

Douglas B Rusch

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

23,309
citations

182225

30
h-index

445137

33
g-index

35
all docs

35
docs citations

35
times ranked

30416
citing authors

#	ARTICLE	IF	CITATIONS
1	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	6.0	12,623
2	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 129-149.	6.0	1,859
3	The Sorcerer II Global Ocean Sampling Expedition: Northwest Atlantic through Eastern Tropical Pacific. <i>PLoS Biology</i> , 2007, 5, e77.	2.6	1,757
4	Improving the <i>Arabidopsis</i> genome annotation using maximal transcript alignment assemblies. <i>Nucleic Acids Research</i> , 2003, 31, 5654-5666.	6.5	1,597
5	The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. <i>PLoS Biology</i> , 2007, 5, e16.	2.6	736
6	A Catalog of Reference Genomes from the Human Microbiome. <i>Science</i> , 2010, 328, 994-999.	6.0	621
7	Genomic insights to SAR86, an abundant and uncultivated marine bacterial lineage. <i>ISME Journal</i> , 2012, 6, 1186-1199.	4.4	511
8	The Dog Genome: Survey Sequencing and Comparative Analysis. <i>Science</i> , 2003, 301, 1898-1903.	6.0	482
9	A Comparison of Whole-Genome Shotgun-Derived Mouse Chromosome 16 and the Human Genome. <i>Science</i> , 2002, 296, 1661-1671.	6.0	344
10	Genomic and functional adaptation in surface ocean planktonic prokaryotes. <i>Nature</i> , 2010, 468, 60-66.	13.7	280
11	The Sorcerer II Global Ocean Sampling Expedition: Metagenomic Characterization of Viruses within Aquatic Microbial Samples. <i>PLoS ONE</i> , 2008, 3, e1456.	1.1	276
12	Community ecology of hot spring cyanobacterial mats: predominant populations and their functional potential. <i>ISME Journal</i> , 2011, 5, 1262-1278.	4.4	206
13	Efficient de novo assembly of single-cell bacterial genomes from short-read data sets. <i>Nature Biotechnology</i> , 2011, 29, 915-921.	9.4	203
14	The YNP metagenome project: environmental parameters responsible for microbial distribution in the Yellowstone geothermal ecosystem. <i>Frontiers in Microbiology</i> , 2013, 4, 67.	1.5	196
15	Metagenomes from High-Temperature Chemotrophic Systems Reveal Geochemical Controls on Microbial Community Structure and Function. <i>PLoS ONE</i> , 2010, 5, e9773.	1.1	186
16	Functional Tradeoffs Underpin Salinity-Driven Divergence in Microbial Community Composition. <i>PLoS ONE</i> , 2014, 9, e89549.	1.1	184
17	Characterization of <i>Prochlorococcus</i> clades from iron-depleted oceanic regions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16184-16189.	3.3	183
18	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, 1464-1475.	1.8	156

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19	Viral photosynthetic reaction center genes and transcripts in the marine environment. <i>ISME Journal</i> , 2007, 1, 492-501.	4.4	122
20	Community Structure and Function of High-Temperature Chlorophototrophic Microbial Mats Inhabiting Diverse Geothermal Environments. <i>Frontiers in Microbiology</i> , 2013, 4, 106.	1.5	112
21	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.	1.1	95
22	<i>Daphnia magna</i> transcriptome by RNA-Seq across 12 environmental stressors. <i>Scientific Data</i> , 2016, 3, 160030.	2.4	89
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.	1.5	73
24	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.	1.5	73
25	The JCVI standard operating procedure for annotating prokaryotic metagenomic shotgun sequencing data. <i>Standards in Genomic Sciences</i> , 2010, 2, 229-237.	1.5	55
26	Metagenomic Analysis of the Indian Ocean Picocyanobacterial Community: Structure, Potential Function and Evolution. <i>PLoS ONE</i> , 2016, 11, e0155757.	1.1	54
27	Marsarchaeota are an aerobic archaeal lineage abundant in geothermal iron oxide microbial mats. <i>Nature Microbiology</i> , 2018, 3, 732-740.	5.9	53
28	Novel, Deep-Branching Heterotrophic Bacterial Populations Recovered from Thermal Spring Metagenomes. <i>Frontiers in Microbiology</i> , 2016, 7, 304.	1.5	48
29	Distribution of microbial terpenoid lipid cyclases in the global ocean metagenome. <i>ISME Journal</i> , 2009, 3, 352-363.	4.4	47
30	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.	4.4	40
31	The distribution, diversity and function of predominant Thermoproteales in high-temperature environments of Yellowstone National Park. <i>Environmental Microbiology</i> , 2016, 18, 4755-4769.	1.8	24
32	Recombination Does Not Hinder Formation or Detection of Ecological Species of <i>Synechococcus</i> Inhabiting a Hot Spring Cyanobacterial Mat. <i>Frontiers in Microbiology</i> , 2015, 6, 1540.	1.5	16
33	Sulfur cycling and host-virus interactions in <i>Aquificales</i> -dominated biofilms from Yellowstone's hottest ecosystems. <i>ISME Journal</i> , 2022, 16, 842-855.	4.4	8
34	Bioinformatics for Genomes and Metagenomes in Ecology Studies. <i>Advanced Topics in Science and Technology in China</i> , 2014, , 203-226.	0.0	0