

# Daniel R Mende

## List of Publications by Year in descending order

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Version: 2024-02-01

43  
papers

28,438  
citations

126907

33  
h-index

243625

44  
g-index

54  
all docs

54  
docs citations

54  
times ranked

33854  
citing authors

#	ARTICLE	IF	CITATIONS
1	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	27.8	9,342
2	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	27.8	5,800
3	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.	14.5	2,575
4	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	12.6	2,137
5	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.	14.5	1,937
6	Potential of fecal microbiota for early-stage detection of colorectal cancer. <i>Molecular Systems Biology</i> , 2014, 10, 766.	7.2	991
7	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013, 493, 45-50.	27.8	783
8	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.	7.1	588
9	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	19.0	442
10	Country-specific antibiotic use practices impact the human gut resistome. <i>Genome Research</i> , 2013, 23, 1163-1169.	5.5	356
11	Accurate and universal delineation of prokaryotic species. <i>Nature Methods</i> , 2013, 10, 881-884.	19.0	311
12	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019, 10, 1014.	12.8	298
13	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, 17989-17994.	7.1	253
14	Deciphering a global network of functionally associated post-translational modifications. <i>Molecular Systems Biology</i> , 2012, 8, 599.	7.2	216
15	Assessment of Metagenomic Assembly Using Simulated Next Generation Sequencing Data. <i>PLoS ONE</i> , 2012, 7, e31386.	2.5	214
16	MOCAT: A Metagenomics Assembly and Gene Prediction Toolkit. <i>PLoS ONE</i> , 2012, 7, e47656.	2.5	208
17	Inter-individual differences in the gene content of human gut bacterial species. <i>Genome Biology</i> , 2015, 16, 82.	8.8	184
18	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.	7.1	179

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19	Environmental drivers of a microbial genomic transition zone in the ocean's interior. <i>Nature Microbiology</i> , 2017, 2, 1367-1373.	13.3	177
20	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	19.0	133
21	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. <i>Nucleic Acids Research</i> , 2017, 45, D529-D534.	14.5	131
22	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.	7.1	120
23	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.	7.1	116
24	GUNC: detection of chimerism and contamination in prokaryotic genomes. <i>Genome Biology</i> , 2021, 22, 178.	8.8	94
25	Towards the biogeography of prokaryotic genes. <i>Nature</i> , 2022, 601, 252-256.	27.8	85
26	Bacteriophage Distributions and Temporal Variability in the Ocean's Interior. <i>MBio</i> , 2017, 8, .	4.1	76
27	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , 2020, 14, 1247-1259.	9.8	74
28	Double-stranded DNA viroplankton dynamics and reproductive strategies in the oligotrophic open ocean water column. <i>ISME Journal</i> , 2020, 14, 1304-1315.	9.8	65
29	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.	9.8	62
30	Consistent mutational paths predict eukaryotic thermostability. <i>BMC Evolutionary Biology</i> , 2013, 13, 7.	3.2	60
31	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.	14.5	60
32	Isolation and Characterization of Bacteria That Degrade Phosphonates in Marine Dissolved Organic Matter. <i>Frontiers in Microbiology</i> , 2017, 8, 1786.	3.5	49
33	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.	14.5	35
34	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.	9.8	28
35	Metapangenomics reveals depth-dependent shifts in metabolic potential for the ubiquitous marine bacterial SAR324 lineage. <i>Microbiome</i> , 2021, 9, 172.	11.1	25
36	Improved Environmental Genomes via Integration of Metagenomic and Single-Cell Assemblies. <i>Frontiers in Microbiology</i> , 2016, 7, 143.	3.5	24

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37	<i>Escherichia ruysiae</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, .	1.7	24
38	Complex marine microbial communities partition metabolism of scarce resources over the diel cycle. <i>Nature Ecology and Evolution</i> , 2022, 6, 218-229.	7.8	21
39	Persistent Core Populations Shape the Microbiome Throughout the Water Column in the North Pacific Subtropical Gyre. <i>Frontiers in Microbiology</i> , 2019, 10, 2273.	3.5	17
40	<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.	1.6	8
41	mOTUs: Profiling Taxonomic Composition, Transcriptional Activity and Strain Populations of Microbial Communities. <i>Current Protocols</i> , 2021, 1, e218.	2.9	8
42	Individuality and temporal stability of the human gut microbiome. <i>Central Asian Journal of Global Health</i> , 2013, 2, 120.	0.6	6
43	Benchmarking the topological accuracy of bacterial phylogenomic workflows using in silico evolution. <i>Microbial Genomics</i> , 2022, 8, .	2.0	1