

Granger G Sutton

List of Publications by Year in descending order

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21
papers

4,437
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687363

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citing authors

#	ARTICLE	IF	CITATIONS
1	A pan-genome method to determine core regions of the <i>Bacillus subtilis</i> and <i>Escherichia coli</i> genomes. <i>F1000Research</i> , 2021, 10, 286.	1.6	5
2	Horizontal transfer and evolution of wall teichoic acid gene cassettes in <i>Bacillus subtilis</i> . <i>F1000Research</i> , 2021, 10, 354.	1.6	4
3	A pan-genome method to determine core regions of the <i>Bacillus subtilis</i> and <i>Escherichia coli</i> genomes. <i>F1000Research</i> , 2021, 10, 286.	1.6	3
4	Newly Named <i>Klebsiella aerogenes</i> (formerly <i>Enterobacter aerogenes</i>) Is Associated with Poor Clinical Outcomes Relative to Other <i>Enterobacter</i> Species in Patients with Bloodstream Infection. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	29
5	COVID-19 pandemic reveals the peril of ignoring metadata standards. <i>Scientific Data</i> , 2020, 7, 188.	5.3	56
6	Large-scale comparative analysis of microbial pan-genomes using PanOCT. <i>Bioinformatics</i> , 2019, 35, 1049-1050.	4.1	27
7	GGRaSP: a R-package for selecting representative genomes using Gaussian mixture models. <i>Bioinformatics</i> , 2018, 34, 3032-3034.	4.1	16
8	<i>Enterobacter hormaechei</i> subsp. <i>hoffmannii</i> subsp. nov., <i>Enterobacter hormaechei</i> subsp. <i>xiangfangensis</i> comb. nov., <i>Enterobacter roggenkampii</i> sp. nov., and <i>Enterobacter muelleri</i> is a later heterotypic synonym of <i>Enterobacter asburiae</i> based on computational analysis of sequenced <i>Enterobacter</i> genomes.. <i>F1000Research</i> , 2018, 7, 521.	1.6	68
9	A draft genome sequence for the <i>Ixodes scapularis</i> cell line, ISE6. <i>F1000Research</i> , 2018, 7, 297.	1.6	49
10	<i>Enterobacter hormaechei</i> subsp. <i>hoffmannii</i> subsp. nov., <i>Enterobacter hormaechei</i> subsp. <i>xiangfangensis</i> comb. nov., <i>Enterobacter roggenkampii</i> sp. nov., and <i>Enterobacter muelleri</i> is a later heterotypic synonym of <i>Enterobacter asburiae</i> based on computational analysis of sequenced <i>Enterobacter</i> genomes.. <i>F1000Research</i> , 2018, 7, 521.	1.6	56
11	LOCUST: a custom sequence locus typer for classifying microbial isolates. <i>Bioinformatics</i> , 2017, 33, 1725-1726.	4.1	16
12	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	17.5	1,512
13	Initial genome sequencing of the sugarcane CP 96-1252 complex hybrid. <i>F1000Research</i> , 2017, 6, 688.	1.6	6
14	Comprehensive Genome Analysis of Carbapenemase-Producing <i>Enterobacter</i> spp.: New Insights into Phylogeny, Population Structure, and Resistance Mechanisms. <i>MBio</i> , 2016, 7, .	4.1	154
15	Genomic insights into the <i>Ixodes scapularis</i> tick vector of Lyme disease. <i>Nature Communications</i> , 2016, 7, 10507.	12.8	450
16	A novel method of consensus pan-chromosome assembly and large-scale comparative analysis reveal the highly flexible pan-genome of <i>Acinetobacter baumannii</i> . <i>Genome Biology</i> , 2015, 16, 143.	9.6	122
17	PanOCT: automated clustering of orthologs using conserved gene neighborhood for pan-genomic analysis of bacterial strains and closely related species. <i>Nucleic Acids Research</i> , 2012, 40, e172-e172.	14.5	227
18	Whole-genome shotgun assembly and comparison of human genome assemblies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1916-1921.	7.1	164

#	ARTICLE	IF	CITATIONS
19	A Whole-Genome Assembly of <i>Drosophila</i> . <i>Science</i> , 2000, 287, 2196-2204.	12.6	1,449
20	Typing and classification of non-tuberculous mycobacteria isolates. <i>F1000Research</i> , 0, 9, 249.	1.6	1
21	Typing and classification of non-tuberculous mycobacteria isolates. <i>F1000Research</i> , 0, 9, 249.	1.6	1