

Nabil-Fareed Alikhan

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

5,618
citations

304368

22
h-index

454577

30
g-index

63
all docs

63
docs citations

63
times ranked

7825
citing authors

#	ARTICLE	IF	CITATIONS
1	Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package. <i>GigaScience</i> , 2022, 11, .	3.3	18
2	Dynamics of <i>Salmonella enterica</i> and antimicrobial resistance in the Brazilian poultry industry and global impacts on public health. <i>PLoS Genetics</i> , 2022, 18, e1010174.	1.5	13
3	CoronaHiT: high-throughput sequencing of SARS-CoV-2 genomes. <i>Genome Medicine</i> , 2021, 13, 21.	3.6	94
4	Extensive microbial diversity within the chicken gut microbiome revealed by metagenomics and culture. <i>PeerJ</i> , 2021, 9, e10941.	0.9	79
5	Large-scale sequencing of SARS-CoV-2 genomes from one region allows detailed epidemiology and enables local outbreak management. <i>Microbial Genomics</i> , 2021, 7, .	1.0	31
6	Genomic diversity of <i>Escherichia coli</i> from healthy children in rural Gambia. <i>PeerJ</i> , 2021, 9, e10572.	0.9	9
7	Genomic diversity of <i>Escherichia coli</i> isolates from backyard chickens and guinea fowl in the Gambia. <i>Microbial Genomics</i> , 2021, 7, .	1.0	13
8	The impact of viral mutations on recognition by SARS-CoV-2 specific T cells. <i>iScience</i> , 2021, 24, 103353.	1.9	57
9	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021, 374, eabl9551.	6.0	111
10	Invasive atypical non-typhoidal <i>Salmonella</i> serovars in The Gambia. <i>Microbial Genomics</i> , 2021, 7, .	1.0	8
11	SARS-CoV-2 variants of concern dominate in Lahore, Pakistan in April 2021. <i>Microbial Genomics</i> , 2021, 7, .	1.0	9
12	The Enterobase user's guide, with case studies on <i>Salmonella</i> transmissions, <i>Yersinia pestis</i> phylogeny, and <i>Escherichia coli</i> core genomic diversity. <i>Genome Research</i> , 2020, 30, 138-152.	2.4	577
13	Emergence of Resistance to Fluoroquinolones and Third-Generation Cephalosporins in <i>Salmonella</i> Typhi in Lahore, Pakistan. <i>Microorganisms</i> , 2020, 8, 1336.	1.6	35
14	Evolution of <i>Salmonella enterica</i> serotype Typhimurium driven by anthropogenic selection and niche adaptation. <i>PLoS Genetics</i> , 2020, 16, e1008850.	1.5	48
15	Emergence of human-adapted <i>Salmonella enterica</i> is linked to the Neolithization process. <i>Nature Ecology and Evolution</i> , 2020, 4, 324-333.	3.4	72
16	Genomic diversity of <i>Salmonella enterica</i> -The UoWUCC 10K genomes project. <i>Wellcome Open Research</i> , 2020, 5, 223.	0.9	43
17	ICTV Virus Taxonomy Profile: Herelleviridae. <i>Journal of General Virology</i> , 2020, 101, 362-363.	1.3	37
18	Genomic diversity of <i>Escherichia coli</i> isolates from non-human primates in the Gambia. <i>Microbial Genomics</i> , 2020, 6, .	1.0	12

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19	Genomic diversity of <i>Salmonella enterica</i> -The UoWUCC 10K genomes project. Wellcome Open Research, 2020, 5, 223.	0.9	38
20	Genome-wide Identification and Characterization of a Superfamily of Bacterial Extracellular Contractile Injection Systems. Cell Reports, 2019, 29, 511-521.e2.	2.9	44
21	Comparative analysis of core genome MLST and SNP typing within a European <i>Salmonella</i> serovar Enteritidis outbreak. International Journal of Food Microbiology, 2018, 274, 1-11.	2.1	150
22	Accurate Reconstruction of Microbial Strains from Metagenomic Sequencing Using Representative Reference Genomes. Lecture Notes in Computer Science, 2018, , 225-240.	1.0	16
23	Principles of Systems Biology, No. 31. Cell Systems, 2018, 7, 133-135.	2.9	0
24	GrapeTree: visualization of core genomic relationships among 100,000 bacterial pathogens. Genome Research, 2018, 28, 1395-1404.	2.4	553
25	Pan-genome Analysis of Ancient and Modern <i>Salmonella enterica</i> Demonstrates Genomic Stability of the Invasive Para C Lineage for Millennia. Current Biology, 2018, 28, 2420-2428.e10.	1.8	65
26	A genomic overview of the population structure of <i>Salmonella</i> . PLoS Genetics, 2018, 14, e1007261.	1.5	476
27	Comparison of classical multi-locus sequence typing software for next-generation sequencing data. Microbial Genomics, 2017, 3, e000124.	1.0	45
28	Mechanisms Involved in Acquisition of <i>bla</i> _{NDM} Genes by IncA/C ₂ and IncFII _Y Plasmids. Antimicrobial Agents and Chemotherapy, 2016, 60, 4082-4088.	1.4	49
29	Molecular Analysis of Asymptomatic Bacteriuria <i>Escherichia coli</i> Strain VR50 Reveals Adaptation to the Urinary Tract by Gene Acquisition. Infection and Immunity, 2015, 83, 1749-1764.	1.0	24
30	BLAST Ring Image Generator (BRIG): simple prokaryote genome comparisons. BMC Genomics, 2011, 12, 402.	1.2	2,691
31	Genome Sequence of the Emerging Pathogen <i>Aeromonas caviae</i> . Journal of Bacteriology, 2011, 193, 1286-1287.	1.0	39
32	Characterising the persistence of RT-PCR positivity and incidence in a community survey of SARS-CoV-2. Wellcome Open Research, 0, 7, 102.	0.9	7