Douglas B Rusch

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/11989237/publications.pdf

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	Sulfur cycling and host-virus interactions in <i>Aquificales</i>-dominated biofilms from Yellowstoneâ€™s hottest ecosystems. ISME Journal, 2022, 16, 842-855.	4.4	8
2	Marsarchaeota are an aerobic archaeal lineage abundant in geothermal iron oxide microbial mats. Nature Microbiology, 2018, 3, 732-740.	5.9	53
3	Speciation and ecological success in dimly lit waters: horizontal gene transfer in a green sulfur bacteria bloom unveiled by metagenomic assembly. ISME Journal, 2017, 11, 201-211.	4.4	40
4	Novel, Deep-Branching Heterotrophic Bacterial Populations Recovered from Thermal Spring Metagenomes. Frontiers in Microbiology, 2016, 7, 304.	1.5	48
5	The distribution, diversity and function of predominant Thermoproteales in highâ€temperature environments of Yellowstone National Park. Environmental Microbiology, 2016, 18, 4755-4769.	1.8	24
6	Daphnia magna transcriptome by RNA-Seq across 12 environmental stressors. Scientific Data, 2016, 3, 160030.	2.4	89
7	Metagenomic Analysis of the Indian Ocean Picocyanobacterial Community: Structure, Potential Function and Evolution. PLoS ONE, 2016, 11, e0155757.	1.1	54
8	Recombination Does Not Hinder Formation or Detection of Ecological Species of Synechococcus Inhabiting a Hot Spring Cyanobacterial Mat. Frontiers in Microbiology, 2015, 6, 1540.	1.5	16
9	Functional Tradeoffs Underpin Salinity-Driven Divergence in Microbial Community Composition. PLoS ONE, 2014, 9, e89549.	1.1	184
10	Bioinformatics for Genomes and Metagenomes in Ecology Studies. Advanced Topics in Science and Technology in China, 2014, , 203-226.	0.0	0
11	The YNP metagenome project: environmental parameters responsible for microbial distribution in the Yellowstone geothermal ecosystem. Frontiers in Microbiology, 2013, 4, 67.	1.5	196
12	Metagenome Sequence Analysis of Filamentous Microbial Communities Obtained from Geochemically Distinct Geothermal Channels Reveals Specialization of Three Aquificales Lineages. Frontiers in Microbiology, 2013, 4, 84.	1.5	73
13	Phylogenetic and Functional Analysis of Metagenome Sequence from High-Temperature Archaeal Habitats Demonstrate Linkages between Metabolic Potential and Geochemistry. Frontiers in Microbiology, 2013, 4, 95.	1.5	73
14	Community Structure and Function of High-Temperature Chlorophototrophic Microbial Mats Inhabiting Diverse Geothermal Environments. Frontiers in Microbiology, 2013, 4, 106.	1.5	112
15	Genomic insights to SAR86, an abundant and uncultivated marine bacterial lineage. ISME Journal, 2012, 6, 1186-1199.	4.4	511
16	Efficient de novo assembly of single-cell bacterial genomes from short-read data sets. Nature Biotechnology, 2011, 29, 915-921.	9.4	203
17	Stalking the Fourth Domain in Metagenomic Data: Searching for, Discovering, and Interpreting Novel, Deep Branches in Marker Gene Phylogenetic Trees. PLoS ONE, 2011, 6, e18011.	1.1	95
18	Community ecology of hot spring cyanobacterial mats: predominant populations and their functional potential. ISME Journal, 2011, 5, 1262-1278.	4.4	206

#	Article	IF	Citations
19	The JCVI standard operating procedure for annotating prokaryotic metagenomic shotgun sequencing data. Standards in Genomic Sciences, 2010, 2, 229-237.	1.5	55
20	Genomic and functional adaptation in surface ocean planktonic prokaryotes. Nature, 2010, 468, 60-66.	13.7	280
21	Metagenomes from High-Temperature Chemotrophic Systems Reveal Geochemical Controls on Microbial Community Structure and Function. PLoS ONE, 2010, 5, e9773.	1.1	186
22	Characterization of<i>Prochlorococcus</i>clades from iron-depleted oceanic regions. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16184-16189.	3.3	183
23	A Catalog of Reference Genomes from the Human Microbiome. Science, 2010, 328, 994-999.	6.0	621
24	Distribution of microbial terpenoid lipid cyclases in the global ocean metagenome. ISME Journal, 2009, 3, 352-363.	4.4	47
25	The Sorcerer II Global Ocean Sampling Expedition: Metagenomic Characterization of Viruses within Aquatic Microbial Samples. PLoS ONE, 2008, 3, e1456.	1.1	276
26	The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. PLoS Biology, 2007, 5, e16.	2.6	736
27	The Sorcerer II Global Ocean Sampling Expedition: Northwest Atlantic through Eastern Tropical Pacific. PLoS Biology, 2007, 5, e77.	2.6	1,757
28	Viral photosynthetic reaction center genes and transcripts in the marine environment. ISME Journal, 2007, 1, 492-501.	4.4	122
29	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. Environmental Microbiology, 2007, 9, 1464-1475.	1.8	156
30	The Dog Genome: Survey Sequencing and Comparative Analysis. Science, 2003, 301, 1898-1903.	6.0	482
31	Improving the Arabidopsis genome annotation using maximal transcript alignment assemblies. Nucleic Acids Research, 2003, 31, 5654-5666.	6.5	1,597
32	A Comparison of Whole-Genome Shotgun-Derived Mouse Chromosome 16 and the Human Genome. Science, 2002, 296, 1661-1671.	6.0	344
33	The Genome Sequence of the Malaria MosquitoAnopheles gambiae. Science, 2002, 298, 129-149.	6.0	1,859
34	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	6.0	12,623