

Daniel R Mende

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

28,438
citations

126708

33
h-index

243296

44
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all docs

54
docs citations

54
times ranked

33854
citing authors

#	ARTICLE	IF	CITATIONS
1	Complex marine microbial communities partition metabolism of scarce resources over the diel cycle. <i>Nature Ecology and Evolution</i> , 2022, 6, 218-229.	3.4	21
2	Towards the biogeography of prokaryotic genes. <i>Nature</i> , 2022, 601, 252-256.	13.7	85
3	Benchmarking the topological accuracy of bacterial phylogenomic workflows using in silico evolution. <i>Microbial Genomics</i> , 2022, 8, .	1.0	1
4	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	9.0	133
5	Combined pigment and metatranscriptomic analysis reveals highly synchronized diel patterns of phenotypic light response across domains in the open oligotrophic ocean. <i>ISME Journal</i> , 2021, 15, 520-533.	4.4	28
6	<i>Escherichia ruyisiae</i> sp. nov., a novel Gram-stain-negative bacterium, isolated from a faecal sample of an international traveller. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	24
7	GUNC: detection of chimerism and contamination in prokaryotic genomes. <i>Genome Biology</i> , 2021, 22, 178.	3.8	94
8	mOTUs: Profiling Taxonomic Composition, Transcriptional Activity and Strain Populations of Microbial Communities. <i>Current Protocols</i> , 2021, 1, e218.	1.3	8
9	Metapangenomics reveals depth-dependent shifts in metabolic potential for the ubiquitous marine bacterial SAR324 lineage. <i>Microbiome</i> , 2021, 9, 172.	4.9	25
10	proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2020, 48, D621-D625.	6.5	60
11	<i>Thermus thermophilus</i> DNA can be used as internal control for process monitoring of clinical metagenomic next-generation sequencing of urine samples. <i>Journal of Microbiological Methods</i> , 2020, 176, 106005.	0.7	8
12	Alternative strategies of nutrient acquisition and energy conservation map to the biogeography of marine ammonia-oxidizing archaea. <i>ISME Journal</i> , 2020, 14, 2595-2609.	4.4	62
13	Double-stranded DNA viroplankton dynamics and reproductive strategies in the oligotrophic open ocean water column. <i>ISME Journal</i> , 2020, 14, 1304-1315.	4.4	65
14	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , 2020, 14, 1247-1259.	4.4	74
15	A distinct lineage of giant viruses brings a rhodopsin photosystem to unicellular marine predators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20574-20583.	3.3	120
16	Persistent Core Populations Shape the Microbiome Throughout the Water Column in the North Pacific Subtropical Gyre. <i>Frontiers in Microbiology</i> , 2019, 10, 2273.	1.5	17
17	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019, 10, 1014.	5.8	298
18	eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. <i>Nucleic Acids Research</i> , 2019, 47, D309-D314.	6.5	2,575

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19	Diel cycling and long-term persistence of viruses in the ocean's euphotic zone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11446-11451.	3.3	116
20	Environmental drivers of a microbial genomic transition zone in the ocean's interior. <i>Nature Microbiology</i> , 2017, 2, 1367-1373.	5.9	177
21	Bacteriophage Distributions and Temporal Variability in the Ocean's Interior. <i>MBio</i> , 2017, 8, .	1.8	76
22	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2017, 45, D529-D534.	6.5	131
23	Isolation and Characterization of Bacteria That Degrade Phosphonates in Marine Dissolved Organic Matter. <i>Frontiers in Microbiology</i> , 2017, 8, 1786.	1.5	49
24	Improved Environmental Genomes via Integration of Metagenomic and Single-Cell Assemblies. <i>Frontiers in Microbiology</i> , 2016, 7, 143.	1.5	24
25	Siderophore-based microbial adaptations to iron scarcity across the eastern Pacific Ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14237-14242.	3.3	179
26	Integration of multi-omics data of a genome-reduced bacterium: Prevalence of post-transcriptional regulation and its correlation with protein abundances. <i>Nucleic Acids Research</i> , 2016, 44, 1192-1202.	6.5	35
27	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. <i>Nucleic Acids Research</i> , 2016, 44, D286-D293.	6.5	1,937
28	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	6.0	2,137
29	Inter-individual differences in the gene content of human gut bacterial species. <i>Genome Biology</i> , 2015, 16, 82.	3.8	184
30	Metabolic dependencies drive species co-occurrence in diverse microbial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6449-6454.	3.3	588
31	Potential of fecal microbiota for early-stage detection of colorectal cancer. <i>Molecular Systems Biology</i> , 2014, 10, 766.	3.2	991
32	Accurate and universal delineation of prokaryotic species. <i>Nature Methods</i> , 2013, 10, 881-884.	9.0	311
33	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	9.0	442
34	Country-specific antibiotic use practices impact the human gut resistome. <i>Genome Research</i> , 2013, 23, 1163-1169.	2.4	356
35	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013, 493, 45-50.	13.7	783
36	Consistent mutational paths predict eukaryotic thermostability. <i>BMC Evolutionary Biology</i> , 2013, 13, 7.	3.2	60

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37	Individuality and temporal stability of the human gut microbiome. Central Asian Journal of Global Health, 2013, 2, 120.	0.6	6
38	Role for urea in nitrification by polar marine Archaea. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17989-17994.	3.3	253
39	Deciphering a global network of functionally associated post-translational modifications. Molecular Systems Biology, 2012, 8, 599.	3.2	216
40	MOCAT: A Metagenomics Assembly and Gene Prediction Toolkit. PLoS ONE, 2012, 7, e47656.	1.1	208
41	Assessment of Metagenomic Assembly Using Simulated Next Generation Sequencing Data. PLoS ONE, 2012, 7, e31386.	1.1	214
42	Enterotypes of the human gut microbiome. Nature, 2011, 473, 174-180.	13.7	5,800
43	A human gut microbial gene catalogue established by metagenomic sequencing. Nature, 2010, 464, 59-65.	13.7	9,342