

Matthew Z Demaere

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6033081/publications.pdf>

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	The genomic basis of trophic strategy in marine bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15527-15533.	7.1	685
2	Critical Assessment of Metagenome Interpretationâ€”a benchmark of metagenomics software. Nature Methods, 2017, 14, 1063-1071.	19.0	635
3	Functional genomic signatures of sponge bacteria reveal unique and shared features of symbiosis. ISME Journal, 2010, 4, 1557-1567.	9.8	278
4	The role of planktonic <i>Flavobacteria</i> in processing algal organic matter in coastal Antarctic Antarctica revealed using metagenomics and metaproteomics. Environmental Microbiology, 2013, 15, 1302-1317.	3.8	277
5	Virophage control of antarctic algal hostâ€”virus dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6163-6168.	7.1	252
6	Global biogeography of SAR11 marine bacteria. Molecular Systems Biology, 2012, 8, 595.	7.2	215
7	An integrative study of a meromictic lake ecosystem in Antarctica. ISME Journal, 2011, 5, 879-895.	9.8	204
8	A metaproteomic assessment of winter and summer bacterioplankton from Antarctic Peninsula coastal surface waters. ISME Journal, 2012, 6, 1883-1900.	9.8	200
9	The Intracellular Chloride Ion Channel Protein CLIC1 Undergoes a Redox-controlled Structural Transition. Journal of Biological Chemistry, 2004, 279, 9298-9305.	3.4	192
10	Crystal Structure of a Soluble Form of the Intracellular Chloride Ion Channel CLIC1 (NCC27) at 1.4-Å Resolution. Journal of Biological Chemistry, 2001, 276, 44993-45000.	3.4	180
11	The genome sequence of the psychrophilic archaeon, <i>Methanococcoides burtonii</i> : the role of genome evolution in cold adaptation. ISME Journal, 2009, 3, 1012-1035.	9.8	178
12	Key microbial drivers in Antarctic aquatic environments. FEMS Microbiology Reviews, 2013, 37, 303-335.	8.6	144
13	CAMISIM: simulating metagenomes and microbial communities. Microbiome, 2019, 7, 17.	11.1	117
14	High level of intergenera gene exchange shapes the evolution of haloarchaea in an isolated Antarctic lake. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 16939-16944.	7.1	105
15	Metaproteogenomic analysis of a dominant green sulfur bacterium from Ace Lake, Antarctica. ISME Journal, 2010, 4, 1002-1019.	9.8	97
16	Biogeographic partitioning of Southern Ocean microorganisms revealed by metagenomics. Environmental Microbiology, 2013, 15, 1318-1333.	3.8	82
17	Metagenomic insights into strategies of carbon conservation and unusual sulfur biogeochemistry in a hypersaline Antarctic lake. ISME Journal, 2013, 7, 1944-1961.	9.8	75
18	bin3C: exploiting Hi-C sequencing data to accurately resolve metagenome-assembled genomes. Genome Biology, 2019, 20, 46.	8.8	66

#	ARTICLE	IF	CITATIONS
19	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
20	Genomic variation and biogeography of Antarctic haloarchaea. <i>Microbiome</i> , 2018, 6, 113.	11.1	32
21	Complete Sequences of Multiple-Drug Resistant IncHI2 ST3 Plasmids in Escherichia coli of Porcine Origin in Australia. <i>Frontiers in Sustainable Food Systems</i> , 2019, 3, .	3.9	31
22	Sim3C: simulation of Hi-C and Meta3C proximity ligation sequencing technologies. <i>GigaScience</i> , 2018, 7, .	6.4	27
23	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
24	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
25	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
26	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
27	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
28	Evaluation of ddRADseq for reduced representation metagenome sequencing. <i>PeerJ</i> , 2017, 5, e3837.	2.0	11
29	Metagenomic Hi-C of a Healthy Human Fecal Microbiome Transplant Donor. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	9
30	A large-scale metagenomic survey dataset of the post-weaning piglet gut lumen. <i>GigaScience</i> , 2021, 10, .	6.4	9
31	Post-weaning shifts in microbiome composition and metabolism revealed by over 25,000 pig gut metagenome-assembled genomes. <i>Microbial Genomics</i> , 2021, 7, .	2.0	9
32	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
33	qc3C: Reference-free quality control for Hi-C sequencing data. <i>PLoS Computational Biology</i> , 2021, 17, e1008839.	3.2	5
34	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
35	Simple high-throughput annotation pipeline (SHAP). <i>Bioinformatics</i> , 2011, 27, 2431-2432.	4.1	3