

# Andrew J Page

## List of Publications by Year in descending order

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Version: 2024-02-01

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	The role of viral genomics in understanding COVID-19 outbreaks in long-term care facilities. <i>Lancet Microbe</i> , The, 2022, 3, e151-e158.	7.3	25
2	SARS-CoV-2 infection and vaccine effectiveness in England (REACT-1): a series of cross-sectional random community surveys. <i>Lancet Respiratory Medicine</i> , the, 2022, 10, 355-366.	10.7	39
3	Rapid increase in Omicron infections in England during December 2021: REACT-1 study. <i>Science</i> , 2022, 375, 1406-1411.	12.6	99
4	Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission. <i>Nature Communications</i> , 2022, 13, 751.	12.8	27
5	Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package. <i>GigaScience</i> , 2022, 11, .	6.4	18
6	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	12.8	10
7	Long-read sequencing for identification of insertion sites in large transposon mutant libraries. <i>Scientific Reports</i> , 2022, 12, 3546.	3.3	3
8	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.	7.1	8
9	Twin peaks: The Omicron SARS-CoV-2 BA.1 and BA.2 epidemics in England. <i>Science</i> , 2022, 376, .	12.6	78
10	Genomic epidemiology of Salmonella Typhi in Central Division, Fiji, 2012 to 2016. <i>The Lancet Regional Health - Western Pacific</i> , 2022, 24, 100488.	2.9	6
11	CoronaHiT: high-throughput sequencing of SARS-CoV-2 genomes. <i>Genome Medicine</i> , 2021, 13, 21.	8.2	94
12	Long-read-sequenced reference genomes of the seven major lineages of enterotoxigenic Escherichia coli (ETEC) circulating in modern time. <i>Scientific Reports</i> , 2021, 11, 9256.	3.3	12
13	Surveillance of SARS-CoV-2 in Zimbabwe shows dominance of variants of concern. <i>Lancet Microbe</i> , The, 2021, 2, e177.	7.3	13
14	A global resource for genomic predictions of antimicrobial resistance and surveillance of Salmonella Typhi at pathogenwatch. <i>Nature Communications</i> , 2021, 12, 2879.	12.8	56
15	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, .	2.0	31
16	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.	6.4	375
17	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	12.6	144
18	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.	6.3	19

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19	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021, 374, eabl9551.	12.6	111
20	Invasive atypical non-typhoidal <i>Salmonella</i> serovars in The Gambia. <i>Microbial Genomics</i> , 2021, 7, .	2.0	8
21	SARS-CoV-2 variants of concern dominate in Lahore, Pakistan in April 2021. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
22	Chemical biology-whole genome engineering datasets predict new antibacterial combinations. <i>Microbial Genomics</i> , 2021, 7, .	2.0	7
23	AlbaTraDIS: Comparative analysis of large datasets from parallel transposon mutagenesis experiments. <i>PLoS Computational Biology</i> , 2020, 16, e1007980.	3.2	17
24	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.	3.0	15
25	TraDIS-Xpress: a high-resolution whole-genome assay identifies novel mechanisms of triclosan action and resistance. <i>Genome Research</i> , 2020, 30, 239-249.	5.5	32
26	' <i>Candidatus Ornithobacterium hominis</i> ': insights gained from draft genomes obtained from nasopharyngeal swabs. <i>Microbial Genomics</i> , 2019, 5, .	2.0	16
27	International genomic definition of pneumococcal lineages, to contextualise disease, antibiotic resistance and vaccine impact. <i>EBioMedicine</i> , 2019, 43, 338-346.	6.1	168
28	The golden death bacillus <i>Chryseobacterium nematophagum</i> is a novel matrix digesting pathogen of nematodes. <i>BMC Biology</i> , 2019, 17, 10.	3.8	12
29	TipToft: detecting plasmids contained in uncorrected long read sequencing data. <i>Journal of Open Source Software</i> , 2019, 4, 1021.	4.6	1
30	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, .	4.1	434
31	The phylogeography and incidence of multi-drug resistant typhoid fever in sub-Saharan Africa. <i>Nature Communications</i> , 2018, 9, 5094.	12.8	98
32	<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.	1.7	31
33	Rapid multi-locus sequence typing direct from uncorrected long reads using <i>Krocus</i> . <i>PeerJ</i> , 2018, 6, e5233.	2.0	19
34	Phylogenetic Analysis of <i>Klebsiella pneumoniae</i> from Hospitalized Children, Pakistan. <i>Emerging Infectious Diseases</i> , 2017, 23, 1872-1875.	4.3	32
35	ARIBA: rapid antimicrobial resistance genotyping directly from sequencing reads. <i>Microbial Genomics</i> , 2017, 3, e000131.	2.0	478
36	Comparison of classical multi-locus sequence typing software for next-generation sequencing data. <i>Microbial Genomics</i> , 2017, 3, e000124.	2.0	45

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37	SaffronTree: Fast, reference-free pseudo-phylogenomic trees from reads or contigs.. Journal of Open Source Software, 2017, 2, 243.	4.6	1
38	Microevolution of Monophasic <i>Salmonella</i> Typhimurium during Epidemic, United Kingdom, 2005–2010. Emerging Infectious Diseases, 2016, 22, 617-624.	4.3	158
39	SNP-sites: rapid efficient extraction of SNPs from multi-FASTA alignments. Microbial Genomics, 2016, 2, e000056.	2.0	888
40	Molecular Surveillance Identifies Multiple Transmissions of Typhoid in West Africa. PLoS Neglected Tropical Diseases, 2016, 10, e0004781.	3.0	46
41	Genomic Analysis of <i>Salmonella enterica</i> Serovar Typhimurium from Wild Passerines in England and Wales. Applied and Environmental Microbiology, 2016, 82, 6728-6735.	3.1	51
42	Global phylogeography and evolutionary history of <i>Shigella dysenteriae</i> type 1. Nature Microbiology, 2016, 1, 16027.	13.3	65
43	An extended genotyping framework for <i>Salmonella enterica</i> serovar Typhi, the cause of human typhoid. Nature Communications, 2016, 7, 12827.	12.8	145
44	The TraDIS toolkit: sequencing and analysis for dense transposon mutant libraries. Bioinformatics, 2016, 32, 1109-1111.	4.1	167
45	Robust high-throughput prokaryote de novo assembly and improvement pipeline for Illumina data. Microbial Genomics, 2016, 2, e000083.	2.0	208
46	A Phylogenetic and Phenotypic Analysis of <i>Salmonella enterica</i> Serovar Weltevreden, an Emerging Agent of Diarrheal Disease in Tropical Regions. PLoS Neglected Tropical Diseases, 2016, 10, e0004446.	3.0	59
47	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). PLoS ONE, 2016, 11, e0152899.	2.5	10
48	GFF3toEMBL: Preparing annotated assemblies for submission to EMBL. Journal of Open Source Software, 2016, 1, 80.	4.6	3
49	Multilocus sequence typing by blast from de novo assemblies against PubMLST. Journal of Open Source Software, 2016, 1, 118.	4.6	81
50	Roary: rapid large-scale prokaryote pan genome analysis. Bioinformatics, 2015, 31, 3691-3693.	4.1	4,099
51	Phylogeographical analysis of the dominant multidrug-resistant H58 clade of <i>Salmonella</i> Typhi identifies inter- and intracontinental transmission events. Nature Genetics, 2015, 47, 632-639.	21.4	403
52	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
53	Epithelial IL-22RA1-Mediated Fucosylation Promotes Intestinal Colonization Resistance to an Opportunistic Pathogen. Cell Host and Microbe, 2014, 16, 504-516.	11.0	237
54	Dense genomic sampling identifies highways of pneumococcal recombination. Nature Genetics, 2014, 46, 305-309.	21.4	371

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55	Characterization of the yehUT Two-Component Regulatory System of Salmonella enterica Serovar Typhi and Typhimurium. PLoS ONE, 2013, 8, e84567.	2.5	16
56	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
57	Using Commodity Graphics Hardware for Real-Time Digital Hologram View-Reconstruction. Journal of Display Technology, 2009, 5, 111-119.	1.2	44
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	Low memory distributed reconstruction of large digital holograms. Optics Express, 2008, 16, 1990.	3.4	13
60	Building Large Phylogenetic Trees on Coarse-Grained Parallel Machines. Algorithmica, 2006, 45, 285-300.	1.3	4
61	Framework for Task Scheduling in Heterogeneous Distributed Computing Using Genetic Algorithms. Artificial Intelligence Review, 2005, 24, 415-429.	15.7	54
62	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