Zamin Iqbal

List of Publications by Year
in descending order

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	The 2021 WHO catalogue of Mycobacterium tuberculosis complex mutations associated with drug resistance: a genotypic analysis. Lancet Microbe, The, 2022, 3, e265-e273.	3.4	114
2	ReadItAndKeep: rapid decontamination of SARS-CoV-2 sequencing reads. Bioinformatics, 2022, 38, 3291-3293.	1.8	5
3	Minos: variant adjudication and joint genotyping of cohorts of bacterial genomes. Genome Biology, 2022, 23, .	3.8	11
4	Drug-Resistant Tuberculosis in Pet Ring-Tailed Lemur, Madagascar. Emerging Infectious Diseases, 2021, 27, 977-979.	2.0	7
5	Global population structure and genotyping framework for genomic surveillance of the major dysentery pathogen, Shigella sonnei. Nature Communications, 2021, 12, 2684.	5.8	65
6	GenTB: A user-friendly genome-based predictor for tuberculosis resistance powered by machine learning. Genome Medicine, 2021, 13, 138.	3.6	27
7	Pandora: nucleotide-resolution bacterial pan-genomics with reference graphs. Genome Biology, 2021, 22, 267.	3.8	26
8	Gramtools enables multiscale variation analysis with genome graphs. Genome Biology, 2021, 22, 259.	3.8	15
9	Exploring bacterial diversity via a curated and searchable snapshot of archived DNA sequences. PLoS Biology, 2021, 19, e3001421.	2.6	60
10	Detection of simple and complex de novo mutations with multiple reference sequences. Genome Research, 2020, 30, 1154-1169.	2.4	7
11	REINDEER: efficient indexing of k-mer presence and abundance in sequencing datasets. Bioinformatics, 2020, 36, i177-i185.	1.8	40
12	DeepAMR for predicting co-occurrent resistance of *Mycobacterium tuberculosis*. Bioinformatics, 2019, 35, 3240-3249.	1.8	38
13	Assessing evolutionary risks of resistance for new antimicrobial therapies. Nature Ecology and Evolution, 2019, 3, 515-517.	3.4	37
14	SNP-IT Tool for Identifying Subspecies and Associated Lineages of *Mycobacterium tuberculosis* Complex. Emerging Infectious Diseases, 2019, 25, 482-488.	2.0	64
15	COBS: A Compact Bit-Sliced Signature Index. Lecture Notes in Computer Science, 2019, , 285-303.	1.0	39
16	Ultrafast search of all deposited bacterial and viral genomic data. Nature Biotechnology, 2019, 37, 152-159.	9.4	123
17	Antibiotic resistance prediction for Mycobacterium tuberculosis from genome sequence data with Mykrobe. Wellcome Open Research, 2019, 4, 191.	0.9	103
18	The global distribution and spread of the mobilized colistin resistance gene mcr-1. Nature Communications, 2018, 9, 1179.	5.8	464

#	Article	IF	Citations
19	Integrating long-range connectivity information into de Bruijn graphs. Bioinformatics, 2018, 34, 2556-2565.	1.8	61
20	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
21	Prediction of Susceptibility to First-Line Tuberculosis Drugs by DNA Sequencing. New England Journal of Medicine, 2018, 379, 1403-1415.	13.9	405
22	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
23	Accuracy of Different Bioinformatics Methods in Detecting Antibiotic Resistance and Virulence Factors from Staphylococcus aureus Whole-Genome Sequences. Journal of Clinical Microbiology, 2018, 56, .	1.8	61
24	Same-Day Diagnostic and Surveillance Data for Tuberculosis via Whole-Genome Sequencing of Direct Respiratory Samples. Journal of Clinical Microbiology, 2017, 55, 1285-1298.	1.8	315
25	A reference data set of 5.4 million phased human variants validated by genetic inheritance from sequencing a three-generation 17-member pedigree. Genome Research, 2017, 27, 157-164.	2.4	338
26	Using reference-free compressed data structures to analyze sequencing reads from thousands of human genomes. Genome Research, 2017, 27, 300-309.	2.4	19
27	Severe infections emerge from commensal bacteria by adaptive evolution. ELife, 2017, 6, .	2.8	93
28	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
29	Towards Point-of-Care Diagnosis of Pulmonary Tuberculosis and Drug Susceptibility Testing by Whole Genome Sequencing of DNA Isolated from Sputum. Canadian Journal of Biotechnology, 2017, 1, 267-267.	0.3	0
30	Inferring Strain Mixture within Clinical Plasmodium falciparum Isolates from Genomic Sequence Data. PLoS Computational Biology, 2016, 12, e1004824.	1.5	19
31	Indels, structural variation, and recombination drive genomic diversity in <i>Plasmodium falciparum</i>. Genome Research, 2016, 26, 1288-1299.	2.4	180
32	A Natural Encoding of Genetic Variation in a Burrows-Wheeler Transform to Enable Mapping and Genome Inference. Lecture Notes in Computer Science, 2016, , 222-233.	1.0	35
33	Identifying lineage effects when controlling for population structure improves power in bacterial association studies. Nature Microbiology, 2016, 1, 16041.	5.9	247
34	Binding of Plasmodium falciparum Merozoite Surface Proteins DBLMSP and DBLMSP2 to Human Immunoglobulin M Is Conserved among Broadly Diverged Sequence Variants. Journal of Biological Chemistry, 2016, 291, 14285-14299.	1.6	27
35	High-Accuracy HLA Type Inference from Whole-Genome Sequencing Data Using Population Reference Graphs. PLoS Computational Biology, 2016, 12, e1005151.	1.5	87
36	Rapid antibiotic-resistance predictions from genome sequence data for Staphylococcus aureus and Mycobacterium tuberculosis. Nature Communications, 2015, 6, 10063.	5.8	479

#	Article	IF	Citations
37	The genomic and phenotypic diversity of Schizosaccharomyces pombe. Nature Genetics, 2015, 47, 235-241.	9.4	174
38	Whole-genome sequencing for prediction of Mycobacterium tuberculosis drug susceptibility and resistance: a retrospective cohort study. Lancet Infectious Diseases, The, 2015, 15, 1193-1202.	4.6	553
39	Improved genome inference in the MHC using a population reference graph. Nature Genetics, 2015, 47, 682-688.	9.4	197
40	A Bayesian Approach to Inferring the Phylogenetic Structure of Communities from Metagenomic Data. Genetics, 2014, 197, 925-937.	1.2	20
41	Rapid Whole-Genome Sequencing for Surveillance of <i>Salmonella enterica</i> Serovar Enteritidis. Emerging Infectious Diseases, 2014, 20, 1306-1314.	2.0	155
42	Integrating mapping-, assembly- and haplotype-based approaches for calling variants in clinical sequencing applications. Nature Genetics, 2014, 46, 912-918.	9.4	937
43	Referenceâ€free <scp>SNP</scp> discovery for the <scp>E</scp>urasian beaver from restriction siteâ€"associated <scp>DNA</scp> pairedâ€end data. Molecular Ecology, 2013, 22, 3141-3150.	2.0	40
44	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
45	High-throughput microbial population genomics using the Cortex variation assembler. Bioinformatics, 2013, 29, 275-276.	1.8	37
46	Identifying and Classifying Trait Linked Polymorphisms in Non-Reference Species by Walking Coloured de Bruijn Graphs. PLoS ONE, 2013, 8, e60058.	1.1	26
47	Evolutionary dynamics of <i>Staphylococcus aureus</i> during progression from carriage to disease. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4550-4555.	3.3	244
48	A Fine-Scale Chimpanzee Genetic Map from Population Sequencing. Science, 2012, 336, 193-198.	6.0	273
49	De novo assembly and genotyping of variants using colored de Bruijn graphs. Nature Genetics, 2012, 44, 226-232.	9.4	564
50	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	13.7	991