Andrew J Page

List of Publications by Year
in descending order

62 papers	**11,924** citations	159585 **30** h-index	123424 **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. Bioinformatics, 2015, 31, 3691-3693.	4.1	4,099
2	Rapid phylogenetic analysis of large samples of recombinant bacterial whole genome sequences using Gubbins. Nucleic Acids Research, 2015, 43, e15-e15.	14.5	1,834
3	SNP-sites: rapid efficient extraction of SNPs from multi-FASTA alignments. Microbial Genomics, 2016, 2, e000056.	2.0	888
4	ARIBA: rapid antimicrobial resistance genotyping directly from sequencing reads. Microbial Genomics, 2017, 3, e000131.	2.0	478
5	Emergence of an Extensively Drug-Resistant *Salmonella enterica* Serovar Typhi Clone Harboring a Promiscuous Plasmid Encoding Resistance to Fluoroquinolones and Third-Generation Cephalosporins. MBio, 2018, 9, .	4.1	434
6	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of Salmonella Typhi identifies inter- and intracontinental transmission events. Nature Genetics, 2015, 47, 632-639.	21.4	403
7	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. Cell Reports, 2021, 35, 109292.	6.4	375
8	Dense genomic sampling identifies highways of pneumococcal recombination. Nature Genetics, 2014, 46, 305-309.	21.4	371
9	Epithelial IL-22RA1-Mediated Fucosylation Promotes Intestinal Colonization Resistance to an Opportunistic Pathogen. Cell Host and Microbe, 2014, 16, 504-516.	11.0	237
10	Robust high-throughput prokaryote de novo assembly and improvement pipeline for Illumina data. Microbial Genomics, 2016, 2, e000083.	2.0	208
11	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. EBioMedicine, 2019, 43, 338-346.	6.1	168
12	The TraDIS toolkit: sequencing and analysis for dense transposon mutant libraries. Bioinformatics, 2016, 32, 1109-1111.	4.1	167
13	Microevolution of Monophasic *Salmonella* Typhimurium during Epidemic, United Kingdom, 2005–2010. Emerging Infectious Diseases, 2016, 22, 617-624.	4.3	158
14	An extended genotyping framework for Salmonella enterica serovar Typhi, the cause of human typhoid. Nature Communications, 2016, 7, 12827.	12.8	145
15	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. Science, 2021, 374, 423-431.	12.6	144
16	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. Science, 2021, 374, eabl9551.	12.6	111
17	Rapid increase in Omicron infections in England during December 2021: REACT-1 study. Science, 2022, 375, 1406-1411.	12.6	99
18	The phylogeography and incidence of multi-drug resistant typhoid fever in sub-Saharan Africa. Nature Communications, 2018, 9, 5094.	12.8	98

#	Article	IF	Citations
19	CoronaHiT: high-throughput sequencing of SARS-CoV-2 genomes. Genome Medicine, 2021, 13, 21.	8.2	94
20	Multi-heuristic dynamic task allocation using genetic algorithms in a heterogeneous distributed system. Journal of Parallel and Distributed Computing, 2010, 70, 758-766.	4.1	85
21	Multilocus sequence typing by blast from de novo assemblies against PubMLST. Journal of Open Source Software, 2016, 1, 118.	4.6	81
22	Twin peaks: The Omicron SARS-CoV-2 BA.1 and BA.2 epidemics in England. Science, 2022, 376, .	12.6	78
23	Global phylogeography and evolutionary history of Shigella dysenteriae type 1. Nature Microbiology, 2016, 1, 16027.	13.3	65
24	A Phylogenetic and Phenotypic Analysis of Salmonella enterica Serovar Weltevreden, an Emerging Agent of Diarrheal Disease in Tropical Regions. PLoS Neglected Tropical Diseases, 2016, 10, e0004446.	3.0	59
25	A global resource for genomic predictions of antimicrobial resistance and surveillance of Salmonella Typhi at pathogenwatch. Nature Communications, 2021, 12, 2879.	12.8	56
26	Framework for Task Scheduling in Heterogeneous Distributed Computing Using Genetic Algorithms. Artificial Intelligence Review, 2005, 24, 415-429.	15.7	54
27	Genomic Analysis of Salmonella enterica Serovar Typhimurium from Wild Passerines in England and Wales. Applied and Environmental Microbiology, 2016, 82, 6728-6735.	3.1	51
28	Molecular Surveillance Identifies Multiple Transmissions of Typhoid in West Africa. PLoS Neglected Tropical Diseases, 2016, 10, e0004781.	3.0	46
29	Comparison of classical multi-locus sequence typing software for next-generation sequencing data. Microbial Genomics, 2017, 3, e000124.	2.0	45
30	Using Commodity Graphics Hardware for Real-Time Digital Hologram View-Reconstruction. Journal of Display Technology, 2009, 5, 111-119.	1.2	44
31	SARS-CoV-2 infection and vaccine effectiveness in England (REACT-1): a series of cross-sectional random community surveys. Lancet Respiratory Medicine,the, 2022, 10, 355-366.	10.7	39
32	Phylogenetic Analysis of *Klebsiella pneumoniae* from Hospitalized Children, Pakistan. Emerging Infectious Diseases, 2017, 23, 1872-1875.	4.3	32
33	TraDIS-Xpress: a high-resolution whole-genome assay identifies novel mechanisms of triclosan action and resistance. Genome Research, 2020, 30, 239-249.	5.5	32
34	Large-scale sequencing of SARS-CoV-2 genomes from one region allows detailed epidemiology and enables local outbreak management. Microbial Genomics, 2021, 7, .	2.0	31
35	Staphylococcus cornubiensis sp. nov., a member of the Staphylococcus intermedius Group (SIG). International Journal of Systematic and Evolutionary Microbiology, 2018, 68, 3404-3408.	1.7	31
36	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission. Nature Communications, 2022, 13, 751.	12.8	27

#	Article	IF	Citations
37	The role of viral genomics in understanding COVID-19 outbreaks in long-term care facilities. Lancet Microbe, The, 2022, 3, e151-e158.	7.3	25
38	Rapid multi-locus sequence typing direct from uncorrected long reads using *Krocus*. PeerJ, 2018, 6, e5233.	2.0	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. The Lancet Global Health, 2021, 9, e1658-e1666.	6.3	19
40	Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package. GigaScience, 2022, 11, .	6.4	18
41	AlbaTraDIS: Comparative analysis of large datasets from parallel transposon mutagenesis experiments. PLoS Computational Biology, 2020, 16, e1007980.	3.2	17
42	Characterization of the yehUT Two-Component Regulatory System of Salmonella enterica Serovar Typhi and Typhimurium. PLoS ONE, 2013, 8, e84567.	2.5	16
43	'Candidatus Ornithobacterium hominis': insights gained from draft genomes obtained from nasopharyngeal swabs. Microbial Genomics, 2019, 5, .	2.0	16
44	A genome-wide analysis of Escherichia coli responses to fosfomycin using TraDIS-Xpress reveals novel roles for phosphonate degradation and phosphate transport systems. Journal of Antimicrobial Chemotherapy, 2020, 75, 3144-3151.	3.0	15
45	Low memory distributed reconstruction of large digital holograms. Optics Express, 2008, 16, 1990.	3.4	13
46	Surveillance of SARS-CoV-2 in Zimbabwe shows dominance of variants of concern. Lancet Microbe, The, 2021, 2, e177.	7.3	13
47	The golden death bacillus Chryseobacterium nematophagum is a novel matrix digesting pathogen of nematodes. BMC Biology, 2019, 17, 10.	3.8	12
48	Long-read-sequenced reference genomes of the seven major lineages of enterotoxigenic Escherichia coli (ETEC) circulating in modern time. Scientific Reports, 2021, 11, 9256.	3.3	12
49	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). PLoS ONE, 2016, 11, e0152899.	2.5	10
50	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. Nature Communications, 2022, 13, 1012.	12.8	10
51	SARS-CoV-2 variants of concern dominate in Lahore, Pakistan in April 2021. Microbial Genomics, 2021, 7, .	2.0	9
52	Invasive atypical non-typhoidal Salmonella serovars in The Gambia. Microbial Genomics, 2021, 7, .	2.0	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. EClinicalMedicine, 2022, 48, 101419.	7.1	8
54	Characterising the persistence of RT-PCR positivity and incidence in a community survey of SARS-CoV-2. Wellcome Open Research, 0, 7, 102.	1.8	7

#	Article	IF	Citations
55	Chemical biology-whole genome engineering datasets predict new antibacterial combinations. Microbial Genomics, 2021, 7, .	2.0	7
56	Genomic epidemiology of Salmonella Typhi in Central Division, Fiji, 2012 to 2016. The Lancet Regional Health - Western Pacific, 2022, 24, 100488.	2.9	6
57	Building Large Phylogenetic Trees on Coarse-Grained Parallel Machines. Algorithmica, 2006, 45, 285-300.	1.3	4
58	Scheduling in a dynamic heterogeneous distributed system using estimation error. Journal of Parallel and Distributed Computing, 2008, 68, 1452-1462.	4.1	4
59	GFF3toEMBL: Preparing annotated assemblies for submission to EMBL. Journal of Open Source Software, 2016, 1, 80.	4.6	3
60	Long-read sequencing for identification of insertion sites in large transposon mutant libraries. Scientific Reports, 2022, 12, 3546.	3.3	3
61	SaffronTree: Fast, reference-free pseudo-phylogenomic trees from reads or contigs.. Journal of Open Source Software, 2017, 2, 243.	4.6	1
62	TipToft: detecting plasmids contained in uncorrected long read sequencing data. Journal of Open Source Software, 2019, 4, 1021.	4.6	1