

Lu Cheng

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12149310/publications.pdf>

Version: 2024-02-01

11
papers

1,300
citations

1039880

9
h-index

1372474

10
g-index

11
all docs

11
docs citations

11
times ranked

2579
citing authors

#	ARTICLE	IF	CITATIONS
1	Directional gene flow and ecological separation in <i>Yersinia enterocolitica</i> . <i>Microbial Genomics</i> , 2015, 1, e000030.	1.0	16
2	Cryptic ecology among host generalist <i>Campylobacter jejuni</i> in domestic animals. <i>Molecular Ecology</i> , 2014, 23, 2442-2451.	2.0	131
3	Random projection based clustering for population genomics. , 2014, , .		13
4	SEK: sparsity exploiting k-mer-based estimation of bacterial community composition. <i>Bioinformatics</i> , 2014, 30, 2423-2431.	1.8	11
5	Dense genomic sampling identifies highways of pneumococcal recombination. <i>Nature Genetics</i> , 2014, 46, 305-309.	9.4	371
6	Bayesian clustering of DNA sequences using Markov chains and a stochastic partition model. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 105-21.	0.2	14
7	Recent Recombination Events in the Core Genome Are Associated with Adaptive Evolution in <i>Enterococcus faecium</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 1524-1535.	1.1	87
8	Hierarchical and Spatially Explicit Clustering of DNA Sequences with BAPS Software. <i>Molecular Biology and Evolution</i> , 2013, 30, 1224-1228.	3.5	568
9	The Evolutionary Path to Extraintestinal Pathogenic, Drug-Resistant <i>Escherichia coli</i> Is Marked by Drastic Reduction in Detectable Recombination within the Core Genome. <i>Genome Biology and Evolution</i> , 2013, 5, 699-710.	1.1	45
10	Bayesian estimation of bacterial community composition from 454 sequencing data. <i>Nucleic Acids Research</i> , 2012, 40, 5240-5249.	6.5	27
11	Bayesian semi-supervised classification of bacterial samples using MLST databases. <i>BMC Bioinformatics</i> , 2011, 12, 302.	1.2	17