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List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

4,303
citations

279798

23
h-index

361022

35
g-index

46
all docs

46
docs citations

46
times ranked

6190
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogenetic diversity analysis of shotgun metagenomic reads describes gut microbiome development and treatment effects in the post-weaned pig. <i>PLoS ONE</i> , 2022, 17, e0270372.	2.5	5
2	A large-scale metagenomic survey dataset of the post-weaning piglet gut lumen. <i>GigaScience</i> , 2021, 10, .	6.4	9
3	Post-weaning shifts in microbiome composition and metabolism revealed by over 25â€™000 pig gut metagenome-assembled genomes. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
4	qc3C: Reference-free quality control for Hi-C sequencing data. <i>PLoS Computational Biology</i> , 2021, 17, e1008839.	3.2	5
5	Metagenomic Hi-C of a Healthy Human Fecal Microbiome Transplant Donor. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	9
6	Identification of a novel lineage of plasmids within phylogenetically diverse subclades of IncHI2-ST1 plasmids. <i>Plasmid</i> , 2019, 102, 56-61.	1.4	6
7	bin3C: exploiting Hi-C sequencing data to accurately resolve metagenome-assembled genomes. <i>Genome Biology</i> , 2019, 20, 46.	8.8	66
8	CAMISIM: simulating metagenomes and microbial communities. <i>Microbiome</i> , 2019, 7, 17.	11.1	117
9	High contiguity genome sequence of a multidrug-resistant hospital isolate of <i>Enterobacter hormaechei</i> . <i>Gut Pathogens</i> , 2019, 11, 3.	3.4	26
10	Complete Sequences of Multiple-Drug Resistant IncHI2 ST3 Plasmids in <i>Escherichia coli</i> of Porcine Origin in Australia. <i>Frontiers in Sustainable Food Systems</i> , 2019, 3, .	3.9	31
11	Australian porcine clonal complex 10 (CC10) <i>Escherichia coli</i> belong to multiple sublineages of a highly diverse global CC10 phylogeny. <i>Microbial Genomics</i> , 2019, 5, .	2.0	25
12	Sim3C: simulation of Hi-C and Meta3C proximity ligation sequencing technologies. <i>GigaScience</i> , 2018, 7, .	6.4	27
13	Genomic variation and biogeography of Antarctic haloarchaea. <i>Microbiome</i> , 2018, 6, 113.	11.1	32
14	Critical Assessment of Metagenome Interpretationâ€™ a benchmark of metagenomics software. <i>Nature Methods</i> , 2017, 14, 1063-1071.	19.0	635
15	Evaluation of ddRADseq for reduced representation metagenome sequencing. <i>PeerJ</i> , 2017, 5, e3837.	2.0	11
16	Comparative genomic analysis of toxin-negative strains of <i>Clostridium difficile</i> from humans and animals with symptoms of gastrointestinal disease. <i>BMC Microbiology</i> , 2016, 16, 41.	3.3	13
17	Deconvoluting simulated metagenomes: the performance of hard- and soft- clustering algorithms applied to metagenomic chromosome conformation capture (3C). <i>PeerJ</i> , 2016, 4, e2676.	2.0	11
18	Microbial ecology of an Antarctic hypersaline lake: genomic assessment of ecophysiology among dominant haloarchaea. <i>ISME Journal</i> , 2014, 8, 1645-1658.	9.8	54

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19	Metagenomic insights into strategies of carbon conservation and unusual sulfur biogeochemistry in a hypersaline Antarctic lake. <i>ISME Journal</i> , 2013, 7, 1944-1961.	9.8	75
20	High level of intergenera gene exchange shapes the evolution of haloarchaea in an isolated Antarctic lake. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16939-16944.	7.1	105
21	Key microbial drivers in Antarctic aquatic environments. <i>FEMS Microbiology Reviews</i> , 2013, 37, 303-335.	8.6	144
22	Biogeographic partitioning of Southern Ocean microorganisms revealed by metagenomics. <i>Environmental Microbiology</i> , 2013, 15, 1318-1333.	3.8	82
23	The role of planktonic Flavobacteria in processing algal organic matter in coastal East Antarctica revealed using metagenomics and metaproteomics. <i>Environmental Microbiology</i> , 2013, 15, 1302-1317.	3.8	277
24	Global biogeography of SAR11 marine bacteria. <i>Molecular Systems Biology</i> , 2012, 8, 595.	7.2	215
25	A metaproteomic assessment of winter and summer bacterioplankton from Antarctic Peninsula coastal surface waters. <i>ISME Journal</i> , 2012, 6, 1883-1900.	9.8	200
26	An integrative study of a meromictic lake ecosystem in Antarctica. <i>ISME Journal</i> , 2011, 5, 879-895.	9.8	204
27	Virophage control of antarctic algal host-virus dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6163-6168.	7.1	252
28	Simple high-throughput annotation pipeline (SHAP). <i>Bioinformatics</i> , 2011, 27, 2431-2432.	4.1	3
29	Metaproteogenomic analysis of a dominant green sulfur bacterium from Ace Lake, Antarctica. <i>ISME Journal</i> , 2010, 4, 1002-1019.	9.8	97
30	Functional genomic signatures of sponge bacteria reveal unique and shared features of symbiosis. <i>ISME Journal</i> , 2010, 4, 1557-1567.	9.8	278
31	The genomic basis of trophic strategy in marine bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15527-15533.	7.1	685
32	The genome sequence of the psychrophilic archaeon, <i>Methanococcoides burtonii</i> : the role of genome evolution in cold adaptation. <i>ISME Journal</i> , 2009, 3, 1012-1035.	9.8	178
33	Metagenomic studies reveal the critical and wide-ranging ecological importance of uncultivated archaea: the role of ammonia oxidizers. <i>BioEssays</i> , 2007, 29, 11-14.	2.5	16
34	The Intracellular Chloride Ion Channel Protein CLIC1 Undergoes a Redox-controlled Structural Transition. <i>Journal of Biological Chemistry</i> , 2004, 279, 9298-9305.	3.4	192
35	Crystal Structure of a Soluble Form of the Intracellular Chloride Ion Channel CLIC1 (NCC27) at 1.4-Å Resolution. <i>Journal of Biological Chemistry</i> , 2001, 276, 44993-45000.	3.4	180