

Daniel R Mende

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

45
papers

18,670
citations

26
h-index

54
g-index

54
ext. papers

24,818
ext. citations

15.9
avg, IF

5.79
L-index

#	Paper	IF	Citations
45	Critical Assessment of Metagenome Interpretation: the second round of challenges.. <i>Nature Methods</i> , 2022 ,	21.6	14
44	Towards the biogeography of prokaryotic genes.. <i>Nature</i> , 2021 ,	50.4	8
43	GUNC: detection of chimerism and contamination in prokaryotic genomes. <i>Genome Biology</i> , 2021 , 22, 178	18.3	16
42	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	11.9	12
41	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,	2.2	5
40	mOTUs: Profiling Taxonomic Composition, Transcriptional Activity and Strain Populations of Microbial Communities. <i>Current Protocols</i> , 2021 , 1, e218		2
39	Metapangenomics reveals depth-dependent shifts in metabolic potential for the ubiquitous marine bacterial SAR324 lineage. <i>Microbiome</i> , 2021 , 9, 172	16.6	4
38	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	11.9	19
37	Double-stranded DNA viroplankton dynamics and reproductive strategies in the oligotrophic open ocean water column. <i>ISME Journal</i> , 2020 , 14, 1304-1315	11.9	31
36	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , 2020 , 14, 1247-1259	11.9	23
35	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	20.1	21
34	<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	2.8	3
33	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	11.5	68
32	Persistent Core Populations Shape the Microbiome Throughout the Water Column in the North Pacific Subtropical Gyre. <i>Frontiers in Microbiology</i> , 2019 , 10, 2273	5.7	7
31	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019 , 10, 1014	17.4	134
30	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	20.1	850
29	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	11.5	70

28	Environmental drivers of a microbial genomic transition zone in the ocean's interior. <i>Nature Microbiology</i> , 2017 , 2, 1367-1373	26.6	91
27	Bacteriophage Distributions and Temporal Variability in the Ocean's Interior. <i>MBio</i> , 2017 , 8,	7.8	39
26	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2017 , 45, D529-D534	20.1	74
25	Isolation and Characterization of Bacteria That Degrade Phosphonates in Marine Dissolved Organic Matter. <i>Frontiers in Microbiology</i> , 2017 , 8, 1786	5.7	26
24	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. <i>Nucleic Acids Research</i> , 2016 , 44, D286-93	20.1	1211
23	Improved Environmental Genomes via Integration of Metagenomic and Single-Cell Assemblies. <i>Frontiers in Microbiology</i> , 2016 , 7, 143	5.7	17
22	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	11.5	121
21	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, 1192-202	20.1	25
20	Inter-individual differences in the gene content of human gut bacterial species. <i>Genome Biology</i> , 2015 , 16, 82	18.3	107
19	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, 6449-54	11.5	366
18	Ocean plankton. Structure and function of the global ocean microbiome. <i>Science</i> , 2015 , 348, 1261359	33.3	1261
17	Potential of fecal microbiota for early-stage detection of colorectal cancer. <i>Molecular Systems Biology</i> , 2014 , 10, 766	12.2	575
16	Accurate and universal delineation of prokaryotic species. <i>Nature Methods</i> , 2013 , 10, 881-4	21.6	234
15	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013 , 10, 1196-9	21.6	340
14	Country-specific antibiotic use practices impact the human gut resistome. <i>Genome Research</i> , 2013 , 23, 1163-9	9.7	269
13	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013 , 493, 45-50	50.4	571
12	Consistent mutational paths predict eukaryotic thermostability. <i>BMC Evolutionary Biology</i> , 2013 , 13, 7	3	47
11	Individuality and temporal stability of the human gut microbiome. <i>Central Asian Journal of Global Health</i> , 2013 , 2, 120	0.8	1

10	MOCAT: a metagenomics assembly and gene prediction toolkit. <i>PLoS ONE</i> , 2012 , 7, e47656	3.7	143
9	Role for urea in nitrification by polar marine Archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 17989-94	11.5	177
8	Deciphering a global network of functionally associated post-translational modifications. <i>Molecular Systems Biology</i> , 2012 , 8, 599	12.2	171
7	Assessment of metagenomic assembly using simulated next generation sequencing data. <i>PLoS ONE</i> , 2012 , 7, e31386	3.7	157
6	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011 , 473, 174-80	50.4	4240
5	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010 , 464, 59-65	50.4	7044
4	Combined pigment and metatranscriptomic analysis reveals synchronized diel patterns of phenotypic light response across domains in the open ocean		2
3	Community-scale Synchronization and Temporal Partitioning of Gene Expression, Metabolism, and Lipid Biosynthesis in Oligotrophic Ocean Surface Waters		6
2	GUNC: Detection of Chimerism and Contamination in Prokaryotic Genomes		3
1	<i>Escherichia ruysiae</i> sp. nov., isolated from an international traveller		3