

Andrew J Page

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

85
papers

6,235
citations

26
h-index

78
g-index

105
ext. papers

10,059
ext. citations

11.2
avg, IF

5.53
L-index

#	Paper	IF	Citations
85	Roary: rapid large-scale prokaryote pan genome analysis. <i>Bioinformatics</i> , 2015 , 31, 3691-3	7.2	1949
84	Rapid phylogenetic analysis of large samples of recombinant bacterial whole genome sequences using Gubbins. <i>Nucleic Acids Research</i> , 2015 , 43, e15	20.1	1007
83	: rapid efficient extraction of SNPs from multi-FASTA alignments. <i>Microbial Genomics</i> , 2016 , 2, e000056	4.4	417
82	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of Salmonella Typhi identifies inter- and intracontinental transmission events. <i>Nature Genetics</i> , 2015 , 47, 632-9	36.3	305
81	Emergence of an Extensively Drug-Resistant Serovar Typhi Clone Harboring a Promiscuous Plasmid Encoding Resistance to Fluoroquinolones and Third-Generation Cephalosporins. <i>MBio</i> , 2018 , 9,	7.8	301
80	ARIBA: rapid antimicrobial resistance genotyping directly from sequencing reads. <i>Microbial Genomics</i> , 2017 , 3, e000131	4.4	283
79	Dense genomic sampling identifies highways of pneumococcal recombination. <i>Nature Genetics</i> , 2014 , 46, 305-309	36.3	269
78	Epithelial IL-22RA1-mediated fucosylation promotes intestinal colonization resistance to an opportunistic pathogen. <i>Cell Host and Microbe</i> , 2014 , 16, 504-16	23.4	186
77	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. <i>Cell Reports</i> , 2021 , 35, 109292	10.6	172
76	Robust high-throughput prokaryote assembly and improvement pipeline for Illumina data. <i>Microbial Genomics</i> , 2016 , 2, e000083	4.4	144
75	The TraDIS toolkit: sequencing and analysis for dense transposon mutant libraries. <i>Bioinformatics</i> , 2016 , 32, 1109-11	7.2	98
74	Microevolution of Monophasic Salmonella Typhimurium during Epidemic, United Kingdom, 2005-2010. <i>Emerging Infectious Diseases</i> , 2016 , 22, 617-24	10.2	96
73	An extended genotyping framework for Salmonella enterica serovar Typhi, the cause of human typhoid. <i>Nature Communications</i> , 2016 , 7, 12827	17.4	88
72	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. <i>EBioMedicine</i> , 2019 , 43, 338-346	8.8	67
71	Multi-heuristic dynamic task allocation using genetic algorithms in a heterogeneous distributed system. <i>Journal of Parallel and Distributed Computing</i> , 2010 , 70, 758-766	4.4	60
70	The phylogeography and incidence of multi-drug resistant typhoid fever in sub-Saharan Africa. <i>Nature Communications</i> , 2018 , 9, 5094	17.4	53
69	Global phylogeography and evolutionary history of Shigella dysenteriae type 1. <i>Nature Microbiology</i> , 2016 , 1, 16027	26.6	47

68	Multilocus sequence typing by blast from de novo assemblies against PubMLST. <i>Journal of Open Source Software</i> , 2016 , 1, 118	5.2	45
67	CoronaHiT: high-throughput sequencing of SARS-CoV-2 genomes. <i>Genome Medicine</i> , 2021 , 13, 21	14.4	40
66	Framework for Task Scheduling in Heterogeneous Distributed Computing Using Genetic Algorithms. <i>Artificial Intelligence Review</i> , 2005 , 24, 415-429	9.7	39
65	A Phylogenetic and Phenotypic Analysis of Salmonella enterica Serovar Weltevreden, an Emerging Agent of Diarrheal Disease in Tropical Regions. <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0004446	4.8	39
64	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021 , 374, 423-431	33.3	35
63	. <i>Journal of Display Technology</i> , 2009 , 5, 111-119		32
62	Genomic Analysis of Salmonella enterica Serovar Typhimurium from Wild Passerines in England and Wales. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 6728-6735	4.8	32
61	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021 , 374, eabl9551	33.3	31
60	Molecular Surveillance Identifies Multiple Transmissions of Typhoid in West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2016 , 10, e0004781	4.8	27
59	Phylogenetic Analysis of Klebsiella pneumoniae from Hospitalized Children, Pakistan. <i>Emerging Infectious Diseases</i> , 2017 , 23, 1872-1875	10.2	26
58	Comparison of classical multi-locus sequence typing software for next-generation sequencing data. <i>Microbial Genomics</i> , 2017 , 3, e000124	4.4	22
57	REACT-1 round 13 final report: exponential growth, high prevalence of SARS-CoV-2 and vaccine effectiveness associated with Delta variant in England during May to July 2021		21
56	Staphylococcus cornubiensis sp. nov., a member of the Staphylococcus intermedius Group (SIG). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018 , 68, 3404-3408	2.2	18
55	TraDIS-Xpress: a high-resolution whole-genome assay identifies novel mechanisms of triclosan action and resistance. <i>Genome Research</i> , 2020 , 30, 239-249	9.7	15
54	REACT-1 round 12 report: resurgence of SARS-CoV-2 infections in England associated with increased frequency of the Delta variant		15
53	ARIBA: rapid antimicrobial resistance genotyping directly from sequencing reads		13
52	A global resource for genomic predictions of antimicrobial resistance and surveillance of Salmonella Typhi at pathogenwatch. <i>Nature Communications</i> , 2021 , 12, 2879	17.4	12
51	Rapid increase in Omicron infections in England during December 2021: REACT-1 study.. <i>Science</i> , 2022 , 375, eabn8347	33.3	11

50	CoronaHiT: High throughput sequencing of SARS-CoV-2 genomes		11
49	Large-scale sequencing of SARS-CoV-2 genomes from one region allows detailed epidemiology and enables local outbreak management. <i>Microbial Genomics</i> , 2021 , 7,	4.4	11
48	Rapid multi-locus sequence typing direct from uncorrected long reads using. <i>PeerJ</i> , 2018 , 6, e5233	3.1	10
47	Low memory distributed reconstruction of large digital holograms. <i>Optics Express</i> , 2008 , 16, 1990-5	3.3	9
46	Stability of the Encoding Plasmids and Surface Expression of CS6 Differs in Enterotoxigenic Escherichia coli (ETEC) Encoding Different Heat-Stable (ST) Enterotoxins (STh and STp). <i>PLoS ONE</i> , 2016 , 11, e0152899	3.7	9
45	The PHA4GE SARS-CoV-2 Contextual Data Specification for Open Genomic Epidemiology		9
44	Robust high throughput prokaryote de novo assembly and improvement pipeline for Illumina data		9
43	Large scale sequencing of SARS-CoV-2 genomes from one region allows detailed epidemiology and enables local outbreak management		9
42	The golden death bacillus Chryseobacterium nematophagum is a novel matrix digesting pathogen of nematodes. <i>BMC Biology</i> , 2019 , 17, 10	7.3	8
41	Candidatus Ornithobacterium hominis insights gained from draft genomes obtained from nasopharyngeal swabs. <i>Microbial Genomics</i> , 2019 , 5,	4.4	7
40	Characterization of the yehUT two-component regulatory system of Salmonella enterica Serovar Typhi and Typhimurium. <i>PLoS ONE</i> , 2013 , 8, e84567	3.7	7
39	SARS-CoV-2 infection and vaccine effectiveness in England (REACT-1): a series of cross-sectional random community surveys.. <i>Lancet Respiratory Medicine</i> , 2022 ,	35.1	7
38	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission.. <i>Nature Communications</i> , 2022 , 13, 751	17.4	7
37	SARS-CoV-2 lineage dynamics in England from January to March 2021 inferred from representative community samples		7
36	REACT-1 study round 14: High and increasing prevalence of SARS-CoV-2 infection among school-aged children during September 2021 and vaccine effectiveness against infection in England		6
35	AlbaTraDIS: Comparative analysis of large datasets from parallel transposon mutagenesis experiments		6
34	Surveillance of SARS-CoV-2 in Zimbabwe shows dominance of variants of concern. <i>Lancet Microbe, The</i> , 2021 , 2, e177	22.2	6
33	A genome-wide analysis of Escherichia coli responses to fosfomycin using TraDIS-Xpress reveals novel roles for phosphonate degradation and phosphate transport systems. <i>Journal of Antimicrobial Chemotherapy</i> , 2020 , 75, 3144-3151	5.1	5

32	Scheduling in a dynamic heterogeneous distributed system using estimation error. <i>Journal of Parallel and Distributed Computing</i> , 2008 , 68, 1452-1462	4.4	4
31	Building Large Phylogenetic Trees on Coarse-Grained Parallel Machines. <i>Algorithmica</i> , 2006 , 45, 285-300.	0.9	4
30	AlbaTraDIS: Comparative analysis of large datasets from parallel transposon mutagenesis experiments. <i>PLoS Computational Biology</i> , 2020 , 16, e1007980	5	4
29	SARS-CoV-2 lineage dynamics in England from September to November 2021: high diversity of Delta sub-lineages and increased transmissibility of AY.4.2		4
28	REACT-1 round 15 final report: Increased breakthrough SARS-CoV-2 infections among adults who had received two doses of vaccine, but booster doses and first doses in children are providing important protection		3
27	SARS-CoV-2 variants of concern dominate in Lahore, Pakistan in April 2021. <i>Microbial Genomics</i> , 2021 , 7,	4.4	3
26	Genomic epidemiology and the role of international and regional travel in the SARS-CoV-2 epidemic in Zimbabwe: a retrospective study of routinely collected surveillance data. <i>The Lancet Global Health</i> , 2021 , 9, e1658-e1666	13.6	3
25	An integrated analysis of contact tracing and genomics to assess the efficacy of travel restrictions on SARS-CoV-2 introduction and transmission in England from June to September, 2020		3
24	Long-read-sequenced reference genomes of the seven major lineages of enterotoxigenic <i>Escherichia coli</i> (ETEC) circulating in modern time. <i>Scientific Reports</i> , 2021 , 11, 9256	4.9	3
23	REACT-1 round 11 report: low prevalence of SARS-CoV-2 infection in the community prior to the third step of the English roadmap out of lockdown		3
22	Rapid increase in Omicron infections in England during December 2021: REACT-1 study		2
21	GFF3toEMBL: Preparing annotated assemblies for submission to EMBL. <i>Journal of Open Source Software</i> , 2016 , 1, 80	5.2	2
20	Application of respiratory metagenomics for COVID-19 patients on the intensive care unit to inform appropriate initial antimicrobial treatment and rapid detection of nosocomial transmission		2
19	A global resource for genomic predictions of antimicrobial resistance and surveillance of <i>Salmonella Typhi</i> at Pathogenwatch		2
18	Socru: Typing of genome level order and orientation in bacteria		2
17	Tatajuba [Exploring the distribution of homopolymer tracts		2
16	The role of viral genomics in understanding COVID-19 outbreaks in long-term care facilities. <i>Lancet Microbe</i> , 2021 ,	22.2	2
15	Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package.. <i>GigaScience</i> , 2022 , 11,	7.6	2

14	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission.. <i>Nature Communications</i> , 2022 , 13, 1012	17.4	2
13	The Omicron SARS-CoV-2 epidemic in England during February 2022		2
12	REACT-1 round 15 interim report: High and rising prevalence of SARS-CoV-2 infection in England from end of September 2021 followed by a fall in late October 2021		1
11	SaffronTree: Fast, reference-free pseudo-phylogenomic trees from reads or contigs.. <i>Journal of Open Source Software</i> , 2017 , 2, 243	5.2	1
10	Rapid Mycobacterium tuberculosis spoligotyping from uncorrected long reads using Galru		1
9	Candidatus <i>Ornithobacterium hominis</i> sp. nov.: insights gained from draft genomes obtained from nasopharyngeal swabs		1
8	A new massively-parallel transposon mutagenesis approach comparing multiple datasets identifies novel mechanisms of action and resistance to triclosan		1
7	Comparison Of Multi-locus Sequence Typing software For next generation sequencing data		1
6	Genomic epidemiology of the SARS-CoV-2 epidemic in Zimbabwe: Role of international travel and regional migration in spread		1
5	Replacement of the Alpha variant of SARS-CoV-2 by the Delta variant in Lebanon between April and June 2021		1
4	Characterising the persistence of RT-PCR positivity and incidence in a community survey of SARS-CoV-2. <i>Wellcome Open Research</i> , 7 , 102	4.8	0
3	Long-read sequencing for identification of insertion sites in large transposon mutant libraries.. <i>Scientific Reports</i> , 2022 , 12, 3546	4.9	0
2	Breakthrough SARS-CoV-2 infections in double and triple vaccinated adults and single dose vaccine effectiveness among children in Autumn 2021 in England: REACT-1 study.. <i>EClinicalMedicine</i> , 2022 , 48, 101419	11.3	0
1	TipToft: detecting plasmids contained in uncorrected long read sequencing data. <i>Journal of Open Source Software</i> , 2019 , 4, 1021	5.2	