

Zamin Iqbal

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

8,254
citations

147726

31
h-index

189801

50
g-index

79
all docs

79
docs citations

79
times ranked

14295
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011, 470, 59-65. | 13.7 | 991 |
| 2 | Integrating mapping-, assembly- and haplotype-based approaches for calling variants in clinical sequencing applications. <i>Nature Genetics</i> , 2014, 46, 912-918. | 9.4 | 937 |
| 3 | De novo assembly and genotyping of variants using colored de Bruijn graphs. <i>Nature Genetics</i> , 2012, 44, 226-232. | 9.4 | 564 |
| 4 | Whole-genome sequencing for prediction of <i>Mycobacterium tuberculosis</i> drug susceptibility and resistance: a retrospective cohort study. <i>Lancet Infectious Diseases</i> , The, 2015, 15, 1193-1202. | 4.6 | 553 |
| 5 | Rapid antibiotic-resistance predictions from genome sequence data for <i>Staphylococcus aureus</i> and <i>Mycobacterium tuberculosis</i> . <i>Nature Communications</i> , 2015, 6, 10063. | 5.8 | 479 |
| 6 | The global distribution and spread of the mobilized colistin resistance gene <i>mcr-1</i> . <i>Nature Communications</i> , 2018, 9, 1179. | 5.8 | 464 |
| 7 | Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. <i>New England Journal of Medicine</i> , 2018, 379, 1403-1415. | 13.9 | 405 |
| 8 | A reference data set of 5.4 million phased human variants validated by genetic inheritance from sequencing a three-generation 17-member pedigree. <i>Genome Research</i> , 2017, 27, 157-164. | 2.4 | 338 |
| 9 | Same-Day Diagnostic and Surveillance Data for Tuberculosis via Whole-Genome Sequencing of Direct Respiratory Samples. <i>Journal of Clinical Microbiology</i> , 2017, 55, 1285-1298. | 1.8 | 315 |
| 10 | A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. <i>Science</i> , 2012, 336, 193-198. | 6.0 | 273 |
| 11 | Identifying lineage effects when controlling for population structure improves power in bacterial association studies. <i>Nature Microbiology</i> , 2016, 1, 16041. | 5.9 | 247 |
| 12 | Evolutionary dynamics of <i>Staphylococcus aureus</i> during progression from carriage to disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4550-4555. | 3.3 | 244 |
| 13 | Improved genome inference in the MHC using a population reference graph. <i>Nature Genetics</i> , 2015, 47, 682-688. | 9.4 | 197 |
| 14 | Indels, structural variation, and recombination drive genomic diversity in <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2016, 26, 1288-1299. | 2.4 | 180 |
| 15 | The genomic and phenotypic diversity of <i>Schizosaccharomyces pombe</i> . <i>Nature Genetics</i> , 2015, 47, 235-241. | 9.4 | 174 |
| 16 | Rapid Whole-Genome Sequencing for Surveillance of <i>Salmonella enterica</i> Serovar Enteritidis. <i>Emerging Infectious Diseases</i> , 2014, 20, 1306-1314. | 2.0 | 155 |
| 17 | Ultrafast search of all deposited bacterial and viral genomic data. <i>Nature Biotechnology</i> , 2019, 37, 152-159. | 9.4 | 123 |
| 18 | The 2021 WHO catalogue of <i>Mycobacterium tuberculosis</i> complex mutations associated with drug resistance: a genotypic analysis. <i>Lancet Microbe</i> , The, 2022, 3, e265-e273. | 3.4 | 114 |

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|----|--|-----|-----------|
| 19 | Antibiotic resistance prediction for Mycobacterium tuberculosis from genome sequence data with Mykrobe. Wellcome Open Research, 2019, 4, 191. | 0.9 | 103 |
| 20 | Severe infections emerge from commensal bacteria by adaptive evolution. ELife, 2017, 6, . | 2.8 | 93 |
| 21 | High-Accuracy HLA Type Inference from Whole-Genome Sequencing Data Using Population Reference Graphs. PLoS Computational Biology, 2016, 12, e1005151. | 1.5 | 87 |
| 22 | Resolving plasmid structures in Enterobacteriaceae using the MinION nanopore sequencer: assessment of MinION and MinION/Illumina hybrid data assembly approaches. Microbial Genomics, 2017, 3, e000118. | 1.0 | 74 |
| 23 | Evaluation of Whole-Genome Sequencing for Mycobacterial Species Identification and Drug Susceptibility Testing in a Clinical Setting: a Large-Scale Prospective Assessment of Performance against Line Probe Assays and Phenotyping. Journal of Clinical Microbiology, 2018, 56, . | 1.8 | 72 |
| 24 | Contributions of intrinsic mutation rate and selfish selection to levels of de novo <i>HRAS</i> mutations in the paternal germline. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20152-20157. | 3.3 | 70 |
| 25 | Global population structure and genotyping framework for genomic surveillance of the major dysentery pathogen, <i>Shigella sonnei</i> . Nature Communications, 2021, 12, 2684. | 5.8 | 65 |
| 26 | SNP-IT Tool for Identifying Subspecies and Associated Lineages of <i>Mycobacterium tuberculosis</i> Complex. Emerging Infectious Diseases, 2019, 25, 482-488. | 2.0 | 64 |
| 27 | Integrating long-range connectivity information into de Bruijn graphs. Bioinformatics, 2018, 34, 2556-2565. | 1.8 | 61 |
| 28 | Accuracy of Different Bioinformatics Methods in Detecting Antibiotic Resistance and Virulence Factors from <i>Staphylococcus aureus</i> Whole-Genome Sequences. Journal of Clinical Microbiology, 2018, 56, . | 1.8 | 61 |
| 29 | Exploring bacterial diversity via a curated and searchable snapshot of archived DNA sequences. PLoS Biology, 2021, 19, e3001421. | 2.6 | 60 |
| 30 | Reference-free SNP discovery for the Eurasian beaver from restriction site-associated DNA paired-end data. Molecular Ecology, 2013, 22, 3141-3150. | 2.0 | 40 |
| 31 | DNA extraction from primary liquid blood cultures for bloodstream infection diagnosis using whole genome sequencing. Journal of Medical Microbiology, 2018, 67, 347-357. | 0.7 | 40 |
| 32 | REINDEER: efficient indexing of <i>k</i> -mer presence and abundance in sequencing datasets. Bioinformatics, 2020, 36, i177-i185. | 1.8 | 40 |
| 33 | COBS: A Compact Bit-Sliced Signature Index. Lecture Notes in Computer Science, 2019, , 285-303. | 1.0 | 39 |
| 34 | DeepAMR for predicting co-occurrent resistance of <i>Mycobacterium tuberculosis</i> . Bioinformatics, 2019, 35, 3240-3249. | 1.8 | 38 |
| 35 | High-throughput microbial population genomics using the Cortex variation assembler. Bioinformatics, 2013, 29, 275-276. | 1.8 | 37 |
| 36 | Assessing evolutionary risks of resistance for new antimicrobial therapies. Nature Ecology and Evolution, 2019, 3, 515-517. | 3.4 | 37 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 37 | A Natural Encoding of Genetic Variation in a Burrows-Wheeler Transform to Enable Mapping and Genome Inference. <i>Lecture Notes in Computer Science</i> , 2016, , 222-233. | 1.0 | 35 |
| 38 | Binding of Plasmodium falciparum Merozoite Surface Proteins DBLMSP and DBLMSP2 to Human Immunoglobulin M Is Conserved among Broadly Diverged Sequence Variants. <i>Journal of Biological Chemistry</i> , 2016, 291, 14285-14299. | 1.6 | 27 |
| 39 | GenTB: A user-friendly genome-based predictor for tuberculosis resistance powered by machine learning. <i>Genome Medicine</i> , 2021, 13, 138. | 3.6 | 27 |
| 40 | Pandora: nucleotide-resolution bacterial pan-genomics with reference graphs. <i>Genome Biology</i> , 2021, 22, 267. | 3.8 | 26 |
| 41 | Identifying and Classifying Trait Linked Polymorphisms in Non-Reference Species by Walking Coloured de Bruijn Graphs. <i>PLoS ONE</i> , 2013, 8, e60058. | 1.1 | 26 |
| 42 | A Bayesian Approach to Inferring the Phylogenetic Structure of Communities from Metagenomic Data. <i>Genetics</i> , 2014, 197, 925-937. | 1.2 | 20 |
| 43 | Inferring Strain Mixture within Clinical Plasmodium falciparum Isolates from Genomic Sequence Data. <i>PLoS Computational Biology</i> , 2016, 12, e1004824. | 1.5 | 19 |
| 44 | Using reference-free compressed data structures to analyze sequencing reads from thousands of human genomes. <i>Genome Research</i> , 2017, 27, 300-309. | 2.4 | 19 |
| 45 | Gramtools enables multiscale variation analysis with genome graphs. <i>Genome Biology</i> , 2021, 22, 259. | 3.8 | 15 |
| 46 | Minos: variant adjudication and joint genotyping of cohorts of bacterial genomes. <i>Genome Biology</i> , 2022, 23, . | 3.8 | 11 |
| 47 | Detection of simple and complex de novo mutations with multiple reference sequences. <i>Genome Research</i> , 2020, 30, 1154-1169. | 2.4 | 7 |
| 48 | Drug-Resistant Tuberculosis in Pet Ring-Tailed Lemur, Madagascar. <i>Emerging Infectious Diseases</i> , 2021, 27, 977-979. | 2.0 | 7 |
| 49 | ReadItAndKeep: rapid decontamination of SARS-CoV-2 sequencing reads. <i>Bioinformatics</i> , 2022, 38, 3291-3293. | 1.8 | 5 |
| 50 | Towards Point-of-Care Diagnosis of Pulmonary Tuberculosis and Drug Susceptibility Testing by Whole Genome Sequencing of DNA Isolated from Sputum. <i>Canadian Journal of Biotechnology</i> , 2017, 1, 267-267. | 0.3 | 0 |