# Nicole E Wheeler

List of Publications by Year
in descending order

| 20 papers | 973 citations | 14 h-index | 19 g-index |
|---|---|---|---|
| | | 623734 | 794594 |
| 29 all docs | 29 docs citations | 29 times ranked | 1482 citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Increased power from conditional bacterial genome-wide association identifies macrolide resistance mutations in Neisseria gonorrhoeae. Nature Communications, 2020, 11, 5374. | 12.8 | 40 |
| 2 | Adaptation to the cervical environment is associated with increased antibiotic susceptibility in Neisseria gonorrhoeae. Nature Communications, 2020, 11, 4126. | 12.8 | 51 |
| 3 | 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 |
| 4 | Computer says â€¦. Significance, 2020, 17, 34-37. | 0.4 | 0 |
| 5 | Evolution of Salmonella enterica serotype Typhimurium driven by anthropogenic selection and niche adaptation. PLoS Genetics, 2020, 16, e1008850. | 3.5 | 48 |
| 6 | Lean, mean, learning machines. Nature Reviews Microbiology, 2020, 18, 266-266. | 28.6 | 1 |
| 7 | Improved Prediction of Bacterial Genotype-Phenotype Associations Using Interpretable Pangenome-Spanning Regressions. MBio, 2020, 11, . | 4.1 | 66 |
| 8 | 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 |
| 9 | An African Salmonella Typhimurium ST313 sublineage with extensive drug-resistance and signatures of host adaptation. Nature Communications, 2019, 10, 4280. | 12.8 | 80 |
| 10 | Joint sequencing of human and pathogen genomes reveals the genetics of pneumococcal meningitis. Nature Communications, 2019, 10, 2176. | 12.8 | 83 |
| 11 | Convergent regulatory evolution and loss of flight in paleognathous birds. Science, 2019, 364, 74-78. | 12.6 | 189 |
| 12 | Tracing outbreaks with machine learning. Nature Reviews Microbiology, 2019, 17, 269-269. | 28.6 | 28 |
| 13 | We are falling behind on TB elimination targets: can whole-genome sequencing guide our efforts?. Thorax, 2019, 74, 833-834. | 5.6 | 1 |
| 14 | Genomic correlates of extraintestinal infection are linked with changes in cell morphology in Campylobacter jejuni. Microbial Genomics, 2019, 5, . | 2.0 | 6 |
| 15 | Breaking the code of antibiotic resistance. Nature Reviews Microbiology, 2018, 16, 262-262. | 28.6 | 11 |
| 16 | Machine learning identifies signatures of host adaptation in the bacterial pathogen Salmonella enterica. PLoS Genetics, 2018, 14, e1007333. | 3.5 | 73 |
| 17 | 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 |
| 18 | Genomic, Transcriptomic, and Phenotypic Analyses of Neisseria meningitidis Isolates from Disease Patients and Their Household Contacts. MSystems, 2017, 2, . | 3.8 | 3 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 19 | A profile-based method for identifying functional divergence of orthologous genes in bacterial genomes. Bioinformatics, 2016, 32, 3566-3574. | 4.1 | 25 |
| 20 | Robust Identification of Noncoding RNA from Transcriptomes Requires Phylogenetically-Informed Sampling. PLoS Computational Biology, 2014, 10, e1003907. | 3.2 | 49 |