

# Stephen D Bentley

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1482507/publications.pdf>

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	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
2	Serotype 1 pneumococcus: epidemiology, genomics, and disease mechanisms. <i>Trends in Microbiology</i> , 2022, 30, 581-592.	7.7	5
3	Comparative Genomics of Disease and Carriage Serotype 1 Pneumococci. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	3
4	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
5	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
6	Genetic background of Cambodian pneumococcal carriage isolates following pneumococcal conjugate vaccine 13. <i>Microbial Genomics</i> , 2022, 8, .	2.0	0
7	Distinct <i>Streptococcus pneumoniae</i> cause invasive disease in Papua New Guinea. <i>Microbial Genomics</i> , 2022, 8, .	2.0	0
8	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
9	Pneumococcal Colonization and Virulence Factors Identified Via Experimental Evolution in Infection Models. <i>Molecular Biology and Evolution</i> , 2021, 38, 2209-2226.	8.9	9
10	Apparent nosocomial adaptation of <i>Enterococcus faecalis</i> predates the modern hospital era. <i>Nature Communications</i> , 2021, 12, 1523.	12.8	69
11	Global genomic pathogen surveillance to inform vaccine strategies: a decade-long expedition in pneumococcal genomics. <i>Genome Medicine</i> , 2021, 13, 84.	8.2	12
12	Emergence and dissemination of antimicrobial resistance in <i>Escherichia coli</i> causing bloodstream infections in Norway in 2002-2017: a nationwide, longitudinal, microbial population genomic study. <i>Lancet Microbe</i> , The, 2021, 2, e331-e341.	7.3	43
13	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
14	The role of interspecies recombination in the evolution of antibiotic-resistant pneumococci. <i>ELife</i> , 2021, 10, .	6.0	21
15	Population genetic structure, serotype distribution and antibiotic resistance of <i>Streptococcus pneumoniae</i> causing invasive disease in children in Argentina. <i>Microbial Genomics</i> , 2021, 7, .	2.0	8
16	<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
17	<i>Streptococcus pneumoniae</i> genomic datasets from an Indian population describing pre-vaccine evolutionary epidemiology using a whole genome sequencing approach. <i>Microbial Genomics</i> , 2021, 7, .	2.0	8
18	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

#	ARTICLE	IF	CITATIONS
19	Early Signals of Vaccine-driven Perturbation Seen in Pneumococcal Carriage Population Genomic Data. <i>Clinical Infectious Diseases</i> , 2020, 70, 1294-1303.	5.8	9
20	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
21	Genetic Variation in <i>Neisseria meningitidis</i> Does Not Influence Disease Severity in Meningococcal Meningitis. <i>Frontiers in Medicine</i> , 2020, 7, 594769.	2.6	8
22	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
23	Producing polished prokaryotic pangenomes with the Panaroo pipeline. <i>Genome Biology</i> , 2020, 21, 180.	8.8	419
24	Investigation of sequential outbreaks of <i>Burkholderia cepacia</i> and multidrug-resistant extended spectrum $\beta$ -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
25	Bacterial genome-wide association study of hyper-virulent pneumococcal serotype 1 identifies genetic variation associated with neurotropism. <i>Communications Biology</i> , 2020, 3, 559.	4.4	11
26	Lineage-specific evolution and gene flow in <i>Listeria monocytogenes</i> are independent of bacteriophages. <i>Environmental Microbiology</i> , 2020, 22, 5058-5072.	3.8	16
27	Carriage Dynamics of Pneumococcal Serotypes in Naturally Colonized Infants in a Rural African Setting During the First Year of Life. <i>Frontiers in Pediatrics</i> , 2020, 8, 587730.	1.9	8
28	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
29	Diversification in immunogenicity genes caused by selective pressures in invasive meningococci. <i>Microbial Genomics</i> , 2020, 6, .	2.0	6
30	Horizontal gene transfer rate is not the primary determinant of observed antibiotic resistance frequencies in <i>Streptococcus pneumoniae</i> . <i>Science Advances</i> , 2020, 6, eaaz6137.	10.3	19
31	The Contribution of Genetic Variation of <i>Streptococcus pneumoniae</i> to the Clinical Manifestation of Invasive Pneumococcal Disease. <i>Clinical Infectious Diseases</i> , 2019, 68, 61-69.	5.8	21
32	Genome-wide epistasis and co-selection study using mutual information. <i>Nucleic Acids Research</i> , 2019, 47, e112-e112.	14.5	36
33	Synergistic Activity of Mobile Genetic Element Defences in <i>Streptococcus pneumoniae</i> . <i>Genes</i> , 2019, 10, 707.	2.4	6
34	Fast and flexible bacterial genomic epidemiology with PopPUNK. <i>Genome Research</i> , 2019, 29, 304-316.	5.5	258
35	Atlas of group A streptococcal vaccine candidates compiled using large-scale comparative genomics. <i>Nature Genetics</i> , 2019, 51, 1035-1043.	21.4	120
36	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

#	ARTICLE	IF	CITATIONS
37	Fast hierarchical Bayesian analysis of population structure. <i>Nucleic Acids Research</i> , 2019, 47, 5539-5549.	14.5	173
38	Joint sequencing of human and pathogen genomes reveals the genetics of pneumococcal meningitis. <i>Nature Communications</i> , 2019, 10, 2176.	12.8	83
39	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. <i>EBioMedicine</i> , 2019, 43, 338-346.	6.1	168
40	PANINI: Pangenome Neighbour Identification for Bacterial Populations. <i>Microbial Genomics</i> , 2019, 5, .	2.0	27
41	Putative novel cps loci in a large global collection of pneumococci. <i>Microbial Genomics</i> , 2019, 5, .	2.0	14
42	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
43	Global emergence and population dynamics of divergent serotype 3 CC180 pneumococci. <i>PLoS Pathogens</i> , 2018, 14, e1007438.	4.7	74
44	Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. <i>Wellcome Open Research</i> , 2018, 3, 33.	1.8	42
45	pyseer: a comprehensive tool for microbial pangenome-wide association studies. <i>Bioinformatics</i> , 2018, 34, 4310-4312.	4.1	208
46	Bayesian inference of ancestral dates on bacterial phylogenetic trees. <i>Nucleic Acids Research</i> , 2018, 46, e134-e134.	14.5	174
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	RhierBAPS: An R implementation of the population clustering algorithm hierBAPS. <i>Wellcome Open Research</i> , 2018, 3, 93.	1.8	198
49	Pneumococcal Capsule Synthesis Locus cps 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	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
51	Frequency-dependent selection in vaccine-associated pneumococcal population dynamics. <i>Nature Ecology and Evolution</i> , 2017, 1, 1950-1960.	7.8	121
52	Phase-variable methylation and epigenetic regulation by type I restriction modification systems. <i>FEMS Microbiology Reviews</i> , 2017, 41, S3-S15.	8.6	110
53	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
54	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

#	ARTICLE	IF	CITATIONS
55	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
56	Pre-vaccine serotype composition within a lineage signposts its serotype replacement – a carriage study over 7 years following pneumococcal conjugate vaccine use in the UK. <i>Microbial Genomics</i> , 2017, 3, e000119.	2.0	26
57	Genome-wide identification of lineage and locus specific variation associated with pneumococcal carriage duration. <i>ELife</i> , 2017, 6, .	6.0	95
58	Sequence element enrichment analysis to determine the genetic basis of bacterial phenotypes. <i>Nature Communications</i> , 2016, 7, 12797.	12.8	190
59	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
60	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
61	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
62	Understanding pneumococcal serotype 1 biology through population genomic analysis. <i>BMC Infectious Diseases</i> , 2016, 16, 649.	2.9	22
63	Comparative Genomics of Carriage and Disease Isolates of <i>Streptococcus pneumoniae</i> Serotype 22F Reveals Lineage-Specific Divergence and Niche Adaptation. <i>Genome Biology and Evolution</i> , 2016, 8, 1243-1251.	2.5	8
64	Phylogenetic Analysis of Invasive Serotype 1 <i>Pneumococcus</i> in South Africa, 1989 to 2013. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1326-1334.	3.9	16
65	Horizontal DNA Transfer Mechanisms of Bacteria as Weapons of Intragenomic Conflict. <i>PLoS Biology</i> , 2016, 14, e1002394.	5.6	127
66	Population genomic datasets describing the post-vaccine evolutionary epidemiology of <i>Streptococcus pneumoniae</i> . <i>Scientific Data</i> , 2015, 2, 150058.	5.3	67
67	The post-vaccine microevolution of invasive <i>Streptococcus pneumoniae</i> . <i>Scientific Reports</i> , 2015, 5, 14952.	3.3	36
68	Selective and Genetic Constraints on Pneumococcal Serotype Switching. <i>PLoS Genetics</i> , 2015, 11, e1005095.	3.5	78
69	Climate induces seasonality in pneumococcal transmission. <i>Scientific Reports</i> , 2015, 5, 11344.	3.3	41
70	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
71	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
72	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

#	ARTICLE	IF	CITATIONS
73	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
74	Region-specific diversification of the highly virulent serotype 1 <i>Streptococcus pneumoniae</i> . <i>Microbial Genomics</i> , 2015, 1, e000027.	2.0	27
75	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
76	Defining the Estimated Core Genome of Bacterial Populations Using a Bayesian Decision Model. <i>PLoS Computational Biology</i> , 2014, 10, e1003788.	3.2	72
77	Heterogeneity in the Frequency and Characteristics of Homologous Recombination in Pneumococcal Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004300.	3.5	84
78	Diversification of bacterial genome content through distinct mechanisms over different timescales. <i>Nature Communications</i> , 2014, 5, 5471.	12.8	173
79	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
80	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. <i>Molecular Ecology</i> , 2014, 23, 2442-2451.	3.9	131
81	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
82	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
83	Two-phase importance sampling for inference about transmission trees. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20141324.	2.6	22
84	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
85	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
86	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
87	Dense genomic sampling identifies highways of pneumococcal recombination. <i>Nature Genetics</i> , 2014, 46, 305-309.	21.4	371
88	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
89	Population genomics of post-vaccine changes in pneumococcal epidemiology. <i>Nature Genetics</i> , 2013, 45, 656-663.	21.4	364
90	Description and Nomenclature of <i>Neisseria meningitidis</i> Capsule Locus. <i>Emerging Infectious Diseases</i> , 2013, 19, 566-573.	4.3	259

#	ARTICLE	IF	CITATIONS
91	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
92	Genome-wide association study identifies vitamin B <sub>5</sub> 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
93	A High-Resolution View of Genome-Wide Pneumococcal Transformation. <i>PLoS Pathogens</i> , 2012, 8, e1002745.	4.7	98
94	Detection of recombination events in bacterial genomes from large population samples. <i>Nucleic Acids Research</i> , 2012, 40, e6-e6.	14.5	179
95	The multidrug-resistant PMEN1 pneumococcus is a paradigm for genetic success. <i>Genome Biology</i> , 2012, 13, R103.	9.6	62
96	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
97	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
98	Rapid Pneumococcal Evolution in Response to Clinical Interventions. <i>Science</i> , 2011, 331, 430-434.	12.6	828
99	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
100	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
101	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
102	Role of Conjugative Elements in the Evolution of the Multidrug-Resistant Pandemic Clone <i>Streptococcus pneumoniae</i> <sup>Spain23F</sup> ST81. <i>Journal of Bacteriology</i> , 2009, 191, 1480-1489.	2.2	168
103	Genetic Analysis of the Capsular Biosynthetic Locus from All 90 Pneumococcal Serotypes. <i>PLoS Genetics</i> , 2006, 2, e31.	3.5	661
104	Evaluation of phylogenetic reconstruction methods using bacterial whole genomes: a simulation based study. <i>Wellcome Open Research</i> , 0, 3, 33.	1.8	18