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List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

4,840
citations

430442

18
h-index

395343

33
g-index

41
all docs

41
docs citations

41
times ranked

10450
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluating the Effects of SARS-CoV-2 Spike Mutation D614G on Transmissibility and Pathogenicity. <i>Cell</i> , 2021, 184, 64-75.e11.	13.5	843
2	SARS-CoV-2 evolution during treatment of chronic infection. <i>Nature</i> , 2021, 592, 277-282.	13.7	802
3	Establishment and lineage dynamics of the SARS-CoV-2 epidemic in the UK. <i>Science</i> , 2021, 371, 708-712.	6.0	335
4	Circulating SARS-CoV-2 spike N439K variants maintain fitness while evading antibody-mediated immunity. <i>Cell</i> , 2021, 184, 1171-1187.e20.	13.5	541
5	Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies. <i>Nature</i> , 2021, 593, 136-141.	13.7	648
6	Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study. <i>Lancet Public Health</i> , The, 2021, 6, e335-e345.	4.7	269
7	gvpA and chiA genes are not uniformly distributed amongst diverse <i>Vibrio cholerae</i> . <i>Microbial Genomics</i> , 2021, 7, .	1.0	2
8	Characterisation of Bacteriophage-Encoded Depolymerases Selective for Key <i>Klebsiella pneumoniae</i> Capsular Exopolysaccharides. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 686090.	1.8	14
9	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. <i>Cell Reports</i> , 2021, 35, 109292.	2.9	375
10	Genomic contextualisation of ancient DNA molecular data from an Argentinian fifth pandemic <i>Vibrio cholerae</i> infection. <i>Microbial Genomics</i> , 2021, 7, .	1.0	0
11	Getting ahead of the competition. <i>Nature Reviews Microbiology</i> , 2021, 19, 551-551.	13.6	0
12	The impact of viral mutations on recognition by SARS-CoV-2 specific T _H cells. <i>iScience</i> , 2021, 24, 103353.	1.9	57
13	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
14	Genomics of the Argentinian cholera epidemic elucidate the contrasting dynamics of epidemic and endemic <i>Vibrio cholerae</i> . <i>Nature Communications</i> , 2020, 11, 4918.	5.8	12
15	An integrated national scale SARS-CoV-2 genomic surveillance network. <i>Lancet Microbe</i> , The, 2020, 1, e99-e100.	3.4	232
16	Type II and type IV toxin-antitoxin systems show different evolutionary patterns in the global <i>Klebsiella pneumoniae</i> population. <i>Nucleic Acids Research</i> , 2020, 48, 4357-4370.	6.5	14
17	“Community evolution”™ “laboratory strains and pedigrees in the age of genomics. <i>Microbiology (United Kingdom)</i> , 2020, 166, 233-238.	0.7	8
18	Loss of RNA Chaperone Hfq Unveils a Toxic Pathway in <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	7

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19	Contrasting patterns of longitudinal population dynamics and antimicrobial resistance mechanisms in two priority bacterial pathogens over 7 years in a single center. <i>Genome Biology</i> , 2019, 20, 184.	3.8	22
20	Novel Insights Into the Spread of Enteric Pathogens Using Genomics. <i>Journal of Infectious Diseases</i> , 2019, 221, S319-S330.	1.9	2
21	Separating Bacteria by Capsule Amount Using a Discontinuous Density Gradient. <i>Journal of Visualized Experiments</i> , 2019, , .	0.2	6
22	The history, genome and biology of NCTC 30: a non-pandemic <i>Vibrio cholerae</i> isolate from World War One. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20182025.	1.2	18
23	High quality reference genomes for toxigenic and non-toxigenic <i>Vibrio cholerae</i> serogroup O139. <i>Scientific Reports</i> , 2019, 9, 5865.	1.6	13
24	Using human iPSC derived small intestinal organoids as a model for enteric disease caused by Enterotoxigenic <i>E. coli</i> and <i>Vibrio cholerae</i> . <i>Access Microbiology</i> , 2019, 1, .	0.2	2
25	The utilisation of organoids and macrophages derived from Human induced pluripotent stem cells as model systems to investigate host-bacterial interactions. <i>Access Microbiology</i> , 2019, 1, .	0.2	1
26	The Capsule Regulatory Network of <i>Klebsiella pneumoniae</i> Defined by density-TraDISort. <i>MBio</i> , 2018, 9, .	1.8	78
27	The Evolution of Gene Regulatory Mechanisms in Bacteria. <i>Grand Challenges in Biology and Biotechnology</i> , 2018, , 125-152.	2.4	4
28	Regulatory Hierarchies Controlling Virulence Gene Expression in <i>Shigella flexneri</i> and <i>Vibrio cholerae</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2686.	1.5	31
29	Defining endemic cholera at three levels of spatiotemporal resolution within Bangladesh. <i>Nature Genetics</i> , 2018, 50, 951-955.	9.4	37
30	Control of virulence gene transcription by indirect readout in <i>Vibrio cholerae</i> and <i>Salmonella enterica</i> serovar Typhimurium. <i>Environmental Microbiology</i> , 2017, 19, 3834-3845.	1.8	26
31	Integrated view of <i>Vibrio cholerae</i> in the Americas. <i>Science</i> , 2017, 358, 789-793.	6.0	128
32	<i>Klebsiella pneumoniae</i> : when a colonizer turns bad. <i>Nature Reviews Microbiology</i> , 2017, 15, 384-384.	13.6	27
33	DNA supercoiling is a fundamental regulatory principle in the control of bacterial gene expression. <i>Biophysical Reviews</i> , 2016, 8, 89-100.	1.5	89
34	DNA supercoiling is a fundamental regulatory principle in the control of bacterial gene expression. <i>Biophysical Reviews</i> , 2016, 8, 209-220.	1.5	73
35	Bacterial pathogen gene regulation: a DNA-structure-centred view of a protein-dominated domain. <i>Clinical Science</i> , 2016, 130, 1165-1177.	1.8	11