

# Nicholas J Croucher

## List of Publications by Year in descending order

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84  
papers

9,006  
citations

66343

42  
h-index

71685

76  
g-index

107  
all docs

107  
docs citations

107  
times ranked

8240  
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	Phandango: an interactive viewer for bacterial population genomics. <i>Bioinformatics</i> , 2018, 34, 292-293.	4.1	468
4	Dense genomic sampling identifies highways of pneumococcal recombination. <i>Nature Genetics</i> , 2014, 46, 305-309.	21.4	371
5	Population genomics of post-vaccine changes in pneumococcal epidemiology. <i>Nature Genetics</i> , 2013, 45, 656-663.	21.4	364
6	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
7	Fast and flexible bacterial genomic epidemiology with PopPUNK. <i>Genome Research</i> , 2019, 29, 304-316.	5.5	258
8	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
9	Sequence element enrichment analysis to determine the genetic basis of bacterial phenotypes. <i>Nature Communications</i> , 2016, 7, 12797.	12.8	190
10	Bayesian inference of ancestral dates on bacterial phylogenetic trees. <i>Nucleic Acids Research</i> , 2018, 46, e134-e134.	14.5	174
11	Diversification of bacterial genome content through distinct mechanisms over different timescales. <i>Nature Communications</i> , 2014, 5, 5471.	12.8	173
12	Pneumococcal Capsular Switching: A Historical Perspective. <i>Journal of Infectious Diseases</i> , 2013, 207, 439-449.	4.0	172
13	Role of Conjugative Elements in the Evolution of the Multidrug-Resistant Pandemic Clone <i>Streptococcus pneumoniae</i> Spain23F <sup>ST81</sup> . <i>Journal of Bacteriology</i> , 2009, 191, 1480-1489.	2.2	168
14	Efficient Inference of Recent and Ancestral Recombination within Bacterial Populations. <i>Molecular Biology and Evolution</i> , 2017, 34, 1167-1182.	8.9	168
15	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. <i>EBioMedicine</i> , 2019, 43, 338-346.	6.1	168
16	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
17	Evolution of antibiotic resistance is linked to any genetic mechanism affecting bacterial duration of carriage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1075-1080.	7.1	133
18	Horizontal DNA Transfer Mechanisms of Bacteria as Weapons of Intragenomic Conflict. <i>PLoS Biology</i> , 2016, 14, e1002394.	5.6	127

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19	Frequency-dependent selection in vaccine-associated pneumococcal population dynamics. <i>Nature Ecology and Evolution</i> , 2017, 1, 1950-1960.	7.8	121
20	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
21	Phase-variable methylation and epigenetic regulation by type I restriction modification systems. <i>FEMS Microbiology Reviews</i> , 2017, 41, S3-S15.	8.6	110
22	Diversification of Colonization Factors in a Multidrug-Resistant <i>Escherichia coli</i> Lineage Evolving under Negative Frequency-Dependent Selection. <i>MBio</i> , 2019, 10, .	4.1	106
23	A High-Resolution View of Genome-Wide Pneumococcal Transformation. <i>PLoS Pathogens</i> , 2012, 8, e1002745.	4.7	98
24	Genome-wide identification of lineage and locus specific variation associated with pneumococcal carriage duration. <i>ELife</i> , 2017, 6, .	6.0	95
25	Interacting networks of resistance, virulence and core machinery genes identified by genome-wide epistasis analysis. <i>PLoS Genetics</i> , 2017, 13, e1006508.	3.5	85
26	Heterogeneity in the Frequency and Characteristics of Homologous Recombination in Pneumococcal Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004300.	3.5	84
27	The application of genomics to tracing bacterial pathogen transmission. <i>Current Opinion in Microbiology</i> , 2015, 23, 62-67.	5.1	84
28	Joint sequencing of human and pathogen genomes reveals the genetics of pneumococcal meningitis. <i>Nature Communications</i> , 2019, 10, 2176.	12.8	83
29	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
30	Impact of 13-Valent Pneumococcal Conjugate Vaccination on <i>Streptococcus pneumoniae</i> Carriage in Young Children in Massachusetts. <i>Journal of the Pediatric Infectious Diseases Society</i> , 2014, 3, 23-32.	1.3	78
31	Selective and Genetic Constraints on Pneumococcal Serotype Switching. <i>PLoS Genetics</i> , 2015, 11, e1005095.	3.5	78
32	Divergent serotype replacement trends and increasing diversity in pneumococcal disease in high income settings reduce the benefit of expanding vaccine valency. <i>Scientific Reports</i> , 2020, 10, 18977.	3.3	76
33	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
34	Genomic and Functional Analysis of Emerging Virulent and Multidrug-Resistant <i>Escherichia coli</i> Lineage Sequence Type 648. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	71
35	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
36	Population genomic datasets describing the post-vaccine evolutionary epidemiology of <i>Streptococcus pneumoniae</i> . <i>Scientific Data</i> , 2015, 2, 150058.	5.3	67

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37	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
38	Comparative Genomic Analysis of Ten <i>Streptococcus pneumoniae</i> Temperate Bacteriophages. <i>Journal of Bacteriology</i> , 2009, 191, 4854-4862.	2.2	64
39	Easy and accurate reconstruction of whole HIV genomes from short-read sequence data with shiver. <i>Virus Evolution</i> , 2018, 4, vey007.	4.9	64
40	The multidrug-resistant PMEN1 pneumococcus is a paradigm for genetic success. <i>Genome Biology</i> , 2012, 13, R103.	9.6	62
41	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
42	Bacterial genomes in epidemiology—present and future. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20120202.	4.0	51
43	Identification, variation and transcription of pneumococcal repeat sequences. <i>BMC Genomics</i> , 2011, 12, 120.	2.8	48
44	Pneumococcal Vaccines: Host Interactions, Population Dynamics, and Design Principles. <i>Annual Review of Microbiology</i> , 2018, 72, 521-549.	7.3	44
45	Distinct Effects on Diversifying Selection by Two Mechanisms of Immunity against <i>Streptococcus pneumoniae</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002989.	4.7	43
46	Emergence and dissemination of antimicrobial resistance in <i>Escherichia coli</i> causing bloodstream infections in Norway in 2002–17: a nationwide, longitudinal, microbial population genomic study. <i>Lancet Microbe</i> , The, 2021, 2, e331-e341.	7.3	43
47	Designing ecologically optimized pneumococcal vaccines using population genomics. <i>Nature Microbiology</i> , 2020, 5, 473-485.	13.3	39
48	Recombination produces coherent bacterial species clusters in both core and accessory genomes. <i>Microbial Genomics</i> , 2015, 1, e000038.	2.0	37
49	Genome-wide epistasis and co-selection study using mutual information. <i>Nucleic Acids Research</i> , 2019, 47, e112-e112.	14.5	36
50	The Emergence of Bacterial “Hopeful Monsters”. <i>MBio</i> , 2014, 5, e01550-14.	4.1	35
51	PANINI: Pangenome Neighbour Identification for Bacterial Populations. <i>Microbial Genomics</i> , 2019, 5, .	2.0	27
52	Stability of the pneumococcal population structure in Massachusetts as PCV13 was introduced. <i>BMC Infectious Diseases</i> , 2015, 15, 68.	2.9	26
53	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
54	Panproteome-wide analysis of antibody responses to whole cell pneumococcal vaccination. <i>ELife</i> , 2018, 7, .	6.0	26

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55	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
56	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . <i>PLoS Biology</i> , 2020, 18, e3000878.	5.6	24
57	Genomic epidemiology of penicillin-non-susceptible <i>Streptococcus pneumoniae</i> . <i>Microbial Genomics</i> , 2019, 5, .	2.0	23
58	Transformation Asymmetry and the Evolution of the Bacterial Accessory Genome. <i>Molecular Biology and Evolution</i> , 2018, 35, 575-581.	8.9	22
59	Methylation Warfare: Interaction of Pneumococcal Bacteriophages with Their Host. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	22
60	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
61	The role of interspecies recombination in the evolution of antibiotic-resistant pneumococci. <i>ELife</i> , 2021, 10, .	6.0	21
62	SuperDCA for genome-wide epistasis analysis. <i>Microbial Genomics</i> , 2018, 4, .	2.0	19
63	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
64	Negative frequency-dependent selection and asymmetrical transformation stabilise multi-strain bacterial population structures. <i>ISME Journal</i> , 2021, 15, 1523-1538.	9.8	17
65	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
66	Identification of pneumococcal colonization determinants in the stringent response pathway facilitated by genomic diversity. <i>BMC Genomics</i> , 2015, 16, 369.	2.8	13
67	Population genomics of pneumococcal carriage in Massachusetts children following introduction of PCV-13. <i>Microbial Genomics</i> , 2019, 5, .	2.0	12
68	Analysing pneumococcal invasiveness using Bayesian models of pathogen progression rates. <i>PLoS Computational Biology</i> , 2022, 18, e1009389.	3.2	10
69	Alterations in chromosomal genes <i>nfsA</i> , <i>nfsB</i> , and <i>ribE</i> are associated with nitrofurantoin resistance in <i>Escherichia coli</i> from the United Kingdom. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
70	Synergistic Activity of Mobile Genetic Element Defences in <i>Streptococcus pneumoniae</i> . <i>Genes</i> , 2019, 10, 707.	2.4	6
71	RCandy: an R package for visualizing homologous recombinations in bacterial genomes. <i>Bioinformatics</i> , 2022, 38, 1450-1451.	4.1	5
72	Genome-wide association, prediction and heritability in bacteria with application to <i>Streptococcus pneumoniae</i> . <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac011.	3.2	5

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73	Targeted control of pneumolysin production by a mobile genetic element in <i>Streptococcus pneumoniae</i> . <i>Microbial Genomics</i> , 2022, 8, .	2.0	5
74	International links between <i>Streptococcus pneumoniae</i> vaccine serotype 4 sequence type (ST) 801 in Northern European shipyard outbreaks of invasive pneumococcal disease. <i>Vaccine</i> , 2022, 40, 1054-1060.	3.8	4
75	Predicting the future distribution of antibiotic resistance using time series forecasting and geospatial modelling. <i>Wellcome Open Research</i> , 0, 5, 194.	1.8	3
76	Comparative Genomics of Disease and Carriage Serotype 1 Pneumococci. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	3
77	Peptide Occurring in Enterobacteriaceae Triggers <i>Streptococcus pneumoniae</i> Cell Death. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 320.	3.9	1
78	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
79	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
80	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
81	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
82	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
83	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
84	Nitrofurantoin-resistant <i>Escherichia coli</i> in the UK: genetic determinants, diversity, and undetected occurrences. <i>Access Microbiology</i> , 2022, 4, .	0.5	0