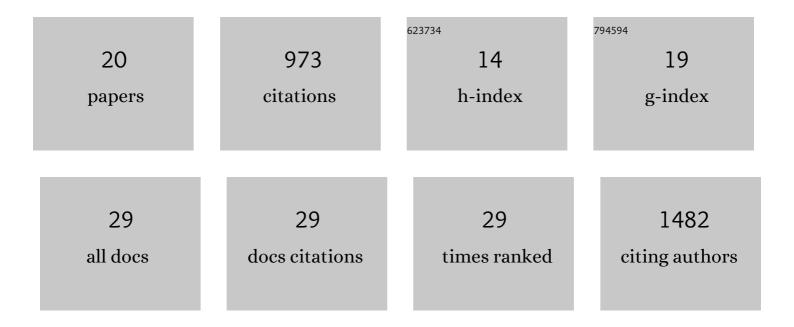
Nicole E Wheeler

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9383604/publications.pdf Version: 2024-02-01



NICOLE E WHEELED

#	Article	IF	CITATIONS
1	Convergent regulatory evolution and loss of flight in paleognathous birds. Science, 2019, 364, 74-78.	12.6	189
2	Joint sequencing of human and pathogen genomes reveals the genetics of pneumococcal meningitis. Nature Communications, 2019, 10, 2176.	12.8	83
3	An African Salmonella Typhimurium ST313 sublineage with extensive drug-resistance and signatures of host adaptation. Nature Communications, 2019, 10, 4280.	12.8	80
4	Machine learning identifies signatures of host adaptation in the bacterial pathogen Salmonella enterica. PLoS Genetics, 2018, 14, e1007333.	3.5	73
5	Improved Prediction of Bacterial Genotype-Phenotype Associations Using Interpretable Pangenome-Spanning Regressions. MBio, 2020, 11, .	4.1	66
6	Evaluation of parameters affecting performance and reliability of machine learning-based antibiotic susceptibility testing from whole genome sequencing data. PLoS Computational Biology, 2019, 15, e1007349.	3.2	64
7	Whole-genome sequencing as part of national and international surveillance programmes for antimicrobial resistance: a roadmap. BMJ Global Health, 2020, 5, e002244.	4.7	60
8	Adaptation to the cervical environment is associated with increased antibiotic susceptibility in Neisseria gonorrhoeae. Nature Communications, 2020, 11, 4126.	12.8	51
9	Robust Identification of Noncoding RNA from Transcriptomes Requires Phylogenetically-Informed Sampling. PLoS Computational Biology, 2014, 10, e1003907.	3.2	49
10	Evolution of Salmonella enterica serotype Typhimurium driven by anthropogenic selection and niche adaptation. PLoS Genetics, 2020, 16, e1008850.	3.5	48
11	Increased power from conditional bacterial genome-wide association identifies macrolide resistance mutations in Neisseria gonorrhoeae. Nature Communications, 2020, 11, 5374.	12.8	40
12	Tracing outbreaks with machine learning. Nature Reviews Microbiology, 2019, 17, 269-269.	28.6	28
13	Why so narrow: Distribution of anti-sense regulated, type I toxin-antitoxin systems compared with type II and type III systems. RNA Biology, 2017, 14, 275-280.	3.1	27
14	A profile-based method for identifying functional divergence of orthologous genes in bacterial genomes. Bioinformatics, 2016, 32, 3566-3574.	4.1	25
15	Breaking the code of antibiotic resistance. Nature Reviews Microbiology, 2018, 16, 262-262.	28.6	11
16	Genomic correlates of extraintestinal infection are linked with changes in cell morphology in Campylobacter jejuni. Microbial Genomics, 2019, 5, .	2.0	6
17	Genomic, Transcriptomic, and Phenotypic Analyses of Neisseria meningitidis Isolates from Disease Patients and Their Household Contacts. MSystems, 2017, 2, .	3.8	3
18	We are falling behind on TB elimination targets: can whole-genome sequencing guide our efforts?. Thorax, 2019, 74, 833-834.	5.6	1

#	Article	IF	CITATIONS
19	Lean, mean, learning machines. Nature Reviews Microbiology, 2020, 18, 266-266.	28.6	1
20	Computer says …. Significance, 2020, 17, 34-37.	0.4	0