

Douglas B Rusch

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.

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	Marsarchaeota are an aerobic archaeal lineage abundant in geothermal iron oxide microbial mats. <i>Nature Microbiology</i> , 2018 , 3, 732-740	26.6	33
32	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> , 2017 , 11, 201-211	11.9	23
31	Daphnia magna transcriptome by RNA-Seq across 12 environmental stressors. <i>Scientific Data</i> , 2016 , 3, 160030	8.2	62
30	Metagenomic Analysis of the Indian Ocean Picocyanobacterial Community: Structure, Potential Function and Evolution. <i>PLoS ONE</i> , 2016 , 11, e0155757	3.7	19
29	Novel, Deep-Branching Heterotrophic Bacterial Populations Recovered from Thermal Spring Metagenomes. <i>Frontiers in Microbiology</i> , 2016 , 7, 304	5.7	16
28	The distribution, diversity and function of predominant Thermoproteales in high-temperature environments of Yellowstone National Park. <i>Environmental Microbiology</i> , 2016 , 18, 4755-4769	5.2	12
27	Recombination Does Not Hinder Formation or Detection of Ecological Species of Synechococcus Inhabiting a Hot Spring Cyanobacterial Mat. <i>Frontiers in Microbiology</i> , 2015 , 6, 1540	5.7	11
26	Functional tradeoffs underpin salinity-driven divergence in microbial community composition. <i>PLoS ONE</i> , 2014 , 9, e89549	3.7	126
25	Bioinformatics for Genomes and Metagenomes in Ecology Studies. <i>Advanced Topics in Science and Technology in China</i> , 2014 , 203-226	0.2	
24	The YNP Metagenome Project: Environmental Parameters Responsible for Microbial Distribution in the Yellowstone Geothermal Ecosystem. <i>Frontiers in Microbiology</i> , 2013 , 4, 67	5.7	133
23	Metagenome sequence analysis of filamentous microbial communities obtained from geochemically distinct geothermal channels reveals specialization of three aquificales lineages. <i>Frontiers in Microbiology</i> , 2013 , 4, 84	5.7	58
22	Phylogenetic and Functional Analysis of Metagenome Sequence from High-Temperature Archaeal Habitats Demonstrate Linkages between Metabolic Potential and Geochemistry. <i>Frontiers in Microbiology</i> , 2013 , 4, 95	5.7	57
21	Community structure and function of high-temperature chlorophototrophic microbial mats inhabiting diverse geothermal environments. <i>Frontiers in Microbiology</i> , 2013 , 4, 106	5.7	64
20	Genomic insights to SAR86, an abundant and uncultivated marine bacterial lineage. <i>ISME Journal</i> , 2012 , 6, 1186-99	11.9	353
19	Efficient de novo assembly of single-cell bacterial genomes from short-read data sets. <i>Nature Biotechnology</i> , 2011 , 29, 915-21	44.5	177
18	Stalking the fourth domain in metagenomic data: searching for, discovering, and interpreting novel, deep branches in marker gene phylogenetic trees. <i>PLoS ONE</i> , 2011 , 6, e18011	3.7	72
17	Community ecology of hot spring cyanobacterial mats: predominant populations and their functional potential. <i>ISME Journal</i> , 2011 , 5, 1262-78	11.9	131

16	Genomic and functional adaptation in surface ocean planktonic prokaryotes. <i>Nature</i> , 2010 , 468, 60-6	50.4	215
15	Metagenomes from high-temperature chemotrophic systems reveal geochemical controls on microbial community structure and function. <i>PLoS ONE</i> , 2010 , 5, e9773	3.7	152
14	Characterization of Prochlorococcus clades from iron-depleted oceanic regions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 16184-9	11.5	139
13	A catalog of reference genomes from the human microbiome. <i>Science</i> , 2010 , 328, 994-9	33.3	508
12	The JCVI standard operating procedure for annotating prokaryotic metagenomic shotgun sequencing data. <i>Standards in Genomic Sciences</i> , 2010 , 2, 229-37		51
11	Distribution of microbial terpenoid lipid cyclases in the global ocean metagenome. <i>ISME Journal</i> , 2009 , 3, 352-63	11.9	42
10	The Sorcerer II Global Ocean Sampling Expedition: metagenomic characterization of viruses within aquatic microbial samples. <i>PLoS ONE</i> , 2008 , 3, e1456	3.7	241
9	The Sorcerer II Global Ocean Sampling expedition: expanding the universe of protein families. <i>PLoS Biology</i> , 2007 , 5, e16	9.7	638
8	The Sorcerer II Global Ocean Sampling expedition: northwest Atlantic through eastern tropical Pacific. <i>PLoS Biology</i> , 2007 , 5, e77	9.7	1476
7	Viral photosynthetic reaction center genes and transcripts in the marine environment. <i>ISME Journal</i> , 2007 , 1, 492-501	11.9	98
6	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> , 2007 , 9, 1464-75	5.2	135
5	The dog genome: survey sequencing and comparative analysis. <i>Science</i> , 2003 , 301, 1898-903	33.3	422
4	Improving the Arabidopsis genome annotation using maximal transcript alignment assemblies. <i>Nucleic Acids Research</i> , 2003 , 31, 5654-66	20.1	939
3	A comparison of whole-genome shotgun-derived mouse chromosome 16 and the human genome. <i>Science</i> , 2002 , 296, 1661-71	33.3	305
2	The genome sequence of the malaria mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002 , 298, 129-49	33.3	1622
1	The sequence of the human genome. <i>Science</i> , 2001 , 291, 1304-51	33.3	10609