

Alison Vaughan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3027272/publications.pdf>

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11
papers

1,045
citations

933447

10
h-index

1281871

11
g-index

12
all docs

12
docs citations

12
times ranked

1936
citing authors

#	ARTICLE	IF	CITATIONS
1	Diagnosis of SARS-CoV-2 Infection with LamPORE, a High-Throughput Platform Combining Loop-Mediated Isothermal Amplification and Nanopore Sequencing. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	3.9	30
2	Ten-year longitudinal molecular epidemiology study of <i>Escherichia coli</i> and <i>Klebsiella</i> species bloodstream infections in Oxfordshire, UK. <i>Genome Medicine</i> , 2021, 13, 144.	8.2	35
3	Viral detection and identification in 20Âmin by rapid single-particle fluorescence in-situ hybridization of viral RNA. <i>Scientific Reports</i> , 2021, 11, 19579.	3.3	16
4	Genomic Epidemiology of Complex, Multispecies, Plasmid-Borne <i>bla</i> _{KPC} Carbapenemase in <i>Enterobacteriales</i> in the United Kingdom from 2009 to 2014. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	26
5	Reconciling the Potentially Irreconcilable? Genotypic and Phenotypic Amoxicillin-Clavulanate Resistance in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	33
6	Optimized use of Oxford Nanopore flowcells for hybrid assemblies. <i>Microbial Genomics</i> , 2020, 6, .	2.0	14
7	<i>Klebsiella quasipneumoniae</i> Provides a Window into Carbapenemase Gene Transfer, Plasmid Rearrangements, and Patient Interactions with the Hospital Environment. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	44
8	Metagenomic Nanopore Sequencing of Influenza Virus Direct from Clinical Respiratory Samples. <i>Journal of Clinical Microbiology</i> , 2019, 58, .	3.9	121
9	Maternal colonization with <i>Streptococcus agalactiae</i> and associated stillbirth and neonatal disease in coastal Kenya. <i>Nature Microbiology</i> , 2016, 1, 16067.	13.3	91
10	Capsular Typing Method for <i>Streptococcus agalactiae</i> Using Whole-Genome Sequence Data. <i>Journal of Clinical Microbiology</i> , 2016, 54, 1388-1390.	3.9	35
11	Diverse Sources of <i>C. difficile</i> Infection Identified on Whole-Genome Sequencing. <i>New England Journal of Medicine</i> , 2013, 369, 1195-1205.	27.0	595