

# Nicole E Wheeler

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9383604/publications.pdf>

Version: 2024-02-01

20  
papers

973  
citations

623734

14  
h-index

794594

19  
g-index

29  
all docs

29  
docs citations

29  
times ranked

1482  
citing authors

#	ARTICLE	IF	CITATIONS
1	Convergent regulatory evolution and loss of flight in paleognathous birds. <i>Science</i> , 2019, 364, 74-78.	12.6	189
2	Joint sequencing of human and pathogen genomes reveals the genetics of pneumococcal meningitis. <i>Nature Communications</i> , 2019, 10, 2176.	12.8	83
3	An African <i>Salmonella</i> Typhimurium ST313 sublineage with extensive drug-resistance and signatures of host adaptation. <i>Nature Communications</i> , 2019, 10, 4280.	12.8	80
4	Machine learning identifies signatures of host adaptation in the bacterial pathogen <i>Salmonella enterica</i> . <i>PLoS Genetics</i> , 2018, 14, e1007333.	3.5	73
5	Improved Prediction of Bacterial Genotype-Phenotype Associations Using Interpretable Pangenome-Spanning Regressions. <i>MBio</i> , 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. <i>PLoS Computational Biology</i> , 2019, 15, e1007349.	3.2	64
7	Whole-genome sequencing as part of national and international surveillance programmes for antimicrobial resistance: a roadmap. <i>BMJ Global Health</i> , 2020, 5, e002244.	4.7	60
8	Adaptation to the cervical environment is associated with increased antibiotic susceptibility in <i>Neisseria gonorrhoeae</i> . <i>Nature Communications</i> , 2020, 11, 4126.	12.8	51
9	Robust Identification of Noncoding RNA from Transcriptomes Requires Phylogenetically-Informed Sampling. <i>PLoS Computational Biology</i> , 2014, 10, e1003907.	3.2	49
10	Evolution of <i>Salmonella enterica</i> serotype Typhimurium driven by anthropogenic selection and niche adaptation. <i>PLoS Genetics</i> , 2020, 16, e1008850.	3.5	48
11	Increased power from conditional bacterial genome-wide association identifies macrolide resistance mutations in <i>Neisseria gonorrhoeae</i> . <i>Nature Communications</i> , 2020, 11, 5374.	12.8	40
12	Tracing outbreaks with machine learning. <i>Nature Reviews Microbiology</i> , 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. <i>RNA Biology</i> , 2017, 14, 275-280.	3.1	27
14	A profile-based method for identifying functional divergence of orthologous genes in bacterial genomes. <i>Bioinformatics</i> , 2016, 32, 3566-3574.	4.1	25
15	Breaking the code of antibiotic resistance. <i>Nature Reviews Microbiology</i> , 2018, 16, 262-262.	28.6	11
16	Genomic correlates of extraintestinal infection are linked with changes in cell morphology in <i>Campylobacter jejuni</i> . <i>Microbial Genomics</i> , 2019, 5, .	2.0	6
17	Genomic, Transcriptomic, and Phenotypic Analyses of <i>Neisseria meningitidis</i> Isolates from Disease Patients and Their Household Contacts. <i>MSystems</i> , 2017, 2, .	3.8	3
18	We are falling behind on TB elimination targets: can whole-genome sequencing guide our efforts?. <i>Thorax</i> , 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 â€¦. Significance, 2020, 17, 34-37.	0.4	0