

Danesh Moradigaravand

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

587
citations

759233

12
h-index

940533

16
g-index

20
all docs

20
docs citations

20
times ranked

1216
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of antibiotic resistance in <i>Escherichia coli</i> from large-scale pan-genome data. <i>PLoS Computational Biology</i> , 2018, 14, e1006258.	3.2	127
2	Recent independent emergence of multiple multidrug-resistant <i>Serratia marcescens</i> clones within the United Kingdom and Ireland. <i>Genome Research</i> , 2016, 26, 1101-1109.	5.5	74
3	Whole genome sequencing reveals high-resolution epidemiological links between clinical and environmental <i>Klebsiella pneumoniae</i> . <i>Genome Medicine</i> , 2017, 9, 6.	8.2	61
4	Phylogenetically informative mutations in genes implicated in antibiotic resistance in <i>Mycobacterium tuberculosis</i> complex. <i>Genome Medicine</i> , 2020, 12, 27.	8.2	58
5	A One Health Study of the Genetic Relatedness of <i>Klebsiella pneumoniae</i> and Their Mobile Elements in the East of England. <i>Clinical Infectious Diseases</i> , 2020, 70, 219-226.	5.8	46
6	Recombination Accelerates Adaptation on a Large-Scale Empirical Fitness Landscape in HIV-1. <i>PLoS Genetics</i> , 2014, 10, e1004439.	3.5	41
7	Population Structure of Multidrug-Resistant <i>Klebsiella oxytoca</i> within Hospitals across the United Kingdom and Ireland Identifies Sharing of Virulence and Resistance Genes with <i>K. pneumoniae</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 574-584.	2.5	35
8	The Evolution of Natural Competence: Disentangling Costs and Benefits of Sex in Bacteria. <i>American Naturalist</i> , 2013, 182, E112-E126.	2.1	29
9	The Effect of Bacterial Recombination on Adaptation on Fitness Landscapes with Limited Peak Accessibility. <i>PLoS Computational Biology</i> , 2012, 8, e1002735.	3.2	23
10	<i>dfrA thyA</i> Double Deletion in <i>para</i> -Aminosalicylic Acid-Resistant <i>Mycobacterium tuberculosis</i> Beijing Strains. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3864-3867.	3.2	20
11	Genomic Epidemiology and Evolution of <i>Escherichia coli</i> in Wild Animals in Mexico. <i>MSphere</i> , 2021, 6, .	2.9	19
12	Wild-Type and Non-Wild-Type <i>Mycobacterium tuberculosis</i> MIC Distributions for the Novel Fluoroquinolone Antofloxacin Compared with Those for Ofloxacin, Levofloxacin, and Moxifloxacin. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 5232-5237.	3.2	15
13	Adaptation through genetic time travel? Fluctuating selection can drive the evolution of bacterial transformation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20132609.	2.6	14
14	The impact of natural transformation on adaptation in spatially structured bacterial populations. <i>BMC Evolutionary Biology</i> , 2014, 14, 141.	3.2	9
15	Machine Learning Prediction of Resistance to Subinhibitory Antimicrobial Concentrations from <i>Escherichia coli</i> Genomes. <i>MSystems</i> , 2021, 6, e0034621.	3.8	6
16	The lipoprotein DolP affects cell separation in <i>Escherichia coli</i> , but not as an upstream regulator of NlpD. <i>Microbiology (United Kingdom)</i> , 2022, 168, .	1.8	2