

# Douglas B Rusch

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/11989237/douglas-b-rusch-publications-by-citations.pdf>

**Version:** 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

33  
papers

18,939  
citations

27  
h-index

35  
g-index

35  
ext. papers

21,690  
ext. citations

14.1  
avg, IF

4.56  
L-index

#	Paper	IF	Citations
33	The sequence of the human genome. <i>Science</i> , <b>2001</b> , 291, 1304-51	33.3	10609
32	The genome sequence of the malaria mosquito <i>Anopheles gambiae</i> . <i>Science</i> , <b>2002</b> , 298, 129-49	33.3	1622
31	The Sorcerer II Global Ocean Sampling expedition: northwest Atlantic through eastern tropical Pacific. <i>PLoS Biology</i> , <b>2007</b> , 5, e77	9.7	1476
30	Improving the Arabidopsis genome annotation using maximal transcript alignment assemblies. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 5654-66	20.1	939
29	The Sorcerer II Global Ocean Sampling expedition: expanding the universe of protein families. <i>PLoS Biology</i> , <b>2007</b> , 5, e16	9.7	638
28	A catalog of reference genomes from the human microbiome. <i>Science</i> , <b>2010</b> , 328, 994-9	33.3	508
27	The dog genome: survey sequencing and comparative analysis. <i>Science</i> , <b>2003</b> , 301, 1898-903	33.3	422
26	Genomic insights to SAR86, an abundant and uncultivated marine bacterial lineage. <i>ISME Journal</i> , <b>2012</b> , 6, 1186-99	11.9	353
25	A comparison of whole-genome shotgun-derived mouse chromosome 16 and the human genome. <i>Science</i> , <b>2002</b> , 296, 1661-71	33.3	305
24	The Sorcerer II Global Ocean Sampling Expedition: metagenomic characterization of viruses within aquatic microbial samples. <i>PLoS ONE</i> , <b>2008</b> , 3, e1456	3.7	241
23	Genomic and functional adaptation in surface ocean planktonic prokaryotes. <i>Nature</i> , <b>2010</b> , 468, 60-6	50.4	215
22	Efficient de novo assembly of single-cell bacterial genomes from short-read data sets. <i>Nature Biotechnology</i> , <b>2011</b> , 29, 915-21	44.5	177
21	Metagenomes from high-temperature chemotrophic systems reveal geochemical controls on microbial community structure and function. <i>PLoS ONE</i> , <b>2010</b> , 5, e9773	3.7	152
20	Characterization of Prochlorococcus clades from iron-depleted oceanic regions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 16184-9	11.5	139
19	Assessing diversity and biogeography of aerobic anoxygenic phototrophic bacteria in surface waters of the Atlantic and Pacific Oceans using the Global Ocean Sampling expedition metagenomes. <i>Environmental Microbiology</i> , <b>2007</b> , 9, 1464-75	5.2	135
18	The YNP Metagenome Project: Environmental Parameters Responsible for Microbial Distribution in the Yellowstone Geothermal Ecosystem. <i>Frontiers in Microbiology</i> , <b>2013</b> , 4, 67	5.7	133
17	Community ecology of hot spring cyanobacterial mats: predominant populations and their functional potential. <i>ISME Journal</i> , <b>2011</b> , 5, 1262-78	11.9	131

16	Functional tradeoffs underpin salinity-driven divergence in microbial community composition. <i>PLoS ONE</i> , <b>2014</b> , 9, e89549	3.7	126
15	Viral photosynthetic reaction center genes and transcripts in the marine environment. <i>ISME Journal</i> , <b>2007</b> , 1, 492-501	11.9	98
14	Stalking the fourth domain in metagenomic data: searching for, discovering, and interpreting novel, deep branches in marker gene phylogenetic trees. <i>PLoS ONE</i> , <b>2011</b> , 6, e18011	3.7	72
13	Community structure and function of high-temperature chlorophototrophic microbial mats inhabiting diverse geothermal environments. <i>Frontiers in Microbiology</i> , <b>2013</b> , 4, 106	5.7	64
12	Daphnia magna transcriptome by RNA-Seq across 12 environmental stressors. <i>Scientific Data</i> , <b>2016</b> , 3, 160030	8.2	62
11	Metagenome sequence analysis of filamentous microbial communities obtained from geochemically distinct geothermal channels reveals specialization of three aquificales lineages. <i>Frontiers in Microbiology</i> , <b>2013</b> , 4, 84	5.7	58
10	Phylogenetic and Functional Analysis of Metagenome Sequence from High-Temperature Archaeal Habitats Demonstrate Linkages between Metabolic Potential and Geochemistry. <i>Frontiers in Microbiology</i> , <b>2013</b> , 4, 95	5.7	57
9	The JCVI standard operating procedure for annotating prokaryotic metagenomic shotgun sequencing data. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 2, 229-37		51
8	Distribution of microbial terpenoid lipid cyclases in the global ocean metagenome. <i>ISME Journal</i> , <b>2009</b> , 3, 352-63	11.9	42
7	Marsarchaeota are an aerobic archaeal lineage abundant in geothermal iron oxide microbial mats. <i>Nature Microbiology</i> , <b>2018</b> , 3, 732-740	26.6	33
6	Speciation and ecological success in dimly lit waters: horizontal gene transfer in a green sulfur bacteria bloom unveiled by metagenomic assembly. <i>ISME Journal</i> , <b>2017</b> , 11, 201-211	11.9	23
5	Metagenomic Analysis of the Indian Ocean Picocyanobacterial Community: Structure, Potential Function and Evolution. <i>PLoS ONE</i> , <b>2016</b> , 11, e0155757	3.7	19
4	Novel, Deep-Branching Heterotrophic Bacterial Populations Recovered from Thermal Spring Metagenomes. <i>Frontiers in Microbiology</i> , <b>2016</b> , 7, 304	5.7	16
3	The distribution, diversity and function of predominant Thermoproteales in high-temperature environments of Yellowstone National Park. <i>Environmental Microbiology</i> , <b>2016</b> , 18, 4755-4769	5.2	12
2	Recombination Does Not Hinder Formation or Detection of Ecological Species of Synechococcus Inhabiting a Hot Spring Cyanobacterial Mat. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 1540	5.7	11
1	Bioinformatics for Genomes and Metagenomes in Ecology Studies. <i>Advanced Topics in Science and Technology in China</i> , <b>2014</b> , 203-226	0.2	