

Nicholas J Croucher

List of Publications by Year in descending order

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Version: 2024-02-01

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	RCandy: an R package for visualizing homologous recombinations in bacterial genomes. <i>Bioinformatics</i> , 2022, 38, 1450-1451.	4.1	5
2	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
3	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
4	Analysing pneumococcal invasiveness using Bayesian models of pathogen progression rates. <i>PLoS Computational Biology</i> , 2022, 18, e1009389.	3.2	10
5	Targeted control of pneumolysin production by a mobile genetic element in <i>Streptococcus pneumoniae</i> . <i>Microbial Genomics</i> , 2022, 8, .	2.0	5
6	Comparative Genomics of Disease and Carriage Serotype 1 Pneumococci. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	3
7	Nitrofurantoin-resistant <i>Escherichia coli</i> in the UK: genetic determinants, diversity, and undetected occurrences. <i>Access Microbiology</i> , 2022, 4, .	0.5	0
8	Negative frequency-dependent selection and asymmetrical transformation stabilise multi-strain bacterial population structures. <i>ISME Journal</i> , 2021, 15, 1523-1538.	9.8	17
9	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
10	The role of interspecies recombination in the evolution of antibiotic-resistant pneumococci. <i>ELife</i> , 2021, 10, .	6.0	21
11	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
12	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
13	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
14	Designing ecologically optimized pneumococcal vaccines using population genomics. <i>Nature Microbiology</i> , 2020, 5, 473-485.	13.3	39
15	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
16	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
17	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . <i>PLoS Biology</i> , 2020, 18, e3000878.	5.6	24
18	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0

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19	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
20	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
21	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
22	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
23	Frequency-dependent selection can forecast evolution in <i>Streptococcus pneumoniae</i> . , 2020, 18, e3000878.		0
24	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
25	Methylation Warfare: Interaction of Pneumococcal Bacteriophages with Their Host. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	22
26	Genome-wide epistasis and co-selection study using mutual information. <i>Nucleic Acids Research</i> , 2019, 47, e112-e112.	14.5	36
27	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
28	Synergistic Activity of Mobile Genetic Element Defences in <i>Streptococcus pneumoniae</i> . <i>Genes</i> , 2019, 10, 707.	2.4	6
29	Fast and flexible bacterial genomic epidemiology with PopPUNK. <i>Genome Research</i> , 2019, 29, 304-316.	5.5	258
30	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
31	Joint sequencing of human and pathogen genomes reveals the genetics of pneumococcal meningitis. <i>Nature Communications</i> , 2019, 10, 2176.	12.8	83
32	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. <i>EBioMedicine</i> , 2019, 43, 338-346.	6.1	168
33	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
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	PANINI: Pangenome Neighbour Identification for Bacterial Populations. <i>Microbial Genomics</i> , 2019, 5, .	2.0	27
36	Population genomics of pneumococcal carriage in Massachusetts children following introduction of PCV-13. <i>Microbial Genomics</i> , 2019, 5, .	2.0	12

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37	Genomic epidemiology of penicillin-non-susceptible <i>Streptococcus pneumoniae</i> . <i>Microbial Genomics</i> , 2019, 5, .	2.0	23
38	Phandango: an interactive viewer for bacterial population genomics. <i>Bioinformatics</i> , 2018, 34, 292-293.	4.1	468
39	Transformation Asymmetry and the Evolution of the Bacterial Accessory Genome. <i>Molecular Biology and Evolution</i> , 2018, 35, 575-581.	8.9	22
40	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
41	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
42	Bayesian inference of ancestral dates on bacterial phylogenetic trees. <i>Nucleic Acids Research</i> , 2018, 46, e134-e134.	14.5	174
43	Pneumococcal Vaccines: Host Interactions, Population Dynamics, and Design Principles. <i>Annual Review of Microbiology</i> , 2018, 72, 521-549.	7.3	44
44	SuperDCA for genome-wide epistasis analysis. <i>Microbial Genomics</i> , 2018, 4, .	2.0	19
45	Panproteome-wide analysis of antibody responses to whole cell pneumococcal vaccination. <i>ELife</i> , 2018, 7, .	6.0	26
46	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
47	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
48	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
49	Frequency-dependent selection in vaccine-associated pneumococcal population dynamics. <i>Nature Ecology and Evolution</i> , 2017, 1, 1950-1960.	7.8	121
50	Phase-variable methylation and epigenetic regulation by type I restriction modification systems. <i>FEMS Microbiology Reviews</i> , 2017, 41, S3-S15.	8.6	110
51	Efficient Inference of Recent and Ancestral Recombination within Bacterial Populations. <i>Molecular Biology and Evolution</i> , 2017, 34, 1167-1182.	8.9	168
52	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
53	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
54	Genome-wide identification of lineage and locus specific variation associated with pneumococcal carriage duration. <i>ELife</i> , 2017, 6, .	6.0	95

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55	Sequence element enrichment analysis to determine the genetic basis of bacterial phenotypes. <i>Nature Communications</i> , 2016, 7, 12797.	12.8	190
56	Horizontal DNA Transfer Mechanisms of Bacteria as Weapons of Intragenomic Conflict. <i>PLoS Biology</i> , 2016, 14, e1002394.	5.6	127
57	Population genomic datasets describing the post-vaccine evolutionary epidemiology of <i>Streptococcus pneumoniae</i> . <i>Scientific Data</i> , 2015, 2, 150058.	5.3	67
58	Identification of pneumococcal colonization determinants in the stringent response pathway facilitated by genomic diversity. <i>BMC Genomics</i> , 2015, 16, 369.	2.8	13
59	Stability of the pneumococcal population structure in Massachusetts as PCV13 was introduced. <i>BMC Infectious Diseases</i> , 2015, 15, 68.	2.9	26
60	Selective and Genetic Constraints on Pneumococcal Serotype Switching. <i>PLoS Genetics</i> , 2015, 11, e1005095.	3.5	78
61	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
62	The application of genomics to tracing bacterial pathogen transmission. <i>Current Opinion in Microbiology</i> , 2015, 23, 62-67.	5.1	84
63	Recombination produces coherent bacterial species clusters in both core and accessory genomes. <i>Microbial Genomics</i> , 2015, 1, e000038.	2.0	37
64	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
65	Heterogeneity in the Frequency and Characteristics of Homologous Recombination in Pneumococcal Evolution. <i>PLoS Genetics</i> , 2014, 10, e1004300.	3.5	84
66	Diversification of bacterial genome content through distinct mechanisms over different timescales. <i>Nature Communications</i> , 2014, 5, 5471.	12.8	173
67	The Emergence of Bacterial ‘‘Hopeful Monsters’’. <i>MBio</i> , 2014, 5, e01550-14.	4.1	35
68	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
69	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
70	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
71	Dense genomic sampling identifies highways of pneumococcal recombination. <i>Nature Genetics</i> , 2014, 46, 305-309.	21.4	371
72	Population genomics of post-vaccine changes in pneumococcal epidemiology. <i>Nature Genetics</i> , 2013, 45, 656-663.	21.4	364

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73	Bacterial genomes in epidemiologyâ€™ present and future. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120202.	4.0	51
74	Dominant Role of Nucleotide Substitution in the Diversification of Serotype 3 Pneumococci over Decades and during a Single Infection. PLoS Genetics, 2013, 9, e1003868.	3.5	81
75	Pneumococcal Capsular Switching: A Historical Perspective. Journal of Infectious Diseases, 2013, 207, 439-449.	4.0	172
76	A High-Resolution View of Genome-Wide Pneumococcal Transformation. PLoS Pathogens, 2012, 8, e1002745.	4.7	98
77	Distinct Effects on Diversifying Selection by Two Mechanisms of Immunity against Streptococcus pneumoniae. PLoS Pathogens, 2012, 8, e1002989.	4.7	43
78	The multidrug-resistant PMEN1 pneumococcus is a paradigm for genetic success. Genome Biology, 2012, 13, R103.	9.6	62
79	Rapid Pneumococcal Evolution in Response to Clinical Interventions. Science, 2011, 331, 430-434.	12.6	828
80	Identification, variation and transcription of pneumococcal repeat sequences. BMC Genomics, 2011, 12, 120.	2.8	48
81	Structure and dynamics of the pan-genome of Streptococcus pneumoniae and closely related species. Genome Biology, 2010, 11, R107.	8.8	321
82	Comparative Genomic Analysis of Ten <i>Streptococcus pneumoniae</i> Temperate Bacteriophages. Journal of Bacteriology, 2009, 191, 4854-4862.	2.2	64
83	Role of Conjugative Elements in the Evolution of the Multidrug-Resistant Pandemic Clone <i>Streptococcus pneumoniae</i> ^{Spain23F}ST81. Journal of Bacteriology, 2009, 191, 1480-1489.	2.2	168
84	Predicting the future distribution of antibiotic resistance using time series forecasting and geospatial modelling. Wellcome Open Research, 0, 5, 194.	1.8	3