Multiple Sporadic Lineages. <i>Genome Biology and Evolution</i> , 2014, 6, 3281-3294.	2.5	63
51	The multidrug-resistant PMEN1 pneumococcus is a paradigm for genetic success. <i>Genome Biology</i> , 2012, 13, R103.	9.6	62
52	Independent evolution of the core and accessory gene sets in the genus <i>Neisseria</i> : insights gained from the genome of <i>Neisseria lactamica</i> isolate 020-06. <i>BMC Genomics</i> , 2010, 11, 652.	2.8	61
53	High multiple carriage and emergence of <i>Streptococcus pneumoniae</i> vaccine serotype variants in Malawian children. <i>BMC Infectious Diseases</i> , 2015, 15, 234.	2.9	56
54	Large scale genomic analysis shows no evidence for pathogen adaptation between the blood and cerebrospinal fluid niches during bacterial meningitis. <i>Microbial Genomics</i> , 2017, 3, e000103.	2.0	53

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55	Emergence of a New Epidemic <i>Neisseria meningitidis</i> Serogroup A Clone in the African Meningitis Belt: High-Resolution Picture of Genomic Changes That Mediate Immune Evasion. <i>MBio</i> , 2014, 5, e01974-14.	4.1	51
56	Recombination in <i>Streptococcus pneumoniae</i> Lineages Increase with Carriage Duration and Size of the Polysaccharide Capsule. <i>MBio</i> , 2016, 7, .	4.1	50
57	Genetic Characterisation of Malawian Pneumococci Prior to the Roll-Out of the PCV13 Vaccine Using a High-Throughput Whole Genome Sequencing Approach. <i>PLoS ONE</i> , 2012, 7, e44250.	2.5	49
58	Whole-genome sequencing reveals clonal expansion of multiresistant <i>Staphylococcus haemolyticus</i> in European hospitals. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2920-2927.	3.0	48
59	Emergence and dissemination of antimicrobial resistance in <i>Escherichia coli</i> causing bloodstream infections in Norway in 2002â€“17: a nationwide, longitudinal, microbial population genomic study. <i>Lancet Microbe</i> , The, 2021, 2, e331-e341.	7.3	43
60	Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. <i>Wellcome Open Research</i> , 2018, 3, 33.	1.8	42
61	Climate induces seasonality in pneumococcal transmission. <i>Scientific Reports</i> , 2015, 5, 11344.	3.3	41
62	Within-host microevolution of <i>Streptococcus pneumoniae</i> is rapid and adaptive during natural colonisation. <i>Nature Communications</i> , 2020, 11, 3442.	12.8	39
63	The post-vaccine microevolution of invasive <i>Streptococcus pneumoniae</i> . <i>Scientific Reports</i> , 2015, 5, 14952.	3.3	36
64	Genome-wide epistasis and co-selection study using mutual information. <i>Nucleic Acids Research</i> , 2019, 47, e112-e112.	14.5	36
65	Population genetic structure, antibiotic resistance, capsule switching and evolution of invasive pneumococci before conjugate vaccination in Malawi. <i>Vaccine</i> , 2017, 35, 4594-4602.	3.8	27
66	Region-specific diversification of the highly virulent serotype 1 <i>Streptococcus pneumoniae</i> . <i>Microbial Genomics</i> , 2015, 1, e000027.	2.0	27
67	PANINI: Pangenome Neighbour Identification for Bacterial Populations. <i>Microbial Genomics</i> , 2019, 5, .	2.0	27
68	Excision-reintegration at a pneumococcal phase-variable restriction-modification locus drives within- and between-strain epigenetic differentiation and inhibits gene acquisition. <i>Nucleic Acids Research</i> , 2018, 46, 11438-11453.	14.5	26
69	Investigation of sequential outbreaks of <i>Burkholderia cepacia</i> and multidrug-resistant extended spectrum Î²-lactamase producing <i>Klebsiella</i> species in a West African tertiary hospital neonatal unit: a retrospective genomic analysis. <i>Lancet Microbe</i> , The, 2020, 1, e119-e129.	7.3	26
70	Pre-vaccine serotype composition within a lineage signposts its serotype replacement â€“ a carriage study over 7 years following pneumococcal conjugate vaccine use in the UK. <i>Microbial Genomics</i> , 2017, 3, e000119.	2.0	26
71	Visualizing variation within Global Pneumococcal Sequence Clusters (GPSCs) and country population snapshots to contextualize pneumococcal isolates. <i>Microbial Genomics</i> , 2020, 6, .	2.0	25
72	Comparative Genomic Analysis of Meningitis- and Bacteremia-Causing Pneumococci Identifies a Common Core Genome. <i>Infection and Immunity</i> , 2015, 83, 4165-4173.	2.2	23

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73	Two-phase importance sampling for inference about transmission trees. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20141324.	2.6	22
74	Understanding pneumococcal serotype 1 biology through population genomic analysis. BMC Infectious Diseases, 2016, 16, 649.	2.9	22
75	The Contribution of Genetic Variation of Streptococcus pneumoniae to the Clinical Manifestation of Invasive Pneumococcal Disease. Clinical Infectious Diseases, 2019, 68, 61-69.	5.8	21
76	The role of interspecies recombination in the evolution of antibiotic-resistant pneumococci. ELife, 2021, 10, .	6.0	21
77	Horizontal gene transfer rate is not the primary determinant of observed antibiotic resistance frequencies in <i>Streptococcus pneumoniae</i> . Science Advances, 2020, 6, eaaz6137.	10.3	19
78	Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. Wellcome Open Research, 0, 3, 33.	1.8	18
79	Phylogenetic Analysis of Invasive Serotype 1 Pneumococcus in South Africa, 1989 to 2013. Journal of Clinical Microbiology, 2016, 54, 1326-1334.	3.9	16
80	Lineage-specific evolution and gene flow in <i>Listeria monocytogenes</i> are independent of bacteriophages. Environmental Microbiology, 2020, 22, 5058-5072.	3.8	16
81	Putative novel cps loci in a large global collection of pneumococci. Microbial Genomics, 2019, 5, .	2.0	14
82	Global genomic pathogen surveillance to inform vaccine strategies: a decade-long expedition in pneumococcal genomics. Genome Medicine, 2021, 13, 84.	8.2	12
83	Bacterial genome-wide association study of hyper-virulent pneumococcal serotype 1 identifies genetic variation associated with neurotropism. Communications Biology, 2020, 3, 559.	4.4	11
84	Early Signals of Vaccine-driven Perturbation Seen in Pneumococcal Carriage Population Genomic Data. Clinical Infectious Diseases, 2020, 70, 1294-1303.	5.8	9
85	Pneumococcal Colonization and Virulence Factors Identified Via Experimental Evolution in Infection Models. Molecular Biology and Evolution, 2021, 38, 2209-2226.	8.9	9
86	Comparative Genomics of Carriage and Disease Isolates of <i>Streptococcus pneumoniae</i> Serotype 22F Reveals Lineage-Specific Divergence and Niche Adaptation. Genome Biology and Evolution, 2016, 8, 1243-1251.	2.5	8
87	Genetic Variation in <i>Neisseria meningitidis</i> Does Not Influence Disease Severity in Meningococcal Meningitis. Frontiers in Medicine, 2020, 7, 594769.	2.6	8
88	Population genetic structure, serotype distribution and antibiotic resistance of <i>Streptococcus pneumoniae</i> causing invasive disease in children in Argentina. Microbial Genomics, 2021, 7, .	2.0	8
89	<i>Streptococcus pneumoniae</i> genomic datasets from an Indian population describing pre-vaccine evolutionary epidemiology using a whole genome sequencing approach. Microbial Genomics, 2021, 7, .	2.0	8
90	Carriage Dynamics of Pneumococcal Serotypes in Naturally Colonized Infants in a Rural African Setting During the First Year of Life. Frontiers in Pediatrics, 2020, 8, 587730.	1.9	8

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91	Synergistic Activity of Mobile Genetic Element Defences in <i>Streptococcus pneumoniae</i> . <i>Genes</i> , 2019, 10, 707.	2.4	6
92	Diversification in immunogenicity genes caused by selective pressures in invasive meningococci. <i>Microbial Genomics</i> , 2020, 6, .	2.0	6
93	Genomic surveillance of invasive <i>Streptococcus pneumoniae</i> isolates in the period pre-PCV10 and post-PCV10 introduction in Brazil. <i>Microbial Genomics</i> , 2021, 7, .	2.0	6
94	<i>Streptococcus pneumoniae</i> serotypes that frequently colonise the human nasopharynx are common recipients of penicillin-binding protein gene fragments from <i>Streptococcus mitis</i> . <i>Microbial Genomics</i> , 2021, 7, .	2.0	5
95	Serotype 1 pneumococcus: epidemiology, genomics, and disease mechanisms. <i>Trends in Microbiology</i> , 2022, 30, 581-592.	7.7	5
96	Persistent and Emerging Pneumococcal Carriage Serotypes in a Rural Gambian Community After 10 Years of Pneumococcal Conjugate Vaccine Pressure. <i>Clinical Infectious Diseases</i> , 2021, 73, e3825-e3835.	5.8	4
97	The effect of recombination on the evolution of a population of <i>Neisseria meningitidis</i> . <i>Genome Research</i> , 2021, 31, 1258-1268.	5.5	4
98	Population genomics of pneumococcal carriage in South Africa following the introduction of the 13-valent pneumococcal conjugate vaccine (PCV13) immunization. <i>Microbial Genomics</i> , 2022, 8, .	2.0	4
99	A Nationwide Outbreak of Invasive Pneumococcal Disease in Israel Caused by <i>Streptococcus Pneumoniae</i> Serotype 2. <i>Clinical Infectious Diseases</i> , 2020, 73, e3768-e3777.	5.8	3
100	Comparative Genomics of Disease and Carriage Serotype 1 Pneumococci. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	3
101	Effect of childhood vaccination and antibiotic use on pneumococcal populations and genome-wide associations with disease among children in Nepal: an observational study. <i>Lancet Microbe</i> , The, 2022, 3, e503-e511.	7.3	2
102	Widespread sharing of pneumococcal strains in a rural African setting: proximate villages are more likely to share similar strains that are carried at multiple timepoints. <i>Microbial Genomics</i> , 2022, 8, .	2.0	1
103	Genetic background of Cambodian pneumococcal carriage isolates following pneumococcal conjugate vaccine 13. <i>Microbial Genomics</i> , 2022, 8, .	2.0	0
104	Distinct <i>Streptococcus pneumoniae</i> cause invasive disease in Papua New Guinea. <i>Microbial Genomics</i> , 2022, 8, .	2.0	0