

Andrew J Page

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

11,924
citations

159525

30
h-index

123376

61
g-index

105
all docs

105
docs citations

105
times ranked

14072
citing authors

#	ARTICLE	IF	CITATIONS
1	Roary: rapid large-scale prokaryote pan genome analysis. <i>Bioinformatics</i> , 2015, 31, 3691-3693.	1.8	4,099
2	Rapid phylogenetic analysis of large samples of recombinant bacterial whole genome sequences using Gubbins. <i>Nucleic Acids Research</i> , 2015, 43, e15-e15.	6.5	1,834
3	SNP-sites: rapid efficient extraction of SNPs from multi-FASTA alignments. <i>Microbial Genomics</i> , 2016, 2, e000056.	1.0	888
4	ARIBA: rapid antimicrobial resistance genotyping directly from sequencing reads. <i>Microbial Genomics</i> , 2017, 3, e000131.	1.0	478
5	Emergence of an Extensively Drug-Resistant <i>Salmonella enterica</i> Serovar Typhi Clone Harboring a Promiscuous Plasmid Encoding Resistance to Fluoroquinolones and Third-Generation Cephalosporins. <i>MBio</i> , 2018, 9, .	1.8	434
6	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of <i>Salmonella</i> Typhi identifies inter- and intracontinental transmission events. <i>Nature Genetics</i> , 2015, 47, 632-639.	9.4	403
7	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.	2.9	375
8	Dense genomic sampling identifies highways of pneumococcal recombination. <i>Nature Genetics</i> , 2014, 46, 305-309.	9.4	371
9	Epithelial IL-22RA1-Mediated Fucosylation Promotes Intestinal Colonization Resistance to an Opportunistic Pathogen. <i>Cell Host and Microbe</i> , 2014, 16, 504-516.	5.1	237
10	Robust high-throughput prokaryote de novo assembly and improvement pipeline for Illumina data. <i>Microbial Genomics</i> , 2016, 2, e000083.	1.0	208
11	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. <i>EBioMedicine</i> , 2019, 43, 338-346.	2.7	168
12	The TraDIS toolkit: sequencing and analysis for dense transposon mutant libraries. <i>Bioinformatics</i> , 2016, 32, 1109-1111.	1.8	167
13	Microevolution of Monophasic <i>Salmonella</i> Typhimurium during Epidemic, United Kingdom, 2005-2010. <i>Emerging Infectious Diseases</i> , 2016, 22, 617-624.	2.0	158
14	An extended genotyping framework for <i>Salmonella enterica</i> serovar Typhi, the cause of human typhoid. <i>Nature Communications</i> , 2016, 7, 12827.	5.8	145
15	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	6.0	144
16	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021, 374, eabl9551.	6.0	111
17	Rapid increase in Omicron infections in England during December 2021: REACT-1 study. <i>Science</i> , 2022, 375, 1406-1411.	6.0	99
18	The phylogeography and incidence of multi-drug resistant typhoid fever in sub-Saharan Africa. <i>Nature Communications</i> , 2018, 9, 5094.	5.8	98

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19	CoronaHiT: high-throughput sequencing of SARS-CoV-2 genomes. <i>Genome Medicine</i> , 2021, 13, 21.	3.6	94
20	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.	2.7	85
21	Multilocus sequence typing by blast from de novo assemblies against PubMLST. <i>Journal of Open Source Software</i> , 2016, 1, 118.	2.0	81
22	Twin peaks: The Omicron SARS-CoV-2 BA.1 and BA.2 epidemics in England. <i>Science</i> , 2022, 376, .	6.0	78
23	Global phylogeography and evolutionary history of <i>Shigella dysenteriae</i> type 1. <i>Nature Microbiology</i> , 2016, 1, 16027.	5.9	65
24	A Phylogenetic and Phenotypic Analysis of <i>Salmonella enterica</i> Serovar Weltevreden, an Emerging Agent of Diarrheal Disease in Tropical Regions. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004446.	1.3	59
25	A global resource for genomic predictions of antimicrobial resistance and surveillance of <i>Salmonella</i> Typhi at pathogenwatch. <i>Nature Communications</i> , 2021, 12, 2879.	5.8	56
26	Framework for Task Scheduling in Heterogeneous Distributed Computing Using Genetic Algorithms. <i>Artificial Intelligence Review</i> , 2005, 24, 415-429.	9.7	54
27	Genomic Analysis of <i>Salmonella enterica</i> Serovar Typhimurium from Wild Passerines in England and Wales. <i>Applied and Environmental Microbiology</i> , 2016, 82, 6728-6735.	1.4	51
28	Molecular Surveillance Identifies Multiple Transmissions of Typhoid in West Africa. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004781.	1.3	46
29	Comparison of classical multi-locus sequence typing software for next-generation sequencing data. <i>Microbial Genomics</i> , 2017, 3, e000124.	1.0	45
30	Using Commodity Graphics Hardware for Real-Time Digital Hologram View-Reconstruction. <i>Journal of Display Technology</i> , 2009, 5, 111-119.	1.3	44
31	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, 10, 355-366.	5.2	39
32	Phylogenetic Analysis of <i>Klebsiella pneumoniae</i> from Hospitalized Children, Pakistan. <i>Emerging Infectious Diseases</i> , 2017, 23, 1872-1875.	2.0	32
33	TraDIS-Xpress: a high-resolution whole-genome assay identifies novel mechanisms of triclosan action and resistance. <i>Genome Research</i> , 2020, 30, 239-249.	2.4	32
34	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, .	1.0	31
35	<i>Staphylococcus cornubiensis</i> sp. nov., a member of the <i>Staphylococcus intermedius</i> Group (SIG). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2018, 68, 3404-3408.	0.8	31
36	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission. <i>Nature Communications</i> , 2022, 13, 751.	5.8	27

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37	The role of viral genomics in understanding COVID-19 outbreaks in long-term care facilities. <i>Lancet Microbe</i> , The, 2022, 3, e151-e158.	3.4	25
38	Rapid multi-locus sequence typing direct from uncorrected long reads using <i>Krocus</i> . <i>PeerJ</i> , 2018, 6, e5233.	0.9	19
39	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.	2.9	19
40	Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package. <i>GigaScience</i> , 2022, 11, .	3.3	18
41	AlbaTraDIS: Comparative analysis of large datasets from parallel transposon mutagenesis experiments. <i>PLoS Computational Biology</i> , 2020, 16, e1007980.	1.5	17
42	Characterization of the yehUT Two-Component Regulatory System of <i>Salmonella enterica</i> Serovar Typhi and Typhimurium. <i>PLoS ONE</i> , 2013, 8, e84567.	1.1	16
43	'Candidatus <i>Ornithobacterium hominis</i> ': insights gained from draft genomes obtained from nasopharyngeal swabs. <i>Microbial Genomics</i> , 2019, 5, .	1.0	16
44	A genome-wide analysis of <i>Escherichia coli</i> 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.	1.3	15
45	Low memory distributed reconstruction of large digital holograms. <i>Optics Express</i> , 2008, 16, 1990.	1.7	13
46	Surveillance of SARS-CoV-2 in Zimbabwe shows dominance of variants of concern. <i>Lancet Microbe</i> , The, 2021, 2, e177.	3.4	13
47	The golden death bacillus <i>Chryseobacterium nematophagum</i> is a novel matrix digesting pathogen of nematodes. <i>BMC Biology</i> , 2019, 17, 10.	1.7	12
48	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.	1.6	12
49	Stability of the Encoding Plasmids and Surface Expression of CS6 Differs in Enterotoxigenic <i>Escherichia coli</i> (ETEC) Encoding Different Heat-Stable (ST) Enterotoxins (STh and STp). <i>PLoS ONE</i> , 2016, 11, e0152899.	1.1	10
50	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	5.8	10
51	SARS-CoV-2 variants of concern dominate in Lahore, Pakistan in April 2021. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
52	Invasive atypical non-typhoidal <i>Salmonella</i> serovars in The Gambia. <i>Microbial Genomics</i> , 2021, 7, .	1.0	8
53	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.	3.2	8
54	Characterising the persistence of RT-PCR positivity and incidence in a community survey of SARS-CoV-2. <i>Wellcome Open Research</i> , 0, 7, 102.	0.9	7

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55	Chemical biology-whole genome engineering datasets predict new antibacterial combinations. <i>Microbial Genomics</i> , 2021, 7, .	1.0	7
56	Genomic epidemiology of Salmonella Typhi in Central Division, Fiji, 2012 to 2016. <i>The Lancet Regional Health - Western Pacific</i> , 2022, 24, 100488.	1.3	6
57	Building Large Phylogenetic Trees on Coarse-Grained Parallel Machines. <i>Algorithmica</i> , 2006, 45, 285-300.	1.0	4
58	Scheduling in a dynamic heterogeneous distributed system using estimation error. <i>Journal of Parallel and Distributed Computing</i> , 2008, 68, 1452-1462.	2.7	4
59	GFF3toEMBL: Preparing annotated assemblies for submission to EMBL. <i>Journal of Open Source Software</i> , 2016, 1, 80.	2.0	3
60	Long-read sequencing for identification of insertion sites in large transposon mutant libraries. <i>Scientific Reports</i> , 2022, 12, 3546.	1.6	3
61	SaffronTree: Fast, reference-free pseudo-phylogenomic trees from reads or contigs.. <i>Journal of Open Source Software</i> , 2017, 2, 243.	2.0	1
62	TipToft: detecting plasmids contained in uncorrected long read sequencing data. <i>Journal of Open Source Software</i> , 2019, 4, 1021.	2.0	1